Table S4. Dataset of RNA-Seq analysis of Rod and Gray

Gene_name	Gray-1	Gray-2	Rod-1	Rod-2	Protein_annotation
Apr1	532.224365	583.95105	570.880005	537.101624	proteinase A
Sep7	16.993624	20.593718	33.519352	41.519829	septin
AAF1	391.498444	312.383759	6.539679	9.7916	Aaf1p
AAH1	49.507473	50.830513	11.552348	9.136788	adenine deaminase
AAP1	104.497978	80.305382	93.758904	91.258873	Aap1p
AAT1	198.970215	224.40657	258.647491	236.619537	aspartate transaminase
AAT21	147.461624	170.480148	123.928169	122.457954	aspartate transaminase
AAT22	68.679169	67.957375	42.563549	38.846783	Aat22p
ABC1	287.439301	348.961914	77.413719	74.074921	protein kinase
ABD1	24.634991	28.455547	46.310429	36.318268	mRNA (guanine-N7)-me
ABG1	61.727631	60.331314	55.457275	74.133415	Abg1p
ABP1	87.04512	79.235931	115.773872	111.738052	hypothetical protein MG
ABP140	21.437561	19.613188	19.731058	23.040966	Abp140p
ABP2	1.675741	2.12466	28.514177	21.496555	Abp2p
ABZ1	11.842416	13.371709	27.171417	25.235703	4-amino-4-deoxychorism
ACB1	150.156509	158.633865	273.640625	263.812439	long-chain fatty acid tran
ACC1	39.525803	36.640312	74.913666	72.875137	acetyl-CoA carboxylase
ACE2	30.706118	25.934216	97.065392	140.368515	DNA-binding transcriptio
ACF2	9.720727	7.531666	14.147871	17.303017	Acf2p
ACH1	460.072815	522.331787	943.094116	895.615601	acetyl-CoA hydrolase
ACO1	838.233276	740.877563	702.154602	727.735596	aconitate hydratase
ACO2	15.409312	15.144094	22.956984	26.219519	aconitate hydratase
ACP1	95.358429	92.306534	160.743591	148.514664	Acp1p
ACP12	217.399109	205.681396	376.912415	364.052338	acyl carrier protein
ACS1	923.547119	772.905945	78.837914	74.07341	acetate--CoA ligase 1
ACS2	150.618073	165.451492	550.532104	535.848572	acetate--CoA ligase
ACT1	1031.544556	1009.268494	1229.472778	1226.227051	actin
ADA2	76.675423	75.234901	48.469433	45.418091	chromatin-binding trans
ADAEC	44.512058	52.102486	19.14732	23.796198	Adaecp
ADE1	138.546707	150.391266	230.132019	217.42543	phosphoribosylaminoimi
ADE12	234.208847	245.811661	91.412926	87.396416	adenylosuccinate synthe
ADE13	264.392944	273.508789	169.055222	164.851059	adenylosuccinase
ADE17	236.944305	233.700348	260.078827	266.298187	bifunctional phosphoribo
ADE2	40.546093	35.455124	23.702267	27.964071	phosphoribosylaminoimi
ADE4	89.055214	85.694221	56.937119	68.380341	amidophosphoribosyltra
ADE5,7	78.240898	89.010086	44.365196	48.924679	phosphoribosylamine-gl
ADE6	33.132866	40.48959	37.898197	40.337917	phosphoribosylformylgly
ADE8	113.778297	111.887581	100.552101	118.099342	phosphoribosylglycinami
ADH1	4023.196289	4136.962402	3699.065186	3132.212158	alcohol dehydrogenase I
ADH2	544.530762	631.700012	351.356293	328.949005	alcohol dehydrogenase
ADH3	37.047539	35.528255	56.017597	64.846481	Adh3p
ADH4	1.792188	2.134933	4.939913	1.598072	Adh4p
ADH5	3811.505859	3286.645996	694.763855	477.842651	Adh5p
ADK1	224.310745	200.430893	175.525497	170.374207	adenylate kinase
ADO1	90.095833	117.79895	132.995255	136.118927	adenosine kinase
ADP1	22.841843	26.474003	20.925001	24.394129	putative ATP-dependent
ADR1	23.434052	22.600397	13.262589	14.94908	DNA-binding transcriptio
AFG1	3.401006	1.901453	11.604747	11.36794	Afg1p
AFG3	38.267761	42.924683	80.555832	75.529915	AAA family ATPase
AFL1	110.597206	101.636398	38.730621	40.377502	inositol polyphosphate ki
AFP99	53.047668	36.14019	7.060848	5.87808	Afp99p
AFT2	26.142262	29.475998	24.378548	23.714767	hypothetical protein W5
AGA1	18.931774	15.430824	9.282731	8.825969	Aga1p
AGC1	111.54332	113.860527	23.190905	21.159327	amino acid transporter
AGE1	20.745155	21.040262	23.030416	33.487427	Age1p
AGE2	42.657845	38.855949	85.774307	86.834824	stromal membrane-asso
AGE3	36.282825	33.303871	73.160278	61.557823	ADP-ribosylation factor
AGM1	15.938155	17.923079	38.352211	62.775711	phosphoacetylglucosami
AGO1	15.72821	12.659238	18.421612	15.695413	Ago1p
AGP2	73.418869	78.239449	210.368774	190.270905	Agp2p
AGP3	19.821157	18.300402	7.294939	7.025704	Agp3p
AHA1	56.334534	50.110504	82.95713	94.453087	Aha1p

AHP1	319.417084	377.778961	207.466461	174.512497	thioredoxin peroxidase
AHP2	115.118675	117.489418	140.142487	130.518219	Ahp2p
AHR1	25.031586	27.314814	0.778732	0	Ahr1p
AIP2	44.363052	49.485031	51.374592	46.36401	D-lactate dehydrogenase
AKL1	27.205078	28.11013	28.820618	33.477879	serine/threonine protein
AKR1	48.737926	55.004711	161.056534	156.750458	palmitoyltransferase
ALA1	45.972919	51.345421	79.901917	85.106895	alanine--tRNA ligase
ALD5	1931.221802	1861.968628	1567.907471	1612.503296	aldehyde dehydrogenase
ALD6	130.705795	116.143593	68.580124	74.106468	Ald6p
ALG1	7.876148	12.087177	19.157618	18.075813	chitobiosyldiphosphodoli
ALG11	13.397138	11.014062	12.695373	11.326022	alpha-1,2-mannosyltrans
ALG2	28.315918	28.193462	38.406879	40.432182	GDP-Man:Man(1)GlcNA
ALG5	14.035932	11.085923	18.989546	14.214002	dolichyl-phosphate beta-
ALG6	8.434219	7.146719	12.129725	19.526255	dolichyl-P-Glc:Man(9)Gl
ALG7	9.089252	8.617078	21.509754	25.11504	UDP-N-acetylglucosami
ALG8	10.072319	7.494907	9.922418	14.338671	dolichyl-P-Glc:Glc1Man(
ALG9	21.582548	18.125137	19.484795	30.0891	dolichyl-P-Man:Man(6)G
ALI1	87.003601	94.504501	127.593483	133.324661	Ali1p
ALK2	39.483971	37.003502	10.993759	9.376591	cytochrome P450 52A2
ALK6	1.089091	3.167553	1.465165	1.613124	Alk6p
ALK8	28.171598	31.101566	12.708381	14.218341	Alk8p
ALO1	247.442245	272.238495	250.481689	237.794113	D-arabinono-1,4-lactone
ALP1	39.14827	45.960747	20.751989	23.478367	Alp1p
ALR1	208.491074	198.238632	38.221836	54.796932	Mg(2+) transporter
ALS1	40.955078	39.69453	8.094165	8.537383	Als1p
ALS2	14.731894	14.445206	10.29615	13.068144	Als2p
ALS3	14.386143	13.786924	15.5002	16.969608	Als3p
ALS4	15.203341	17.866549	10.9635	14.079369	Als4p
ALS5	16.152302	14.145532	6.954407	9.724913	Als5p
ALS6	11.209738	10.627385	8.345366	10.663601	RecName: Full=Agglutin
ALS7	168.086823	167.051285	273.520203	280.792786	Als7p
ALS9	6.77632	5.662554	6.468522	8.345686	flocculin
ALT1	34.206596	28.514378	18.232107	22.09688	alanine transaminase
AMN1	11.275475	12.10894	28.991484	41.283661	hypothetical protein ME
AMO1	12.156096	12.402427	6.572461	3.97067	Amo1p
AMO2	18.469452	18.746712	53.185745	48.795387	primary-amine oxidase
AMS1	112.091797	102.849197	45.218506	49.528912	alpha-mannosidase
ANB1	1028.356445	1183.594238	1052.205688	1004.869568	translation elongation fa
ANP1	29.546934	26.135445	31.02179	38.704617	Anp1p
ANT1	13.970103	15.606526	6.566411	9.195624	hypothetical protein ME
AOX1	7.040864	9.799413	9.530026	9.875094	Aox1p
AOX2	1574.637207	1677.005615	1216.11731	998.983398	Aox2p
APA2	25.429306	35.486214	25.79615	33.686226	bifunctional AP-4-A phos
APC1	7.199141	6.844595	18.983118	17.831806	anaphase promoting co
APE2	80.960503	93.571747	159.151443	168.634216	metallo-aminopeptidase
APE3	47.255154	45.036922	99.118996	127.638298	Ape3p
APG7	12.351577	11.699479	19.343912	18.651781	Apg7p
APL2	7.561722	9.36807	20.970047	19.331186	hypothetical protein W5
APL4	14.454271	13.368902	39.471779	35.445301	Apl4p
APL5	7.729826	7.755672	13.345972	14.981165	Apl5p
APM1	34.487984	32.760681	64.346565	70.427177	Apm1p
APM4	13.244056	12.602053	20.042297	19.276163	Apm4p
APN1	46.887745	44.31337	90.315193	59.487011	DNA-(apurinic or apyrim
APN2	4.275712	6.123278	18.010052	19.324377	DNA-(apurinic or apyrim
APS3	29.665207	27.324539	42.879604	34.464741	Aps3p
APT1	67.032761	66.100708	71.056183	57.943638	adenine phosphoribosylt
AQY1	172.513504	239.001801	79.930687	56.996723	Aqy1p
ARA1	20.669706	18.274248	16.19445	15.671097	D-arabinose 1-dehydrog
ARC1	97.814072	107.81115	93.306068	86.478584	Arc1p
ARC15	79.708641	83.238609	117.533104	103.946823	Arc15p
ARC18	13.45699	14.502818	39.289165	36.292381	Arc18p
ARC19	20.409294	37.000725	63.850727	51.244644	Arc19p
ARC35	37.694942	42.004436	70.616234	64.016762	hypothetical protein MG
ARC40	61.531261	81.896828	121.974854	132.988022	Arc40p

ARD	1719.657959	1916.642944	2054.459961	1710.761353	Ardp
ARE2	8.240436	11.174923	9.925474	10.056065	sterol acyltransferase
ARF1	493.907837	468.255859	617.135559	340.460907	Arf1p
ARF2	430.054535	421.615784	527.75946	605.608704	Arf family GTPase
ARF3	53.037025	80.606171	81.113998	96.757355	Arf3p
ARG1	290.887878	306.678772	202.148621	181.190933	argininosuccinate syntha
ARG11	17.604191	21.016062	14.808733	15.972668	Arg11p
ARG2	8.955022	10.067773	9.664436	11.98757	acetyl-CoA:L-glutamate
ARG3	16.505854	18.920601	28.84375	26.578295	ornithine carbamoyltrans
ARG4	62.334759	66.585518	66.569908	84.734962	argininosuccinate lyase
ARG5,6	28.196234	33.852749	21.00988	21.401709	bifunctional acetylglutam
ARG8	32.777756	39.935974	25.144073	18.790121	acetylornithine transami
ARG81	9.082603	10.705448	25.180323	24.112101	Arg81p
ARG83	3.219348	2.836649	5.551992	3.73586	Arg83p
ARH2	15.585965	26.663223	12.216522	12.942617	ferredoxin-NADP+ reduc
ARL1	44.807362	41.334553	79.910149	81.052521	Arf family GTPase
ARL3	35.683846	31.420301	33.760605	48.044151	Arf family GTPase
ARO1	18.492962	20.885351	30.36125	34.354706	Aro1p
ARO10	156.661102	165.068649	288.426392	268.402588	phenylpyruvate decarbo
ARO2	73.633781	70.957726	131.503448	140.06279	bifunctional chorismate
ARO3	57.805576	61.27821	57.898979	57.590092	3-deoxy-7-phosphohept
ARO4	84.693863	69.825684	65.756294	66.953049	3-deoxy-7-phosphohept
ARO7	14.069019	17.697842	32.206203	26.114681	chorismate mutase
ARO8	76.328789	97.840652	182.659088	149.705643	bifunctional 2-aminoadip
ARO80	8.532163	5.436841	13.074183	11.999698	Aro80p
ARO9	10.709655	13.063382	36.794422	38.05238	aromatic-amino-acid:2-o
ARP1	4.163485	4.637852	16.266064	15.46981	actin-related protein 1
ARP2	99.813011	102.060745	174.350296	179.396667	actin-related protein, pu
ARP3	58.086441	65.991257	119.224442	78.620743	actin-related protein 3
ARP4	18.902554	26.108892	37.532719	40.539516	Arp4p
ARP8	27.694351	25.327229	36.54274	40.875412	Arp8p
ARP9	16.578543	25.298147	67.950714	76.489105	Arp9p
ARR3	128.356049	157.678635	47.981384	36.513992	Arr3p
ARV1	2.243164	6.53998	7.090415	7.879267	hypothetical protein MG
ARX1	97.868263	94.309464	36.88369	38.432735	metalloprotease ARX1
ASC1	933.628113	1015.213379	1032.009399	881.652466	guanine nucleotide-bindi
ASE1	6.023274	6.638108	27.934786	34.537136	Ase1p
ASF1	9.879127	10.251206	60.675938	52.563633	histone chaperone ASF1
ASG1	16.179457	15.762299	33.497673	32.724945	Asg1p
ASG7	11.831292	12.087636	4.061264	4.931159	Asg7p
ASH1	116.236206	104.990791	257.345276	349.064514	DNA-binding transcriptio
ASH2	23.126532	24.735319	67.419136	64.659828	Ash2p
ASK1	11.303158	13.401648	38.795952	35.629501	Ask1p
ASM3	17.490366	18.910204	13.03721	11.511131	hypothetical protein MG
ASN1	135.862915	146.221268	216.005966	198.490845	asparagine synthase (gl
ASR1	27.721331	32.624737	4.845396	5.398287	Asr1p
ASR2	57.109898	55.345695	63.799351	56.58942	Asr2p
ASR3	660.843018	648.775024	281.889557	271.541382	Asr3p
ATC1	10.19816	10.035733	9.141759	7.813844	alpha,alpha-trehalase
ATF1	21.558702	14.940515	20.797157	20.77264	Atf1p
ATG1	69.26844	69.199234	96.617699	79.868332	serine/threonine protein
ATG15	33.77496	35.586159	21.667479	20.721849	triglyceride lipase
ATG9	12.945391	13.766954	9.52031	11.253884	autophagy protein
ATM1	6.184138	9.648468	9.578669	12.255761	ATP-binding cassette Fe
ATO1	1301.918091	1067.111816	0.910273	1.899332	Ato1p
ATO10	18.592518	15.926431	11.593912	13.555842	Ato10p
ATO2	36.12212	48.196346	3.125527	2.786993	Ato2p
ATO5	2.145343	0.319706	3.345356	2.157533	Ato5p
ATO6	29.268694	24.095121	7.049398	11.133586	Ato6p
ATO7	727.094849	428.589355	1.068037	2.404016	Ato7p
ATO9	0.87318	0.885029	1.953032	0.150862	Ato9p
ATP1	1103.894775	1079.015503	1068.474487	1096.598389	F1F0 ATP synthase sub
ATP14	549.924866	537.126709	616.746826	698.535095	F1F0 ATP synthase sub
ATP16	1358.79834	1239.016235	1469.144653	1251.235107	F1F0 ATP synthase sub

ATP17	647.768311	606.783081	847.573242	772.041504	F1F0 ATP synthase sub
ATP18	306.553528	320.359741	299.756256	269.067352	ATP synthase J chain, m
ATP19	309.284943	313.811768	420.662231	359.344208	F1F0 ATP synthase sub
ATP2	1296.287598	1223.144287	1211.892578	1235.191895	F1F0 ATP synthase sub
ATP20	230.218735	205.630066	289.603851	264.835327	F1F0 ATP synthase sub
ATP3	556.849548	504.228912	663.362976	685.908997	F1F0 ATP synthase sub
ATP4	665.809692	701.116821	826.847656	750.727295	F1F0 ATP synthase sub
ATP5	643.360962	672.57843	712.947266	613.963379	F1F0 ATP synthase sub
ATP7	336.164886	330.618713	435.66452	467.374176	F1F0 ATP synthase sub
ATS1	40.272747	36.594223	49.875866	45.001717	Ats1p
ATX1	69.408928	79.118797	348.98584	426.238739	copper metallochaperon
AUR1	269.264374	290.324585	111.20742	115.793022	inositol phosphorylceram
AUT7	379.68631	409.816132	235.220627	213.276978	ubiquitin-like protein
AVT1	18.415981	16.799055	4.221303	3.428916	Avt1p
AVT4	9.168591	10.355854	13.127179	15.417097	Avt4p
AVT7	31.439434	38.852043	39.503269	42.160725	conserved hypothetical
AXL1	16.392859	17.234304	21.66489	21.750496	Axl1p
AXL2	66.124641	62.20834	99.954857	96.015579	hypothetical protein ME
AYR1	71.989784	73.888031	75.272514	77.790581	acylglycerone-phosphate
AYR2	60.796825	71.613609	36.664722	38.133759	Ayr2p
BAS1	41.362301	39.375778	32.671299	33.642967	hypothetical protein MG
BAT21	18.101849	24.033991	33.8395	40.755684	branched-chain-amino-a
BAT22	95.538956	95.128014	77.195412	65.308693	Bat22p
BBC1	67.054497	65.352669	62.904438	66.711792	Bbc1p
BCK1	4.568465	5.874892	11.733603	9.586637	mitogen-activated protei
BCR1	204.056152	183.011322	46.302849	51.452644	Bcr1p
BCY1	192.80545	199.725708	355.238007	340.915314	cAMP-dependent protein
BDF1	137.980957	131.909851	250.712982	279.139252	RecName: Full=Bromod
BEM1	79.980202	91.997154	96.34201	98.192589	phosphatidylinositol-3-ph
BEM2	19.102978	16.405958	27.923922	33.820847	Bem2p
BEM3	19.683475	17.774906	15.55659	14.130696	Bem3p
BET2	34.430687	37.941624	47.048645	35.547611	Rab geranylgeranyltrans
BET4	6.802849	9.831006	27.105457	19.019653	Rab geranylgeranyltrans
BFA1	26.790684	26.008717	35.679375	35.980186	Bfa1p
BFR1	119.622482	138.044983	109.847237	119.695274	Bfr1p
BGL2	422.217743	493.924927	546.550537	571.978638	glucan 1,3-beta-glucosid
BGL22	10.361506	11.969957	8.295974	9.633151	Bgl22p
BIG1	10.716952	10.463394	23.29796	16.340324	Big1p
BIO2	14.292643	11.272881	6.461213	7.155755	biotin synthase
BIO32	6.586811	7.576247	5.89946	6.4983	Bio32p
BLM3	19.001799	18.481651	19.342958	23.970993	Blm3p
BLP1	4979.402832	5041.154297	3794.018066	3722.330566	Blp1p
BMH1	962.90033	969.338318	1543.619141	1716.584839	14-3-3 family protein
BMS1	46.372391	41.377968	24.459085	28.737385	GTPase
BMT1	17.859253	21.480934	156.17807	179.684174	Bmt1p
BMT3	65.085571	70.449883	65.79425	57.49403	Bmt3p
BMT4	16.061306	12.172361	172.248886	201.677841	beta-1,2-mannosyltransf
BMT5	84.279594	96.174362	86.118484	98.310257	Bmt5p
BMT6	94.61058	106.4925	66.329643	65.173355	Bmt6p
BMT7	12.882146	9.749351	6.259601	8.395344	Bmt7p
BMT8	6.21729	2.960635	8.724449	6.436531	hypothetical protein ME
BMT9	12.701763	15.123835	7.322945	6.38543	Bmt9p
BNA4	186.416885	205.287613	406.797058	309.53183	kynurenine 3-monooxyg
BNI1	22.174458	19.254549	34.396896	32.003242	formin
BNI4	13.724714	12.167133	12.958618	16.331852	Bni4p
BNR1	4.603117	4.044742	6.855365	8.384505	Bnr1p
BOI2	67.554726	59.0042	54.723625	63.559429	Boi2p
BPH1	5.394302	4.222221	13.9829	11.932165	Bph1p
BRE1	106.455833	101.278152	145.98613	171.256622	E3 ubiquitin-protein ligas
BRF1	29.631157	34.038929	51.378006	60.511116	transcription factor IIIB 7
BRG1	56.871838	91.313095	14.385485	19.156038	Brg1p
BRN1	5.196895	8.398381	25.744102	29.701612	condensin subunit
BRO1	19.383804	13.355801	19.797092	21.53352	Bro1p
BTA1	103.70826	106.544647	19.941965	17.268909	Bta1p

BTS1	10.942402	10.756577	29.461952	20.686596	farnesyltranstransferase
BUB1	9.554914	9.832513	44.436581	38.078354	protein kinase
BUB2	5.922764	4.095907	21.958279	24.561977	Bub2p
BUB3	253.820145	251.769699	286.369049	283.654144	Bub3p
BUD14	57.927601	53.315334	33.012905	38.865265	protein phosphatase reg
BUD16	3.016608	3.825549	3.750877	5.471383	pyridoxal kinase
BUD2	23.059874	23.713198	35.684673	34.023117	hypothetical protein MG1
BUD20	4.408373	5.469805	3.09136	2.378844	Bud20p
BUD21	75.381905	94.279549	49.146103	54.938404	Bud21p
BUD22	39.222565	37.591755	22.686344	19.124176	hypothetical protein MGI
BUD23	48.595474	52.832127	31.852484	30.684069	18S rRNA (guanine1575
BUD31	37.001373	37.042755	37.441704	35.748795	U2 snRNP complex subu
BUD5	32.624176	29.912062	16.859667	16.015879	Ras family guanine nucle
BUD6	14.834196	16.456034	34.76149	26.932177	Bud6p
BUD7	34.025082	34.30431	55.434525	52.24411	hypothetical protein MEQ
BUL1	6.140979	7.79569	3.965253	2.2542	Bul1p
BUL4	2.487855	3.917516	5.230632	6.400499	Bul4p
BUR2	8.763254	8.598329	15.836909	18.904703	protein BUR2
BZZ1	18.30007	21.580812	31.436398	30.630217	Bzz1p
C100020CA	70.829971	55.141121	52.370785	28.319435	hypothetical protein CAA
C100030CA	42.421326	42.531239	41.082607	19.902395	hypothetical protein CAA
C100090WA	15.776589	14.575809	13.171374	17.575823	hypothetical protein CAA
C100100CA	56.565655	49.855099	54.902515	43.504017	CDP-diacylglycerol-glyce
C100160CA	399.663422	414.790894	216.439301	196.752335	nucleolin
C100190CA	167.799606	141.083466	708.985413	604.134644	hypothetical protein CAA
C100200CA	59.71373	72.902145	111.10321	69.326653	hypothetical protein CAA
C100210CA	128.831757	122.443558	162.901978	174.214828	hypothetical protein CAA
C100270WA	104.524246	92.645241	74.119743	67.412766	hypothetical protein CAA
C100310WA	138.732712	151.426117	46.587841	43.864292	hypothetical protein CAA
C100320WA	28.339952	23.284468	53.931702	52.446022	MJ0936 family phosphod
C100330CA	57.105762	42.65049	87.968491	85.839218	CCR4-NOT core subunit
C100370WA	98.25	90.091797	113.289398	112.732391	hypothetical protein CAA
C100380CA	39.227962	39.010338	43.478832	41.993317	hypothetical protein MEQ
C100410CA	75.945343	95.365517	78.916	87.685333	hexadecenal dehydroger
C100420WA	58.511009	58.973827	69.153145	63.57238	hypothetical protein CAA
C100430WA	40.667568	46.017879	65.484779	71.552757	phosphoinositide binding
C100450CA	142.952011	146.967941	182.32518	184.039825	hypothetical protein CAA
C100460WA	376.150085	395.049774	532.174744	442.642822	hypothetical protein CAA
C100470CA	15.469298	20.541956	41.208321	47.06171	N-acetylphosphatidyletha
C100510WA	14.002923	13.342475	15.912892	14.723754	3-methyl-2-oxobutanoate
C100520WA	52.832905	54.46912	48.48859	44.503296	phosphoglycerate mutas
C100530CA	12.957594	12.627263	8.465373	10.599531	hypothetical protein CAA
C100540CA	36.504948	44.987709	24.500612	26.531305	hypothetical protein CAA
C100570CA	11.510025	11.083054	23.260916	19.900539	hypothetical protein CAA
C100580WA	29.176067	26.758736	24.785624	27.245386	hypothetical protein CAA
C100630WA	16.344328	15.438827	29.400782	24.799639	hypothetical protein CAA
C100660CA	50.460831	38.827084	66.754753	67.193481	t-SNARE syntaxin
C100700WA	49.362709	73.854599	114.892136	133.840836	hypothetical protein CAA
C100760WA	69.685074	68.598579	123.983429	105.721069	hypothetical protein CAA
C100790WA	2.652464	3.558016	8.581344	10.244761	hypothetical protein CAA
C100810WA	3.908491	4.922936	10.000624	10.724034	UDP-N-acetylglucosamir
C100820WA	5.168372	6.330859	11.192758	10.454764	hypothetical protein CAA
C100830WA	7.979991	6.904109	7.512219	8.265856	hypothetical protein CAA
C100860WA	24.21118	28.521196	19.192245	23.776028	hypothetical protein CAA
C100880WA	10.320388	10.803828	3.243552	3.348674	hypothetical protein CAA
C100890WA	15.784605	15.83726	24.235691	25.042833	ERMES complex Ca(2+)
C100910WA	13.863703	14.434153	44.04665	39.94677	upstream activation facto
C100920WA	14.751654	13.804949	16.565462	14.396958	hypothetical protein MEV
C100970WA	8.283081	5.206552	25.180103	25.375164	hypothetical protein CAA
C100980WA	67.710716	58.322487	137.963669	117.082741	hypothetical protein CAA
C101000CA	15.083961	14.75372	26.737679	25.54158	origin recognition comple
C101010WA	192.310638	201.974213	264.304779	271.772003	hypothetical protein CAA
C101040WA	43.405766	48.830669	34.792477	26.33564	hypothetical protein CAA
C101050CA	75.577705	82.236656	93.576088	92.653244	trans-2-enoyl-CoA reduc

C101070CA	24.340117	20.296379	64.481628	67.861542	hypothetical protein CAA
C101080WA	6.902265	6.566671	28.013594	26.180733	hypothetical protein CAA
C101090CA	194.935638	180.154358	624.934387	548.987183	hypothetical protein MG
C101130WA	259.760742	285.046021	97.432549	102.696671	ubiquitin-binding SDF ub
C101140CA	52.437595	60.414471	27.104565	30.77931	hypothetical protein MG
C101150CA	27.274584	27.492674	14.053783	14.824287	tRNA methyltransferase
C101160CA	86.343323	69.681755	47.334854	41.744705	exosome non-catalytic c
C101180CA	2.070111	4.721742	1.301155	3.516294	hypothetical protein CAA
C101190CA	12.138596	9.546438	19.407104	20.563015	N,N-dimethylaniline mon
C101210WA	42.461357	58.576481	30.863312	42.176159	hypothetical protein CAA
C101220CA	68.684479	54.148624	46.242657	57.379036	hypothetical protein CAA
C101250WA	30.370207	29.129332	58.652931	56.396576	hypothetical protein CAA
C101290CA	6.145506	8.447212	8.963008	11.589209	hypothetical protein I503
C101300WA	48.162842	44.374954	93.590088	99.962563	hypothetical protein CAA
C101340CA	11.907011	18.105358	32.323322	22.942537	hypothetical protein CAA
C101360CA	106.139046	91.950798	33.094971	32.692856	glycogenin glucosyltrans
C101390CA	25.120539	25.024683	48.018932	56.115078	hypothetical protein CAA
C101400CA	37.780067	35.256588	40.220634	31.691969	sphinganine kinase
C101460WA	12.036312	12.592787	12.008384	15.409685	hypothetical protein CAA
C101470WA	63.332241	63.158291	77.19912	86.362679	hypothetical protein MG
C101490WA	659.286926	742.854431	893.452454	764.86731	hypothetical protein CAA
C101510WA	3.172343	3.742572	2.872992	3.892576	hypothetical protein CAA
C101530CA	92.316795	97.989296	116.363632	112.110207	arginine--tRNA ligase
C101540WA	22.499447	18.452431	44.061607	47.862854	hypothetical protein CAA
C101580WA	85.474686	68.922722	159.122696	187.489548	mitochondrial 54S ribos
C101590CA	33.491386	32.923782	48.977818	47.09927	DNA-directed RNA poly
C101610CA	18.737101	14.43402	34.972248	37.487968	hypothetical protein CAA
C101620CA	187.245102	190.980759	143.816833	124.904427	hypothetical protein CAA
C101630WA	224.159866	223.774933	94.961143	81.237045	hypothetical protein CAA
C101680CA	37.671852	43.105125	102.912064	71.048531	hypothetical protein CAA
C101710WA	88.965828	100.523918	34.663494	40.12764	hypothetical protein CAA
C101750WA	11.696562	13.673205	14.260432	16.850607	hypothetical protein W5
C101800WA	24.128593	25.011925	57.052101	69.34655	hypothetical protein CAA
C101820CA	17.474215	22.456001	27.229397	31.814688	TFIIH complex kinase s
C101840CA	53.46257	51.395561	49.790363	57.118706	hypothetical protein CAA
C101850CA	60.389915	62.819286	83.109497	79.973648	hypothetical protein CAA
C101860WA	78.756096	92.758095	111.423347	114.215477	transcription elongation
C101890CA	142.235565	155.191025	47.810539	59.683723	hypothetical protein CAA
C101900CA	11.606602	7.458169	13.495157	19.696835	hypothetical protein CAA
C101910WA	74.817787	78.593376	72.717194	76.722603	hypothetical protein CAA
C101930WA	134.613113	160.977844	61.68721	65.761185	hypothetical protein CAA
C101940CA	31.147556	26.269186	38.558712	32.960323	signal recognition particl
C101950CA	51.037663	59.677891	82.598808	62.50938	hypothetical protein MG
C101970WA	3.241083	1.931987	0	0	hypothetical protein CAA
C102000WA	30.611408	36.901085	39.311691	40.069942	conserved hypothetical
C102020WA	12.887361	14.205236	20.415766	31.524652	5-formyltetrahydrofolate
C102030CA	37.306599	30.419909	46.719025	38.080547	conserved hypothetical
C102040CA	38.510677	37.009029	44.098621	48.241669	putative ubiquitin-specifi
C102060WA	243.10939	250.571838	616.554871	562.037781	hypothetical protein CAA
C102090CA	9.720727	13.980093	14.712235	16.115913	hypothetical protein CAA
C102100WA	4.381265	4.697015	17.94714	26.390913	hypothetical protein CAA
C102160WA	35.466972	36.86047	43.025333	39.862125	TRAPP subunit
C102200CA	29.874643	33.273369	107.62471	109.189545	autophagy protein 5
C102210WA	83.085007	66.849884	266.621429	367.288696	hypothetical protein CAA
C102220CA	35.040447	34.102547	59.474457	62.29052	YjeF family domain-cont
C102240WA	46.065838	47.557476	46.75835	50.713299	karyopherin beta
C102270CA	171.128326	174.239517	32.63483	27.222746	hypothetical protein CAA
C102290CA	15.712283	18.693834	38.028278	40.875385	ATP synthase complex
C102300WA	12.197167	11.540121	25.507494	31.336256	prefolding complex chap
C102310CA	27.647984	21.376534	40.637867	49.440704	chromatin DNA-binding
C102320CA	41.217838	50.252007	58.381756	55.001152	6-phosphofructo-2-kinas
C102330CA	515.972351	737.297119	768.106995	718.208557	ribosomal 60S subunit p
C102370CA	10.412529	10.387561	44.062809	49.268478	hypothetical protein CAA
C102380CA	7.169116	11.030319	21.740217	15.238472	Arf family GTPase

C102390WA	8.731246	7.432695	10.120266	12.12554	hypothetical protein CAA
C102410CA	32.44352	28.835234	155.832947	178.208542	hypothetical protein CAA
C102430CA	24.251751	23.379219	18.831984	23.1443	hypothetical protein CAA
C102440CA	15.39377	13.466578	17.220873	22.423489	ubiquitin-specific proteas
C102450CA	49.818958	69.917236	33.89835	29.583374	hypothetical protein CAA
C102470WA	20.611912	44.909203	36.959488	56.558994	hypothetical protein CAA
C102490CA	12.703969	14.768129	34.723824	36.517052	hypothetical protein CAA
C102500WA	9.174617	6.93302	20.216831	22.769442	hypothetical protein CAA
C102510WA	14.461173	20.949924	33.574692	32.527378	hypothetical protein CAA
C102650WA	228.129547	213.05603	297.977417	189.783829	hypothetical protein CAA
C102670CA	8.563205	6.89191	1.912494	1.660189	hypothetical protein CAA
C102680CA	15.828548	17.446985	24.824656	23.963531	hypothetical protein CAA
C102690CA	2.119009	1.309603	1.176516	0.794164	hypothetical protein CAA
C102700CA	1321.565063	1286.307373	2337.187744	1802.858032	hypothetical protein CAA
C102720WA	13.498361	12.303938	30.76428	23.110117	hypothetical protein CAA
C102730WA	32.466774	25.971493	22.91407	48.730953	hypothetical protein MG
C102740CA	4.305071	4.038509	14.26431	6.635861	hypothetical protein CAA
C102750CA	54.606838	51.296398	129.077469	135.060562	hypothetical protein CAA
C102760WA	63.397339	65.937057	90.273552	93.329216	guanine nucleotide exch
C102770WA	50.620499	34.367573	64.494545	63.803864	--
C102780WA	77.303894	80.852745	60.195805	37.297924	carboxymethylenebuten
C102800WA	5.16221	5.859858	22.578403	19.757669	hypothetical protein CAA
C102830WA	11.646317	11.57396	19.232672	12.908199	hypothetical protein CAA
C102850WA	36.117916	32.80323	16.991781	16.965342	protein VTS1
C102890CA	23.228439	18.272463	91.986023	85.994072	hypothetical protein CAA
C102900CA	11.779767	11.583437	33.456997	25.070049	mRNA splicing protein
C102910CA	3.768551	5.697409	8.487848	8.886808	protein kinase regulatory
C102940CA	86.649452	90.741859	99.205383	89.539673	hypothetical protein CAA
C102950WA	44.21619	40.519707	53.264679	55.262238	hypothetical protein CAA
C102960CA	33.077049	29.719608	35.177593	38.558475	hypothetical protein CAA
C102970WA	34.441475	43.733303	49.469948	45.425671	hypothetical protein CAA
C103040WA	29.252069	29.308561	35.42841	27.947367	hypothetical protein CAA
C103050WA	14.324746	12.708363	20.45676	21.30261	hypothetical protein CAA
C103100WA	27.118748	29.531149	34.092758	35.923321	hypothetical protein CAA
C103120WA	300.161804	314.338562	340.469055	287.003632	hypothetical protein CAA
C103140WA	13.36523	21.157837	22.292439	27.717407	hypothetical protein MG
C103150CA	31.324167	31.69142	22.281199	13.177608	hypothetical protein ME
C103170CA	4.211356	5.065533	6.055799	5.668984	hypothetical protein CAA
C103180WA	4.067732	2.25146	16.149248	11.658795	lipoyl(octanoyl) transfera
C103240WA	43.808895	59.124321	51.710773	47.443615	hypothetical protein CAA
C103260WA	5.985474	6.179437	11.369908	11.14364	hypothetical protein MEV
C103270WA	91.553703	96.82711	110.508987	119.03331	putative peptide hydrolas
C103280WA	97.572861	99.607689	185.528015	178.819977	mitochondrial 37S riboso
C103310WA	126.67675	115.917709	128.545471	141.326141	hypothetical protein CAA
C103330CA	8.034995	8.804228	12.279012	18.922173	hypothetical protein CAA
C103360WA	27.411913	26.173962	39.823868	36.399059	chromatin-remodeling A
C103370WA	390.103821	413.713501	305.869476	263.241455	polyadenylate-binding pr
C103400WA	11.353484	8.456904	9.598285	7.546686	hypothetical protein MEK
C103410WA	10.33224	7.278608	26.987164	37.692974	hypothetical protein CAA
C103430WA	9.364483	9.151188	11.26153	12.467795	triglyceride lipase
C103440CA	34.63913	35.807896	77.433533	67.002716	hypothetical protein CAA
C103450CA	13.446969	13.108355	25.958431	19.522755	hypothetical protein CAA
C103460CA	6.30902	5.180284	43.79533	48.70322	hypothetical protein CAA
C103470CA	0.15735	0.502193	2.27197	1.729511	putative serine/threonine
C103490WA	29.756746	24.805244	39.15815	38.647858	hypothetical protein CAA
C103510CA	192.129654	197.987625	239.507721	254.372192	hypothetical protein CAA
C103540CA	21.07728	25.431385	44.983845	31.278753	hypothetical protein CAA
C103600WA	64.911163	73.608162	90.543961	118.658966	dolichyl-diphosphooligos
C103620CA	307.85083	320.343567	341.881042	345.495758	ribosomal 40S subunit p
C103630WA	3.886933	3.345655	5.204422	7.19741	hypothetical protein CAA
C103660WA	36.234909	24.684566	27.509533	17.227045	hypothetical protein CAA
C103690WA	72.22744	64.860374	87.030746	105.003525	conserved hypothetical p
C103720CA	41.566235	55.696487	38.270462	42.51564	hypothetical protein CAA
C103750WA	16.561207	26.545488	34.791653	31.060272	hypothetical protein CAA

C103790CA	192.09227	195.142105	69.143616	76.88382	peptidylprolyl isomerase
C103830CA	42.114399	35.265541	34.233849	33.715065	exosome complex comp
C103840WA	8.407035	18.917791	32.361233	25.830198	hypothetical protein CAA
C103870CA	4.767686	5.439829	11.180906	9.683092	hypothetical protein CAA
C103890WA	0.156936	0.14393	0	0.525225	hypothetical protein CAA
C103910CA	7.171183	5.525055	6.824671	7.621335	hypothetical protein CAA
C103920CA	5.720106	6.639078	10.600345	11.811279	palmitoyltransferase
C103930WA	9.177484	13.616021	46.644238	38.772621	hypothetical protein MG
C103940WA	231.956482	231.888519	369.027985	396.124207	succinate dehydrogenas
C103950CA	8.565776	10.223195	14.195625	13.094502	hypothetical protein CAA
C103960CA	4.745157	5.961726	6.449389	4.882001	hypothetical protein CAA
C103990WA	8.645976	11.356939	19.933758	17.108757	hypothetical protein CAA
C104010CA	50.861187	56.736076	3.779288	5.248737	hypothetical protein CAA
C104030WA	10.564415	10.387105	30.183849	34.387882	aspartate--tRNA ligase
C104040CA	48.749352	53.446064	30.798063	29.4916	RNA-binding RNA proce
C104090CA	5.543313	9.330215	11.715279	13.026798	hypothetical protein CAA
C104110WA	65.617424	60.250191	24.339613	19.100025	lysophosphatidic acid ac
C104120CA	17.402924	22.290319	36.686047	28.490673	U2 snRNP complex sub
C104150CA	5.131421	10.188203	11.843165	6.540425	hypothetical protein ME
C104160CA	4.205684	4.518798	14.641936	12.26963	putative ADP-ribose 1&a
C104180WA	2211.29834	2272.807129	8156.817871	7390.179688	hypothetical protein CAA
C104190CA	27.427019	21.207735	24.816408	27.507692	hypothetical protein CAA
C104200CA	57.926888	64.303055	45.202629	53.653763	nucleoporin
C104220CA	199.354294	188.616669	154.851425	113.711151	competence/damage-in
C104230WA	57.265572	53.869293	126.710907	104.73539	26S proteasome regulat
C104270CA	0.083632	0	1.355168	0.3978	hypothetical protein CAA
C104280CA	4.355147	5.216772	7.999832	6.760912	GPI-anchor transamidas
C104340CA	6.526693	9.274796	23.06666	20.796789	hypothetical protein CAA
C104350CA	5.489144	4.270938	2.682751	2.818292	hypothetical protein CAA
C104360CA	953.991882	952.097351	1149.578247	1004.314575	hypothetical protein CAA
C104370CA	107.492149	100.448814	150.142746	164.492905	mitochondrial 37S ribos
C104430CA	41.950672	39.409187	72.785378	57.783741	sepiapterin reductase fa
C104440WA	1.33575	1.095376	0.9335	0.799539	hypothetical protein CAA
C104460CA	55.777138	49.898617	26.629324	28.687788	hypothetical protein CAA
C104470CA	64.95813	45.450249	87.33197	69.079201	hypothetical protein CAA
C104490WA	90.72641	103.430809	202.169357	179.117828	hypothetical protein CAA
C104510WA	9.285749	10.216518	11.407199	7.971867	hypothetical protein CAA
C104530CA	13.846002	16.075361	20.572674	18.813961	tRNA (uracil) methyltrans
C104560WA	10.646907	11.959355	15.237936	21.1439	ubiquitin-protein ligase
C104580CA	20.748959	33.218792	32.110382	28.086788	hypothetical protein CAA
C104590WA	1107.236694	1159.798584	581.163818	650.426025	hypothetical protein CAA
C104600CA	68.629601	75.803123	182.408142	176.124847	hypothetical protein CAA
C104620WA	15.204252	20.086687	34.287823	29.169289	hypothetical protein CAA
C104630CA	12.603235	9.827764	23.257088	25.054394	putative aminophospholi
C104640WA	44.613171	42.833374	65.324753	56.840382	triacylglycerol lipase
C104690CA	0.214062	0.745883	0	0.216201	hypothetical protein CAA
C104700CA	16.896921	12.794138	13.140064	14.530819	hypothetical protein CAA
C104710CA	90.815239	86.591713	33.301037	33.954319	hypothetical protein CAA
C104720WA	245.455109	240.971558	63.950974	55.191105	hypothetical protein CAA
C104780CA	7.352325	6.516324	10.039067	15.598786	hypothetical protein CAA
C104790WA	45.462101	42.824337	76.722839	63.259483	hypothetical protein CA
C104800CA	4.603455	5.427425	1.202339	1.667108	hypothetical protein CAA
C104820CA	23.298292	20.566574	75.061806	74.42804	putative mitochondrial 5
C104840CA	16.20014	23.130379	26.766529	23.614571	hypothetical protein CAA
C104860WA	11.547793	14.320016	22.26473	21.696119	hypothetical protein CAA
C104910CA	64.299637	59.906796	57.968151	57.33667	hypothetical protein CAA
C104930CA	7.989711	8.748005	2.911227	3.30909	hypothetical protein CAA
C104940CA	10.760776	10.109925	12.501648	9.615803	hypothetical protein CAA
C104960CA	7.709096	5.186374	22.054987	26.043444	SCF ubiquitin ligase com
C104970WA	19.876343	20.726978	48.168774	45.148037	translation initiation fact
C104980CA	35.441921	36.654709	51.141346	44.579903	hypothetical protein CAA
C104990CA	13.271379	24.999561	24.992712	26.092916	hypothetical protein CAA
C105010CA	18.002495	23.382713	29.012106	23.047651	conserved hypothetical
C105100WA	6.738816	7.182985	15.712966	16.512951	hypothetical protein CAA

C105120WA	17.843081	18.377863	24.646429	17.589287	amino acid transporter
C105150CA	2.194357	9.609346	0	0.222584	hypothetical protein CAA
C105160CA	1795.246948	1815.680176	625.699036	536.526428	hypothetical protein CAA
C105180CA	84.419899	116.98243	178.643967	214.357819	hypothetical protein CAA
C105190CA	88.637726	78.260612	116.153954	119.285439	hypothetical protein CAA
C105200CA	123.84317	100.576767	111.16584	119.58062	hypothetical protein CAA
C105210CA	60.535812	63.378975	198.955368	181.662567	hypothetical protein CAA
C105220CA	6.153283	10.646707	9.348603	14.750222	hypothetical protein CAA
C105230WA	19.137501	22.428907	21.416559	23.866879	DNA-directed RNA poly
C105250WA	0.33313	0.254407	0	0.342435	uncharacterized protein
C105270CA	57.768791	66.558968	140.860886	115.202866	hypothetical protein CAA
C105280WA	12.253197	13.023021	22.595612	18.913717	conserved hypothetical
C105320CA	10.054813	8.595693	27.3221	24.958862	hypothetical protein ME
C105330CA	11.104528	12.202788	11.096587	11.220357	hypothetical protein MG
C105360CA	29.640984	35.03397	46.17083	30.394867	non-canonical poly(A) p
C105370CA	8.074153	8.847678	11.351997	13.029782	protein kinase
C105380CA	4.417355	5.20118	9.153593	9.930499	DNA-binding protein
C105390CA	12.37319	14.454514	38.473305	35.540836	hypothetical protein CAA
C105400CA	11.390568	12.710977	13.322337	16.027033	hypothetical protein CAA
C105420WA	46.096565	58.661835	101.511078	111.127289	hypothetical protein CAA
C105440CA	42.403469	50.565014	35.011024	32.780827	hypothetical protein CAA
C105450WA	0	0	0.094428	0	hypothetical protein MG
C105480CA	2.553384	1.837451	6.140092	7.887922	hypothetical protein CAA
C105490CA	69.906685	69.302841	89.863106	111.245293	hypothetical protein CAA
C105520WA	34.437866	31.02095	11.457994	17.893984	Transcription is positivel
C105540CA	34.279762	34.823448	33.877037	27.59881	hypothetical protein CAA
C105610WA	15.726848	9.5797	20.457972	16.768673	glutamyl-tRNA(Gln) ami
C105630CA	82.688782	84.700294	57.654682	62.266502	hypothetical protein CAA
C105650WA	26.331182	31.359167	31.025995	23.066906	hypothetical protein MG1
C105660CA	27.381159	26.805077	44.114689	43.82325	hypothetical protein CAA
C105670WA	55.030273	58.045601	70.652794	85.962326	putative aminopeptidase
C105690CA	8.507424	6.282587	4.133196	2.860131	hypothetical protein CAA
C105720WA	1411.460571	1560.427368	1399.657959	1318.798218	ribosomal 60S subunit p
C105740CA	2.215312	4.293881	13.655648	12.318075	hypothetical protein CAA
C105750CA	5.872272	4.899954	7.98314	10.56162	hypothetical protein CAA
C105780WA	28.016159	22.934809	67.536339	71.344948	chromatin structure-rem
C105790WA	66.162872	61.176571	173.57399	142.305573	hypothetical protein CAA
C105800CA	8.447578	10.028336	20.770086	12.483814	hypothetical protein CAA
C105830WA	0	0.580941	1.182396	0.736312	hypothetical protein CAA
C105890WA	36.241917	44.195423	25.72776	36.339993	hypothetical protein CAA
C105900WA	30.644516	27.952578	43.262981	48.397282	hypothetical protein W5
C105920WA	14.237685	15.854674	14.73473	14.507972	hypothetical protein CAA
C105930CA	7.017868	5.630579	7.642815	10.07678	glutamine amidotransfer
C105950CA	33.277645	43.712219	38.139427	39.155411	hypothetical protein MG7
C105970WA	1.516783	0.65852	1.423278	1.647442	hypothetical protein CAA
C105980WA	8.101686	7.708285	6.571853	6.606872	hypothetical protein ME
C105990CA	10.451937	14.634433	17.608099	12.087951	hypothetical protein CAA
C106000WA	14.566798	8.239881	22.341251	25.992428	hypothetical protein CAA
C106030CA	3.650044	4.715811	16.378267	21.574184	hypothetical protein CAA
C106050CA	327.409027	335.552704	400.846741	387.348175	conserved hypothetical
C106070WA	76.607239	88.714691	235.050537	206.349762	putative mitochondrial 3
C106090CA	33.837765	38.712685	27.143236	33.44516	serine/threonine protein
C106120CA	0.28013	0.700893	5.305798	5.960814	hypothetical protein CAA
C106150WA	0	0	1.008956	0	hypothetical protein ME
C106160WA	0.081808	0.143749	0	1.576371	hypothetical protein CAA
C106200WA	8.991478	8.245649	18.527512	14.507171	hypothetical protein CAA
C106220CA	0.145321	0.835711	0.412335	0	hypothetical protein CAA
C106250WA	7.55277	6.741312	12.5687	15.883521	hypothetical protein CAA
C106270WA	4.097754	3.136587	15.425649	16.775787	hypothetical protein CAA
C106320WA	14.069995	14.795255	19.751894	18.014339	hypothetical protein CAA
C106340WA	36.527843	28.978497	50.973511	66.285866	hypothetical protein CAA
C106350WA	157.811356	155.804672	229.872208	229.093613	hypothetical protein CAA
C106360WA	7.560065	9.105213	11.641813	19.027205	protein-serine/threonine
C106380CA	28.809374	40.391224	25.686567	21.611973	hypothetical protein CAA

C106390WA	15.213586	15.868642	28.748598	29.777483	ubiquitin-specific proteas
C106400CA	32.135052	38.787289	48.094006	45.805798	hypothetical protein MG5
C106410WA	4.926661	4.860639	5.345057	5.944434	hypothetical protein CAA
C106420CA	6.429097	7.627777	14.671377	15.633101	hypothetical protein CAA
C106430CA	0.434326	0.16139	0.41587	0.513233	Protein not essential for
C106440CA	7.415754	9.498027	16.233496	15.445449	hypothetical protein CAA
C106470WA	1054.72998	1065.120239	1125.017212	866.931274	hypothetical protein CO
C106480CA	297.145508	328.821167	358.248688	368.685364	hypothetical protein CAA
C106500WA	66.559769	39.48357	59.393646	85.199669	hypothetical protein CAA
C106510CA	16.708055	17.687056	13.721758	15.673124	hypothetical protein CAA
C106530CA	16.090071	13.607089	11.32809	13.841227	putative ubiquitin-specifi
C106540CA	42.432709	39.257069	22.031502	23.425655	exosome non-catalytic c
C106560WA	8.831793	9.881525	14.646331	12.983936	hypothetical protein CAA
C106590CA	31.885302	39.575378	64.661758	67.414955	hypothetical protein CAA
C106600WA	134.139145	120.998718	94.72715	106.648094	hypothetical protein ME
C106620CA	4.937005	8.875505	1.066058	0	hypothetical protein CAA
C106630WA	9.285434	10.24543	13.488479	12.103742	chromatin-binding protei
C106640CA	285.762512	317.718323	242.336212	139.50766	hypothetical protein CAA
C106650WA	74.296898	101.26989	63.595501	59.124958	peptide alpha-N-acetyltra
C106660WA	34.920494	41.0345	20.364515	20.010849	hypothetical protein CAA
C106670WA	5.91749	5.836	7.536908	7.440364	hypothetical protein CAA
C106700WA	12.567152	10.308623	23.965099	27.979132	hypothetical protein CAA
C106710WA	33.820084	34.025349	48.427734	48.027023	serine/threonine-protein
C106720CA	12.302	8.432254	21.124647	24.363386	hypothetical protein CAA
C106750WA	21.915342	18.505081	16.303066	13.289023	hypothetical protein CAA
C106770WA	28.407902	21.883135	20.516315	19.861938	putative oxidoreductase
C106800WA	26.568827	25.705885	22.351912	22.406202	decapping nuclease
C106820WA	74.798294	78.752571	83.792709	90.09462	hypothetical protein CAA
C106840CA	124.309448	123.099365	238.192001	226.792053	hypothetical protein CAA
C106860WA	4.007332	4.721592	1.009193	1.669224	hypothetical protein MEY
C106870CA	10.303043	6.683692	1.544	1.88935	hypothetical protein CAA
C106890CA	1153.519165	1166.482056	1148.662354	830.9245	ribosomal 60S subunit pr
C106910CA	12.599651	10.899049	15.135304	16.671768	hypothetical protein MG
C106920CA	6.576875	8.168037	9.339947	12.861409	hypothetical protein CAA
C106970CA	42.254578	50.276806	79.748833	63.840981	hypothetical protein CAA
C106980CA	89.894417	84.120018	40.039886	46.988178	hypothetical protein CAA
C107010WA	31.789131	28.175705	49.341217	66.445381	hypothetical protein W5
C107040CA	22.268633	17.341377	144.364655	127.737671	hypothetical protein CAA
C107050CA	6.235632	4.053089	9.963955	8.94942	ATP-dependent 5'
C107060CA	71.788887	99.731499	79.765289	71.63662	hypothetical protein CAA
C107080WA	52.590469	58.57962	222.356003	210.325165	hypothetical protein L15
C107090CA	18.747328	17.559443	19.549782	21.058569	hypothetical protein L15
C107100CA	8.988271	8.026814	16.276533	16.459236	hypothetical protein CAA
C107130CA	99.901039	91.874886	20.329712	24.124544	hypothetical protein CAA
C107150WA	173.909317	118.002907	128.13768	159.289429	hypothetical protein CAA
C107160CA	3791.975586	3188.879639	7492.739258	7505.754883	hypothetical protein CAA
C107210CA	27.717512	28.809406	23.506899	28.341534	hypothetical protein CAA
C107220WA	1121.464355	1059.101318	1518.113892	1620.627441	hypothetical protein CAA
C107260CA	12.108756	13.319903	24.930355	28.307808	hypothetical protein CAA
C107280CA	31.270592	19.582375	37.96804	34.921612	TFIIH complex subunit
C107340WA	16.518908	14.800745	32.718761	33.752445	chromatin-remodeling A
C107360WA	14.841988	15.011711	19.970612	21.583767	hypothetical protein CAA
C107390WA	24.048737	34.87088	58.301865	60.389156	hypothetical protein CAA
C107400CA	18.432602	16.175291	6.181335	9.480154	Protein not essential for
C107440WA	14.483594	13.063515	14.010453	16.230667	hypothetical protein CAA
C107470CA	1.3682	1.176433	5.580616	5.475784	double-stranded DNA-de
C107480CA	0.272948	0.447317	1.213012	0.373942	hypothetical protein CAA
C107490CA	4.509473	4.445633	21.379648	26.097742	DNA-directed DNA poly
C107510WA	12.910197	14.580186	20.868412	30.782486	hypothetical protein CAA
C107530WA	387.687805	302.393188	224.79303	190.147446	predicted protein
C107560WA	10.580188	10.180261	18.201921	27.426983	hypothetical protein CAA
C107570CA	5.466372	8.272777	13.472631	8.72388	hypothetical protein CAA
C107590CA	4.897717	4.336904	6.515037	8.808094	hypothetical protein CAA
C107610CA	1.284155	1.848	4.622387	4.074188	hypothetical protein ME

C107630WA	67.466934	85.605087	87.467911	98.377113	hypothetical protein CAW
C107640CA	4.059058	3.869383	2.975214	3.662697	hypothetical protein CAA
C107650WA	4.590212	4.462693	0.440263	3.289566	hypothetical protein CAA
C107660WA	4.334296	4.378699	2.832189	4.361196	hypothetical protein CAA
C107690CA	15.124649	19.510841	12.056643	14.195678	importin-alpha export rec
C107780WA	11.411332	11.497261	19.162457	25.636953	hypothetical protein MG5
C107790CA	36.184757	34.635685	14.191905	8.59679	protein CMS1
C107810CA	7.29376	6.49475	12.700254	12.420077	hypothetical protein CAA
C107820WA	8.955496	7.026672	8.734087	13.753795	hypothetical protein CAA
C107830CA	15.235462	18.728033	17.336514	24.807793	hypothetical protein CAA
C107840WA	109.653038	109.680244	79.25032	78.241394	nicotinate-nucleotide dip
C107850CA	3.337057	2.388895	11.919271	11.606227	anaphase promoting cor
C107860WA	1.637893	1.331564	7.806933	7.028539	hypothetical protein CAA
C107920WA	211.209824	257.370911	396.702209	492.429108	hypothetical protein CAA
C107950CA	25.466717	19.854195	21.811987	21.797579	hypothetical protein CAA
C107960WA	21.505142	17.431667	14.77929	16.37504	hypothetical protein CAA
C107980CA	666.223206	655.209534	381.074738	415.307861	hypothetical protein MG3
C107990CA	172.090408	142.907089	18.863632	21.605539	hypothetical protein CAA
C108040WA	64.55706	60.108185	32.175842	32.334236	hypothetical protein CAA
C108050WA	224.726913	257.437134	337.360474	296.868713	hypothetical protein CAA
C108080CA	236.373886	233.296082	320.543915	265.559753	hypothetical protein CAA
C108110WA	32.366898	30.563576	41.321392	45.166542	hypothetical protein CAA
C108140WA	12.481462	13.489478	35.617657	45.220104	hypothetical protein CAA
C108150CA	8.981592	8.964242	20.098045	43.809425	hypothetical protein CAA
C108160WA	42.471153	49.752735	101.426338	111.521454	hypothetical protein CAA
C108180CA	27.745474	32.142757	36.627277	35.103333	oxysterol-binding protein
C108240CA	7.678629	4.197373	5.544789	2.95829	hypothetical protein CAA
C108340CA	277.944641	259.812622	107.765938	96.082153	hypothetical protein CAA
C108350CA	10651.35742	10717.25391	11512.45801	10535.27148	hypothetical protein CAA
C108390CA	16.363844	17.00452	26.471859	23.98447	WD repeat-containing pr
C108440CA	20.528612	17.296989	70.703545	47.946011	hypothetical protein CAA
C108470WA	46.578979	61.184082	78.599472	90.845451	hypothetical protein CAA
C108490WA	19.829859	25.879503	43.878799	46.330658	kynureninase
C108520CA	56.512592	41.390881	94.529663	104.28923	mitochondrial 54S riboso
C108530WA	18.791809	13.973495	9.949566	12.17949	hypothetical protein CAA
C108540CA	103.240944	112.490288	106.438881	111.392296	serine/threonine-protein
C108610CA	6212.413574	6960.835449	3092.848389	2748.720215	hypothetical protein CAA
C108630WA	39.048717	49.182907	59.920486	56.668873	hypothetical protein MEU
C108660CA	11.418869	8.846108	27.385708	23.619877	hypothetical protein CAA
C108680CA	39.473629	41.971424	66.819656	73.126686	frequenin
C108690WA	63.090462	64.917282	138.85199	127.020103	succinate dehydrogenas
C108700WA	23.227741	25.670639	29.140497	27.080572	hypothetical protein CAA
C108710WA	21.071409	15.804867	36.218174	33.504276	hypothetical protein CAA
C108730WA	12.28359	11.458007	26.094358	38.456818	Golgi transport complex
C108760WA	10.436071	6.346868	17.488205	15.371461	hypothetical protein CAA
C108770WA	23.576471	23.093788	16.007692	11.681237	hypothetical protein CAA
C108780WA	45.616142	38.16132	36.067043	35.452885	alkaline phosphatase
C108800WA	11.217757	11.341683	8.897479	10.208868	hypothetical protein CAA
C108820CA	13.974672	13.161154	16.117752	21.771936	aminoacyl-tRNA hydrola
C108830CA	3.91431	2.990204	2.370663	3.961707	hypothetical protein CAA
C108840WA	3.154825	3.745521	3.646464	6.538719	hypothetical protein CAA
C108860CA	5.672266	5.538718	6.955677	9.184662	phosphatidylinositol-3-ph
C108890CA	6.982046	6.931433	26.738188	34.181297	U2 snRNP complex subu
C108900WA	28.00255	28.975407	5.394397	4.117711	Hap43p-induced protein
C108910CA	7.134342	3.778476	9.919375	12.479545	hypothetical protein CAA
C108920WA	50.571167	51.362862	94.177704	86.955788	37S ribosomal protein S
C108930CA	118.21891	123.920372	184.525482	192.718338	hypothetical protein CAA
C109000WA	8.42067	12.380328	15.926914	10.781174	hypothetical protein CAA
C109020WA	168.835251	157.140594	178.365311	194.057846	hypothetical protein CAA
C109060CA	6.426964	8.049543	16.15234	16.471336	Protein not essential for
C109070WA	12.322695	10.853046	18.233631	19.512335	poly(A)-specific ribonucle
C109110WA	5.048672	3.296339	14.341779	14.17124	hypothetical protein CAA
C109130WA	93.723343	105.361328	28.505775	32.847061	hypothetical protein CAA
C109210CA	58.09758	64.951164	11.257521	9.232678	basic amino acid transpo

C109220WA	56.379673	47.336212	5.260974	3.618642	hypothetical protein CAA
C109240CA	5.552486	4.591495	1.085474	1.191554	hypothetical protein CAA
C109280WA	7.614114	8.531562	16.622425	17.038589	hypothetical protein CAA
C109300CA	1.03216	0.200237	1.07745	1.090635	hypothetical protein CAA
C109310CA	12.734909	12.569304	24.73497	29.103863	hypothetical protein CAA
C109320CA	763.042969	764.115784	65.248428	81.751343	hypothetical protein CAA
C109330WA	104.866936	99.53553	25.295748	18.590797	hypothetical protein CAA
C109340CA	11.746288	13.951546	9.587461	8.823915	hypothetical protein CAA
C109350WA	106.845337	102.990776	226.682571	212.260712	cap-associated protein C
C109360CA	31.703846	29.793818	37.881599	33.803158	hypothetical protein CAA
C109390WA	5.417464	6.442263	12.323645	9.67257	tRNA dimethylallyltransfe
C109430WA	14.46696	16.54649	4.825616	4.646179	hypothetical protein CAA
C109440WA	22.412182	19.80452	21.649515	27.077681	inorganic diphosphatase
C109470CA	25.000603	19.206036	31.140627	30.393875	hypothetical protein CAA
C109500WA	0.052525	2.761542	0	0	hypothetical protein CAA
C109520CA	127.704742	114.880646	132.911194	115.001671	hypothetical protein CAA
C109540WA	78.481255	69.657845	22.949579	22.479809	hypothetical protein I503
C109550WA	38.208424	18.77869	4.599514	6.717041	hypothetical protein CAA
C109570WA	16.415348	24.573528	43.241562	34.890713	hypothetical protein CAA
C109610WA	18.504019	16.136805	23.757881	25.194029	hypothetical protein CAA
C109620CA	47.049313	37.603172	44.454231	68.075371	hypothetical protein CAA
C109650WA	339.957886	334.254822	214.359879	196.29361	hypothetical protein CAA
C109670CA	58.572556	53.479553	123.751839	108.968254	hypothetical protein CAA
C109700WA	1.202774	1.285105	2.252921	0	hypothetical protein CAA
C109710CA	53.369148	61.34444	25.938938	22.997538	hypothetical protein CAA
C109740CA	10.664155	10.353803	11.444653	14.793032	hypothetical protein CAA
C109750WA	30.386223	26.083437	23.575634	18.024704	GET complex subunit
C109770WA	35.955025	42.083473	57.322247	39.100143	hypothetical protein CAA
C109780CA	40.658752	45.622017	12.766535	13.704276	putative ferric-chelate re
C109790CA	36.392063	38.625347	25.710026	23.399977	TRAMP complex RNA-b
C109810WA	18.14151	21.93527	17.95083	23.272087	hypothetical protein CAA
C109840CA	169.330505	158.251404	80.064102	80.591682	protein Cut8
C109850CA	83.108482	100.355255	97.539688	87.551407	hypothetical protein MG
C109910CA	62.011505	50.650799	141.594757	145.230713	hypothetical protein CAA
C109930WA	3.18274	8.099201	4.558993	4.343603	hypothetical protein CAA
C109940WA	62.815315	37.49276	67.609749	40.365238	hypothetical protein CAA
C109950CA	54.847355	65.653618	89.521431	92.664467	hypothetical protein CAA
C109980CA	48.530579	55.438766	67.328842	64.484947	acylglycerol lipase
C110050WA	7.802232	9.142022	0.419842	0.78983	hypothetical protein CAA
C110060CA	44.471981	39.592354	9.519198	9.194538	hypothetical protein CAA
C110080WA	15.512026	22.107002	52.952881	57.476467	U2-type spliceosomal co
C110090CA	15.546429	17.234268	44.486504	50.018986	hypothetical protein CAA
C110110WA	1.959752	1.17287	1.37112	1.961884	hypothetical protein CAA
C110120CA	79.485374	74.919754	138.187363	110.734093	transcription factor TFIIE
C110140CA	102.701797	106.24192	76.885948	80.057961	hypothetical protein CAA
C110170WA	4.103505	7.889502	9.856943	8.513721	hypothetical protein CAA
C110190WA	162.374054	156.900055	119.115074	112.911575	hypothetical protein MG1
C110200CA	56.089355	72.20652	19.470791	23.919233	hypothetical protein CAA
C110230CA	13.371872	14.768911	20.532417	24.455772	hypothetical protein ME
C110240CA	22.359005	21.293341	29.831615	16.355333	bifunctional 4-hydroxy-4-
C110250CA	19.81567	16.690104	25.677685	23.259468	hypothetical protein CAA
C110280CA	78.447563	81.310562	186.910202	151.471634	hypothetical protein CAA
C110310WA	19.035896	16.728907	17.012691	16.104517	hypothetical protein CAA
C110320WA	7.283399	8.804915	9.303582	18.001284	N-acetylglucosaminylpho
C110330CA	9.154071	9.88577	21.485279	29.682505	hypothetical protein CAA
C110340WA	6.611194	5.303413	14.189681	10.919037	hypothetical protein CAA
C110350CA	51.166298	50.710094	9.965672	10.299106	conserved hypothetical p
C110360CA	163.694046	151.31839	182.98703	149.781509	hypothetical protein CAA
C110410WA	20.316021	14.244316	28.99457	40.820843	hypothetical protein CAA
C110420CA	7.52835	8.255718	8.137653	11.064586	hypothetical protein CAA
C110440WA	36.726543	39.240025	18.702023	17.400545	hypothetical protein ME
C110460WA	41.644737	39.233543	33.013103	44.117043	hypothetical protein CAA
C110470WA	87.755737	110.546036	164.346909	156.123505	mitochondrial 37S ribos
C110500WA	31.483492	36.277832	201.500931	155.440857	hypothetical protein CAA

C110510WA	12.391576	16.048021	20.14715	20.716274	hypothetical protein CAA
C110520WA	4.566856	3.346681	7.538375	9.362339	hypothetical protein MEU
C110540CA	11.558484	8.47974	17.187016	20.693289	hypothetical protein CAA
C110560CA	7.841441	7.719667	11.86205	11.008517	hypothetical protein CAA
C110570CA	8.765816	9.755434	3.277162	3.816096	hypothetical protein CAA
C110580CA	1206.179932	1194.454346	49.838024	47.602055	hypothetical protein CAA
C110620WA	200.798279	225.44783	138.78038	136.6987	centromere/microtubule-
C110630CA	2.828674	1.987201	2.767768	2.839602	hypothetical protein CAA
C110680CA	43.2892	43.08923	22.843597	24.468409	tricalbin
C110690WA	17.08625	14.104702	29.986269	34.788364	hypothetical protein CAA
C110710CA	6.183845	4.49852	8.188905	5.523053	hypothetical protein CAA
C110730WA	25.420183	24.906244	29.729179	28.48135	hypothetical protein CAA
C110750CA	68.222603	51.456966	86.156693	82.285957	H(+)-transporting V0 sec
C110810WA	0.542066	1.357709	1.192934	1.567147	hypothetical protein CAA
C110820CA	12.243001	15.819839	27.68289	26.872961	aspartyl aminopeptidase
C110840CA	585.013245	555.341431	350.268951	282.169586	hypothetical protein CAA
C110850WA	0	0.415317	0	1.134728	hypothetical protein MG
C110880WA	84.081947	84.546555	43.204758	48.385323	snoRNA-binding rRNA-p
C110890CA	109.025177	105.616241	138.764526	139.825684	hypothetical protein CAA
C110910CA	14.171387	14.478374	29.177008	28.122931	hypothetical protein CAA
C110920WA	8.510999	7.208598	22.86281	19.648096	transcription factor TFIII
C110950CA	38.053547	30.903627	23.411737	27.486853	protein kinase
C110960WA	16.166683	24.909903	33.725632	49.100391	hypothetical protein CAA
C110970WA	33.545757	31.935146	17.384384	17.473557	hypothetical protein MG3
C110980WA	0.720786	1.406096	0	0.583272	conserved hypothetical p
C111000CA	126.483139	104.291924	63.627163	74.348488	hypothetical protein CAA
C111010CA	20.398033	24.417683	23.960596	24.581745	hypothetical protein CAA
C111020WA	8.162104	8.845776	8.139514	8.873818	hypothetical protein CAA
C111050WA	1.646119	1.087641	4.808492	1.873194	hypothetical protein CAA
C111080WA	618.846741	734.40625	107.928314	141.699402	6-phosphofructo-2-kinas
C111090CA	17.631243	21.47703	26.808302	36.047016	polyadenylation factor su
C111100WA	43.493816	47.047546	52.209549	53.3806	acireductone dioxygenas
C111110CA	31.600985	34.418003	26.721687	47.140205	tubulin-binding prefolding
C111120CA	68.459709	91.163414	136.509537	135.223053	hypothetical protein CAA
C111140WA	15.606711	16.959438	25.549551	17.273016	mannosylinositol phosph
C111150WA	25.219011	27.250431	33.567764	36.377037	hypothetical protein CAA
C111160CA	100.075325	72.881981	70.896339	71.322121	ubiquitin-related modifier
C111200WA	24.759407	22.75695	10.36452	11.693905	hypothetical protein CAA
C111250WA	44.760956	54.847725	89.168762	81.45433	microtubule-binding prot
C111260CA	57.158852	48.846298	72.524811	64.109581	--
C111270WA	3139.843262	3066.56958	1656.229126	1440.697754	hypothetical protein CAA
C111280WA	20.758919	21.664288	23.602854	25.888809	hypothetical protein CAA
C111290WA	12.820902	10.727268	18.017799	13.736307	hypothetical protein CAA
C111300CA	11.878601	10.624625	27.114334	19.943762	mRNA splicing protein
C111320CA	6177.966797	6614.442383	1277.455566	1100.69812	hypothetical protein CAA
C111370CA	8.550344	7.508755	8.941051	11.465817	hypothetical protein CAA
C111390WA	0	0	1.87029	1.960089	hypothetical protein CAA
C111410CA	37.476086	29.617207	5.818611	14.964477	hypothetical protein ME
C111430WA	12.088784	10.401237	14.979241	14.867305	hypothetical protein L15
C111510CA	20.536144	29.518438	16.809299	14.605649	hypothetical protein CAA
C111530CA	0.421282	0.471985	0	0	sulfonate dioxygenase
C111560CA	9.754552	10.37223	23.021505	25.202934	hypothetical protein CAA
C111570WA	3.693634	8.80905	10.205651	9.172384	hypothetical protein CAA
C111580WA	66.802284	46.489399	116.237923	88.486267	hypothetical protein CAA
C111600WA	47.566456	45.742855	70.365822	77.58062	hypothetical protein CAA
C111610CA	14.48613	17.428444	13.747864	14.270753	hypothetical protein CAA
C111620WA	9.704932	10.698214	23.018383	16.15444	hypothetical protein CAA
C111670WA	1523.561523	1502.127686	408.850464	315.149506	hypothetical protein CAA
C111680CA	187.581589	151.617981	44.698044	46.998314	hypothetical protein CAA
C111690WA	36.055134	35.321575	33.748108	29.922874	hypothetical protein CAA
C111710CA	1.349721	0.789832	3.548444	2.997506	hypothetical protein CAA
C111720WA	6.862064	4.390398	24.211618	35.279331	hypothetical protein CAA
C111730WA	24.218079	17.950817	24.528093	39.109394	hypothetical protein MG5
C111740WA	5.275677	4.471518	18.652538	14.087067	hypothetical protein CAA

C111760CA	59.64238	52.643997	102.783989	108.359619	hypothetical protein CAA
C111770CA	53.56588	55.96014	16.261135	17.905058	hypothetical protein L15
C111790WA	10.686053	15.209373	29.737789	28.55481	bifunctional thymidylate/
C111800CA	9.225127	9.813406	21.916538	20.565165	hypothetical protein CAA
C111850WA	218.787369	202.114334	655.102295	706.733948	hypothetical protein CAA
C111860WA	30.043272	32.000252	41.898418	48.122761	hypothetical protein CAA
C111880WA	135.740219	135.246307	189.336563	127.43412	mitochondrial 54S ribos
C111890WA	36.967453	37.240482	39.78577	47.814751	hypothetical protein CAA
C111900CA	11.845136	15.925159	18.882084	17.079895	hypothetical protein W5
C111910WA	7.389795	4.258543	8.503798	10.590574	hypothetical protein CAA
C111920WA	24.657684	22.3846	37.998562	40.775925	hypothetical protein CAA
C111930WA	32.614395	24.56563	88.459732	104.48317	CCR4-NOT transcription
C111940CA	3.909316	3.811149	6.509734	6.600389	hypothetical protein CAA
C111950WA	9.839901	8.848515	15.060573	10.039176	hypothetical protein CAA
C111960CA	65.998795	75.539864	154.045731	129.264236	hypothetical protein CAA
C111970CA	7.716877	5.932052	12.29257	13.401356	hypothetical protein CAA
C111990WA	322.646576	222.866425	3551.224609	4049.317871	hypothetical protein CAA
C112000CA	1.530975	1.782912	2.711497	3.085835	hypothetical protein CAA
C112060CA	9.10775	8.201944	17.941221	20.525747	hypothetical protein CAA
C112070CA	7.725711	8.331467	15.284806	13.527646	hypothetical protein CAA
C112090CA	0.451184	1.064917	3.46084	3.14122	Hap43p-repressed prote
C112110CA	6.546677	7.697664	27.585796	28.382792	hypothetical protein CAA
C112120WA	4.549736	2.320975	9.013876	11.046997	hypothetical protein CAA
C112140WA	76.676765	91.818291	86.77433	78.220909	hypothetical protein CAA
C112150CA	19.729208	17.840759	34.203491	20.300236	hypothetical protein CAA
C112170CA	13.610942	14.950257	25.520363	29.453726	hypothetical protein MG
C112180CA	9.432268	12.326128	25.162638	26.776134	hypothetical protein CAA
C112240CA	6.222352	12.179051	17.444237	16.177616	putative alanine--tRNA li
C112250CA	67.855431	53.946972	95.031235	91.03894	hypothetical protein CAA
C112280CA	14.063044	22.730032	38.47646	36.442959	mitochondrial 54S ribos
C112330WA	0.116268	0	0	0	hypothetical protein CAA
C112350WA	24.321201	24.429321	24.950027	24.272375	exosome catalytic subun
C112370WA	84.612984	80.72905	62.738289	88.987595	hypothetical protein CAA
C112400CA	36.548168	31.916407	27.804731	33.389385	hypothetical protein CAA
C112430WA	10.257226	8.120822	13.628962	20.606308	hypothetical protein CAA
C112440WA	11.655788	11.363841	11.758739	10.820039	RNA exonuclease 4
C112470WA	11.188148	13.041826	3.55664	1.099568	hypothetical protein CAA
C112480WA	5.985527	9.933175	7.512394	13.202307	hypothetical protein CAA
C112530CA	10.236672	13.972973	10.177191	10.065943	hypothetical protein MG3
C112540WA	3.929656	7.439379	11.735497	19.373213	hypothetical protein CAA
C112570CA	146.52153	156.134369	83.868156	81.298103	Elongator subunit
C112580WA	123.559418	126.517967	85.757843	92.351295	hypothetical protein MG9
C112610WA	116.344254	133.95285	141.644745	122.967239	mitochondrial 54S ribos
C112630CA	20.514284	15.882692	30.316555	31.740084	U2-type spliceosomal co
C112640WA	6.033263	10.80602	26.393776	38.768188	hypothetical protein CAA
C112650CA	36.323616	45.466404	58.895077	64.429138	ubiquitin-conjugating en
C112660WA	5.887166	5.571349	15.172013	13.715411	mitotic spindle assembly
C112670CA	2.388176	2.779612	5.939533	5.012399	U4/U6-U5 snRNP compl
C112680WA	107.159195	118.18029	52.883308	54.664894	ribosome assembly prot
C112690CA	3.470006	5.4171	10.769997	15.138991	hypothetical protein CAA
C112700WA	8.498916	7.006536	5.339034	6.473145	hypothetical protein CAA
C112710CA	20.879915	20.616249	15.603935	17.939573	hypothetical protein MG
C112720CA	4.400064	6.155705	2.724963	4.886187	hypothetical protein CAA
C112740WA	5.746997	6.189707	6.693198	6.546484	hypothetical protein CAA
C112750CA	22.377661	23.746073	18.40629	16.990372	hypothetical protein CAA
C112760WA	30.555998	33.441685	42.000088	35.303352	protein-transporting prot
C112800WA	2.12346	0.845129	5.812793	3.877423	microfibrillar-associated
C112810WA	23.744062	24.668194	42.354385	31.176868	2,5-diamino-6-(ribosylam
C112820CA	105.262703	116.966713	96.131943	73.198105	DNA-directed RNA poly
C112830CA	22.747589	19.892668	12.294878	11.667166	hypothetical protein CAA
C112840WA	58.969894	52.692173	81.50296	63.440449	hypothetical protein ME
C112860CA	10.790434	13.566923	17.433807	22.620955	hypothetical protein CAA
C112870CA	8.400681	3.870608	5.415581	5.522755	hypothetical protein CAA
C112880CA	16.408657	20.214054	70.839088	63.93074	hypothetical protein CAA

C112900WA	7.607445	12.096666	12.109729	11.334196	hypothetical protein CAA
C112910WA	186.297119	211.402695	309.892914	249.394592	hypothetical protein CAA
C112920CA	38.647999	45.065441	63.080967	60.061165	hypothetical protein MG7
C112930CA	3.756667	5.242734	2.568698	2.543022	hypothetical protein CAA
C112940CA	2.130572	0.882453	1.140594	0	hypothetical protein CAA
C112950WA	4.130122	4.169195	5.157529	6.131093	hypothetical protein CAA
C113010WA	8.958224	11.864151	17.328964	19.69795	hypothetical protein CAA
C113030CA	23.284882	26.867878	37.582119	36.743977	cysteine--tRNA ligase
C113060CA	48.810757	49.34919	142.210983	148.125854	elongation factor G, mito
C113100WA	8.746305	13.614658	0.972148	1.374459	hypothetical protein CAA
C113130CA	19.285999	18.53459	24.712509	24.879168	hypothetical protein CAA
C113180WA	2.198034	0.285824	3.217115	3.15653	hypothetical protein CAA
C113190WA	967.64563	961.613159	3010.024902	2348.213135	hypothetical protein CAA
C113240WA	37.246132	41.593872	102.014473	129.235947	hypothetical protein CAA
C113250WA	445.990509	556.169373	293.576874	294.75885	hypothetical protein CAA
C113260WA	117.546173	135.97963	234.205322	196.898788	FK506-binding protein 2
C113270WA	28.360659	43.958008	78.281937	72.943092	nicotinamide-nucleotide
C113280CA	93.292068	90.990089	185.340027	149.805008	H(+)-transporting V0 sec
C113290WA	1.980178	1.740229	1.389531	0.862964	hypothetical protein I503
C113320CA	157.1465	166.794693	269.519287	298.215332	hypothetical protein MGK
C113330CA	291.559265	293.605286	227.621872	225.080765	spermine synthase
C113370WA	16.198469	17.971432	14.433934	16.591776	hypothetical protein CAA
C113380WA	27.398174	26.985783	19.594006	21.721695	hypothetical protein CAA
C113390WA	4.287166	3.555695	5.602073	6.515705	hypothetical protein MG3
C113430CA	28.467314	39.537529	27.502045	21.013559	hypothetical protein MG3
C113490CA	6.610291	8.273948	7.81509	10.362779	hypothetical protein CAA
C113560WA	13.36157	11.528585	15.774376	16.564198	ssDNA endodeoxyribonu
C113590WA	1.430789	3.114023	5.851462	3.801723	hypothetical protein CAA
C113600WA	2.834098	2.766224	5.893229	4.324722	hypothetical protein CAA
C113650CA	13.146804	13.604926	15.148534	9.859375	hypothetical protein CAA
C113690CA	632.770264	623.585876	1059.606812	1003.208862	vesicle membrane recep
C113720WA	9.400381	10.935978	9.543801	12.574251	hypothetical protein MEQ
C113750CA	6.409222	3.986369	10.881199	11.549387	hypothetical protein CAA
C113770CA	2.987666	4.2365	10.756474	11.870624	hypothetical protein CAA
C113790CA	38.499603	42.087334	41.958778	45.325153	hypothetical protein CAA
C113810WA	109.455338	70.984161	113.020264	140.101334	hypothetical protein MEC
C113820CA	98.625732	94.57177	27.377544	25.64934	hypothetical protein CAA
C113840WA	84.92215	87.733978	68.314461	70.500336	divalent metal ion transp
C113880CA	157.289841	155.116821	99.589783	107.351845	hypothetical protein CAA
C113950CA	5.836906	6.565775	9.246301	8.783916	hypothetical protein CAA
C114020WA	2.67978	7.561201	5.999458	9.038243	hypothetical protein CAA
C114030WA	49.126259	54.217564	70.984177	65.983368	hypothetical protein CAA
C114040WA	9.669982	9.020084	14.644219	13.62207	hypothetical protein CAA
C114050CA	15.139022	12.709496	16.198904	15.715952	ATP-dependent 3'
C114060WA	83.023399	93.370583	66.892014	54.701107	17-beta-hydroxysteroid d
C114080WA	16.5368	18.237787	18.23023	20.421589	snoRNA-binding rRNA-p
C114090WA	165.638412	202.625992	376.105377	328.202332	hypothetical protein CAA
C114160WA	5.087366	3.481635	6.257226	4.020174	hypothetical protein MG3
C114170WA	29.457825	28.203876	43.1661	42.722572	E3 ubiquitin-protein ligas
C114180WA	82.950775	84.945831	26.745037	26.419445	hypothetical protein CAA
C114190CA	342.826233	264.428284	220.851089	183.752365	type 1 protein phosphata
C114200WA	36.978947	40.49749	57.689175	53.566032	hypothetical protein CAA
C114240WA	35.115532	37.956547	86.890877	98.114639	hypothetical protein CAA
C114250CA	39.446987	32.945045	19.153339	16.912098	hypothetical protein CAA
C114270WA	13.354291	13.972618	12.882565	25.522842	arylformamidase
C114310WA	22.882868	39.155643	64.52137	41.936989	deoxycytidine monophos
C114320CA	42.407204	31.97578	69.08606	57.200481	hypothetical protein CAA
C114330WA	13.521593	12.624491	30.682177	27.288008	tRNA-5-taurinomethyluri
C114350WA	342.618805	283.011993	119.435814	99.648521	hypothetical protein CAA
C114380CA	19.365437	22.289179	28.084007	23.070667	hypothetical protein MGC
C114410WA	100.212044	90.711395	135.236191	106.738205	RNA-binding protein
C114430CA	63.177097	51.94664	75.154793	61.13221	hypothetical protein CAA
C114450CA	92.124496	82.676636	105.739128	93.799583	putative Xaa-Pro dipepti
C114460WA	137.460953	142.173615	179.5905	125.229805	proteasome regulatory p

C114470WA	41.387878	45.313641	54.175705	46.937756	U4/U6.U5 tri-snRNP-ass
C114480WA	18.251722	20.541632	18.025503	10.955201	hypothetical protein CAA
C114500CA	148.868576	152.599533	290.568481	261.385498	hypothetical protein MEC
C114520WA	141.772339	137.661713	127.708038	74.053291	hypothetical protein MGM
C114530WA	202.432404	222.494507	330.698578	333.563324	hypothetical protein CAA
C114550CA	36.560844	42.327896	93.516869	96.796364	hypothetical protein MG9
C114560CA	26.728424	29.708191	50.206623	51.418018	hypothetical protein CAA
C114580CA	48.54538	39.718243	50.0867	47.71677	hypothetical protein CAA
C114630CA	2.797816	3.596714	1.704159	3.81166	hypothetical protein CAA
C200060CA	96.053314	85.199829	98.9869	64.310623	hypothetical protein CAA
C200090WA	64.817429	46.513565	59.515331	40.395203	hypothetical protein CAA
C200110WA	97.951485	85.958176	133.576035	94.376968	hypothetical protein CAA
C200170CA	31.746218	34.229435	38.593426	31.119165	tRNA threonylcarbamoyl
C200180CA	28.680227	27.413363	212.147263	159.19899	hypothetical protein CAA
C200190CA	56.803009	59.853176	78.069427	73.994148	hypothetical protein MEC
C200200WA	41.215397	47.686325	48.294399	62.250614	mRNA splicing protein
C200220CA	50.872326	49.004349	63.727493	60.746498	transcription factor IIF su
C200230WA	17.735361	13.473498	19.536034	22.805565	arginyltransferase
C200270CA	37.41526	42.787811	41.046341	31.492168	hypothetical protein CAA
C200280CA	14.679109	23.926292	14.473767	11.578665	U2-type spliceosomal co
C200290WA	18.864803	21.093084	19.951971	23.360439	J-type chaperone
C200310WA	0.00443	0.626732	0	0.461464	hypothetical protein CAA
C200320WA	57.893223	58.729134	69.306931	56.466854	GET complex subunit
C200350WA	6.537244	6.377391	11.541883	12.4005	DNA helicase
C200360CA	101.573799	104.344467	82.316986	87.410675	hypothetical protein CAA
C200390CA	14.346151	20.046539	19.909195	18.11779	cystathionine beta-lyase
C200400CA	176.211411	151.157379	228.141479	235.827408	hypothetical protein CAA
C200410CA	33.449471	30.508797	13.196117	12.960485	hypothetical protein L150
C200420WA	87.674957	94.851097	70.957199	73.397682	hypothetical protein CAA
C200490WA	21.992353	20.158371	34.127567	29.724609	hypothetical protein CAA
C200510WA	10.277035	8.97335	18.545795	16.45672	hypothetical protein CAA
C200540WA	53.12397	48.652321	37.054047	30.966721	hypothetical protein CAA
C200550WA	6.287706	8.146258	12.795231	13.878922	hypothetical protein CAA
C200570WA	53.131794	51.614315	105.752251	108.489525	hypothetical protein CAA
C200590WA	18.293016	14.024416	22.810585	28.598207	hypothetical protein CAA
C200600CA	146.628433	165.36026	189.320404	135.16806	hypothetical protein CAA
C200620CA	13.31572	8.784839	14.187837	12.149901	protein-lysine N-methyltr
C200630CA	6.287015	5.660686	9.275517	4.290289	allantoicase
C200640WA	4.100831	6.540608	4.368056	3.260157	hypothetical protein CAA
C200650WA	5.277935	5.012949	3.618546	4.988496	hypothetical protein MEC
C200690WA	4.497757	7.513348	6.855162	7.657377	hypothetical protein CAA
C200700WA	28.08914	28.199308	64.263321	75.443207	m-AAA protease subunit
C200730CA	6.749609	5.802168	5.758515	7.723115	hypothetical protein CAA
C200740CA	97.083679	99.570488	138.942276	126.563148	hypothetical protein CAA
C200750WA	58.332066	57.565266	12.218368	17.27022	hypothetical protein CAA
C200760CA	991.235657	1004.830139	423.370331	374.387177	hypothetical protein CAA
C200770WA	42.527599	60.065548	18.394339	26.579025	hypothetical protein CAA
C200790CA	101.046219	102.384712	82.964012	100.199493	diacylglycerol kinase
C200810CA	10.641245	12.925324	16.262959	14.171907	hypothetical protein CAA
C200820WA	6.92035	10.811649	20.554018	18.337317	hypothetical protein CAA
C200830CA	27.052185	28.28603	42.912018	53.296558	chromatin structure-rem
C200840WA	17.54283	19.615446	30.985128	25.177847	NAPDH-dependent diflav
C200860CA	89.735435	95.893867	1.075152	0	hypothetical protein CAA
C200870WA	57.24371	62.651966	107.215584	148.994263	hypothetical protein CAA
C200880WA	30.307032	29.504719	48.487591	44.529602	hypothetical protein CAA
C200890WA	5.087139	2.194781	4.336077	3.343876	hypothetical protein CAA
C200900WA	2.171622	0	0	0	hypothetical protein CAA
C200920WA	125.536247	123.803864	188.089233	208.184998	hypothetical protein CAA
C200940WA	614.677795	660.004272	772.905884	726.78064	hypothetical protein CAA
C201030WA	114.086494	130.582886	211.628922	206.955093	mitochondrial 54S ribosc
C201040WA	42.886681	53.905598	110.631119	91.794899	hypothetical protein CAA
C201050WA	28.837177	40.435699	20.257381	23.300877	hypothetical protein CAA
C201060CA	25.310745	33.943733	23.990808	23.815481	hypothetical protein CAA
C201070WA	63.863407	62.770241	42.592968	49.722023	DNA-directed RNA polyr

C201140CA	0.976213	0.826247	2.642064	2.420101	hypothetical protein CAA
C201160WA	11.895144	9.414059	21.331959	19.937941	S-methyl-5-thioribose-1-
C201170CA	10.859286	10.624022	19.296463	18.884949	hypothetical protein CAA
C201190CA	6.243991	10.969747	22.749228	18.928232	hypothetical protein CAA
C201220WA	20.889124	23.646433	35.805721	37.588848	linker nucleoporin
C201230WA	15.155552	12.328094	26.625465	30.381363	hypothetical protein CAA
C201240CA	4.336665	4.095821	7.095366	7.562917	hypothetical protein CAA
C201250WA	7.553421	6.633484	37.566967	29.931749	hypothetical protein CAA
C201260WA	4.979661	5.686738	23.899704	25.147755	hypothetical protein CAA
C201310WA	10.761209	15.089721	16.6084	17.932848	hypothetical protein CAA
C201320WA	20.823729	21.422802	24.320414	37.629372	proteasome regulatory p
C201340WA	68.432838	69.042168	57.62859	64.627792	hypothetical protein MEM
C201370CA	52.203876	50.24284	36.603424	46.282818	hypothetical protein MGS
C201390WA	42.00729	36.541428	42.536339	52.445301	epsin
C201420CA	8.705362	9.253186	28.981485	33.159039	hypothetical protein CAA
C201440CA	73.939293	71.075035	110.994461	109.264824	dynein light chain
C201450CA	3.115541	5.308377	5.64416	3.339465	cyanamide hydratase
C201460CA	0	0	0.251446	0	hypothetical protein CAA
C201490CA	19.82814	17.380955	28.613768	27.815414	transcription factor ssl1
C201500WA	2.127515	2.277719	3.403557	2.810875	hypothetical protein CAA
C201510CA	7.530452	3.3028	8.51733	6.731943	tRNA(adenine34) deami
C201530CA	21.456839	22.012285	29.136749	32.878735	glutamine-dependent NA
C201540WA	11.454473	11.293214	7.981355	4.776665	hypothetical protein CAA
C201570WA	8.985732	6.93607	12.467744	11.172474	hypothetical protein CAA
C201630WA	15.789396	8.989644	19.646004	28.785051	hypothetical protein CAA
C201650WA	25.058826	23.112608	25.886688	21.827101	mRNA (N6-adenosine)-
C201660CA	490.687439	483.568909	705.066284	555.750977	hypothetical protein CAA
C201680CA	47.625454	51.87751	26.244617	26.817776	hypothetical protein CAA
C201690WA	429.668304	422.224731	328.041962	340.393219	hypothetical protein CAA
C201720CA	50.389576	83.443405	124.953934	118.166702	hypothetical protein CAA
C201730WA	7.998674	8.376683	15.09238	24.044096	conserved hypothetical
C201740CA	102.024101	111.98996	329.133423	399.383728	mitochondrial 54S ribos
C201750CA	595.409424	610.41748	1665.332275	1899.969482	hypothetical protein CAA
C201760CA	20.827721	20.553207	19.063559	23.337143	hypothetical protein CAA
C201800WA	11.949327	11.015579	12.132071	8.67718	hypothetical protein CAA
C201820CA	9.618731	10.467958	12.144189	13.420654	hypothetical protein CAA
C201860CA	8.867295	7.734246	24.454992	18.510334	putative acireductone sy
C201870CA	5.010125	7.892273	11.579047	13.482893	hypothetical protein MG1
C201900CA	13.542776	12.413755	22.369198	26.963789	hypothetical protein CAA
C201910WA	11.327786	10.574437	16.62278	21.372395	hypothetical protein CAA
C201920CA	9.787827	10.349277	17.494852	16.398058	hypothetical protein CAA
C201930CA	17.561605	23.362362	48.768806	54.375916	hypothetical protein CAA
C202000WA	67.69635	79.478165	117.908066	100.052689	hypothetical protein CAA
C202020WA	11.637582	10.488015	18.757895	23.377663	ubiquitin-specific proteas
C202040WA	7.360238	7.379788	12.526611	12.29346	hypothetical protein CAA
C202050CA	17.925951	15.071801	37.316109	61.993713	hypothetical protein CAA
C202090WA	19.291811	17.696795	30.30471	34.137512	hypothetical protein CAA
C202110CA	14.006536	19.680546	21.231571	23.510416	hypothetical protein CAA
C202120WA	61.392403	75.528137	102.056664	96.286819	RNA polymerase specific
C202130CA	0	0.581585	0	2.994114	hypothetical protein CAA
C202140CA	0.482984	0	0	0	hypothetical protein CAA
C202150CA	30.364826	30.033699	32.080894	30.850155	cleavage polyadenylation
C202170WA	39.231728	48.177044	44.149628	48.107887	hypothetical protein CAA
C202180WA	136.927612	141.661682	14.396394	16.159775	Zn(2+) transporter
C202190CA	4.580402	1.95024	12.601499	20.401512	hypothetical protein CAA
C202200WA	57.133801	48.84726	31.426579	40.006336	Zn(2+) transporter
C202220CA	6.683218	4.008703	2.525098	0.800369	hypothetical protein CAA
C202230CA	18.325531	20.239529	8.869482	7.438016	hypothetical protein CAA
C202260WA	74.910751	78.17746	198.018906	240.862778	hypothetical protein CAA
C202270CA	92.748421	83.948967	165.039963	167.419205	mitochondrial 37S ribos
C202280WA	44.378254	27.655071	135.290726	132.384247	hypothetical protein CAA
C202290CA	6.376221	4.042805	7.88828	9.006185	polynucleotide 3'-
C202300WA	13.853213	10.453951	18.265667	13.970726	U4/U6-U5 snRNP compl
C202310WA	125.733696	117.176453	175.2155	201.036118	hypothetical protein CAA

C202330WA	1.60391	0.399771	2.213603	1.331405	hypothetical protein CAA
C202360CA	16.750023	20.501299	39.646076	39.138348	hypothetical protein W5
C202390WA	1553.400757	1291.93811	3248.070312	3404.326904	hypothetical protein CAA
C202410WA	147.092224	160.349915	93.389763	70.709206	hypothetical protein CAA
C202420CA	10.895899	10.954187	13.524651	16.161554	tRNA dihydrouridine syn
C202440WA	16.325802	14.277065	22.75161	23.484619	hypothetical protein CAA
C202490CA	6.266344	8.015461	10.191417	9.830956	putative acid anhydride
C202500WA	19.656235	15.042034	40.056179	42.375263	hypothetical protein CAA
C202520WA	23.296715	30.69838	14.869524	18.204315	hypothetical protein CAA
C202530WA	38.78767	45.14357	0.26456	0.207712	hypothetical protein CAA
C202540WA	21.173689	21.800722	13.59761	16.790468	hypothetical protein CAA
C202550CA	4.05155	8.070976	18.554764	15.618532	hypothetical protein CAA
C202570WA	25.584936	28.003056	11.344529	13.595321	hypothetical protein CAA
C202580WA	148.026337	131.051498	30.591013	22.60405	hypothetical protein CAA
C202620WA	58.535316	48.037197	117.182953	108.532295	hypothetical protein CAA
C202630WA	13.617679	15.522378	17.274755	13.997887	hypothetical protein CAA
C202640CA	18.373552	13.348121	13.232459	10.095731	hypothetical protein CAA
C202660WA	17.888681	16.063791	61.768177	57.492546	hypothetical protein L15
C202670CA	6.377524	15.014842	26.182383	33.196777	hypothetical protein CAA
C202700CA	14.272567	15.310337	37.914238	30.464357	aminodeoxychorismate
C202710CA	99.237061	108.173904	51.744389	65.997543	hypothetical protein CAA
C202720WA	36.709133	45.394146	48.225304	48.209499	hypothetical protein CAA
C202730WA	53.700443	54.323742	68.907997	67.934402	polyubiquitin-binding pro
C202750CA	0.355428	0.345851	0.74993	1.437967	hypothetical protein CAA
C202770WA	65.348099	73.507408	83.858032	87.289169	splicing factor U2AF 65
C202790CA	1.937271	1.809582	1.32836	0.948675	hypothetical protein CAA
C202800WA	104.890182	126.104553	279.127045	223.205704	hypothetical protein CAA
C202820CA	29.468328	34.69173	38.915051	32.60743	putative hydrolase
C202840CA	4.873804	6.388265	14.317309	15.459114	UPF0507 protein
C202870WA	21.562771	33.844418	72.569878	84.24353	TRAPP complex core su
C202900WA	26.54538	30.843977	42.224976	42.362297	hypothetical protein CAA
C202910WA	9.35573	3.639003	26.44685	29.341097	hypothetical protein CAA
C202920WA	1589.630493	1951.868408	1208.626709	1197.403076	hypothetical protein CAA
C202930CA	76.6828	88.724274	112.027733	100.939163	hypothetical protein MG
C202950WA	34.019535	26.765974	26.051252	22.333744	kynurenine--oxoglutarate
C202960CA	8.49684	12.127157	12.382351	9.414506	S-adenosylmethionine-d
C203000CA	14.009766	19.138346	7.282805	8.319556	hypothetical protein CAA
C203020CA	41.489929	46.270046	43.662853	42.688297	hypothetical protein CAA
C203110WA	15.175817	10.824205	12.594485	22.962339	hypothetical protein CAA
C203130WA	50.304443	48.647713	61.081184	47.721748	protein-arginine N-methy
C203140CA	15.500319	16.755024	15.554311	14.789679	putative carboxylic ester
C203150CA	7.506589	5.75655	11.018329	10.233039	hypothetical protein CAA
C203170WA	4.758677	3.803196	11.106014	21.708588	hypothetical protein CAA
C203210WA	133.988388	95.229851	74.015297	102.035263	hypothetical protein CAA
C203260WA	24.220533	29.030626	32.880867	28.434437	hypothetical protein CAA
C203290WA	84.090691	63.325336	96.595695	91.791916	hypothetical protein CAA
C203340WA	17.441252	16.088614	28.042477	31.497473	hypothetical protein CAA
C203360WA	15.571528	20.639166	27.813883	26.813971	AMP deaminase
C203410WA	22.347069	22.988382	22.071178	24.255453	hypothetical protein CAA
C203420CA	10.18037	12.626604	7.440919	8.492863	hypothetical protein CAA
C203450WA	16.915226	14.264115	35.477921	31.810577	hypothetical protein CAA
C203460CA	18.553158	27.137455	71.258522	54.496593	hypothetical protein CAA
C203490CA	9.904295	10.990072	28.305126	34.540222	hypothetical protein CAA
C203500WA	83.547615	88.371964	62.458195	74.529587	hypothetical protein ME
C203530WA	33.495407	38.140755	20.908541	18.39361	putative metalloreductas
C203550CA	13.87635	14.02307	26.145184	30.98852	hypothetical protein MG
C203560CA	54.437012	66.6138	130.299957	129.941696	mitochondrial 54S ribos
C203570CA	43.832779	42.389065	49.207813	52.700134	hypothetical protein CAA
C203630WA	0.134463	0.713395	0	2.154227	hypothetical protein CAA
C203690CA	0.701496	0.440556	0.563613	0.708535	hypothetical protein CAA
C203700WA	7.595652	9.875264	15.287054	11.664216	amidase
C203710WA	2.658437	2.533716	0.38969	0.465839	hypothetical protein ME
C203760CA	103.236755	102.603897	49.697674	47.764397	protein kinase
C203780CA	14.192906	12.95364	14.139272	16.707619	phosphoprotein phospha

C203800CA	37.095417	30.303305	80.967613	81.465492	hypothetical protein CAA
C203830WA	14.579288	19.006014	13.774595	17.601009	diphthine--ammonia ligas
C203880CA	37.851265	14.259064	39.926807	68.985725	small nuclear ribonucleo
C203890WA	3.400833	7.888171	29.269382	28.346666	hypothetical protein CAA
C203900CA	19.86116	20.389351	32.273853	42.005798	hypothetical protein CAA
C203910CA	4.200964	4.631609	10.779475	10.888583	alpha-1,2-mannosidase
C203930CA	20.081387	17.364618	48.802128	40.569862	hypothetical protein CAA
C203950WA	77.564621	72.701431	139.658905	110.007256	mitochondrial 54S ribos
C203970WA	13.397668	13.72333	48.946838	53.711548	hypothetical protein MG5
C204000CA	8.118765	7.038871	2.666133	1.060381	hypothetical protein MG
C204080WA	135.244934	136.21727	58.063465	67.605499	hypothetical protein MG1
C204090WA	0.545582	3.181853	2.178671	3.138734	hypothetical protein CAA
C204100WA	8.925748	10.093796	14.004733	19.056526	hypothetical protein CAA
C204110WA	5.209579	6.395252	20.487827	18.478138	hypothetical protein CAA
C204120CA	81.727524	81.871872	43.875175	44.115967	nucleolar protein 12
C204130WA	14.557171	13.960033	30.780024	30.838287	Rpd3L histone deacetyla
C204160WA	13.782236	12.897335	34.022655	37.697731	hypothetical protein CAA
C204170CA	1054.041016	1062.648926	2174.770996	2044.077759	hypothetical protein CAA
C204180CA	19.850731	17.73695	34.254379	31.092653	hypothetical protein CAA
C204280WA	159.714432	159.016739	96.835114	92.106537	hypothetical protein CAA
C204300CA	28.991869	37.980061	27.825119	31.195971	hypothetical protein CAA
C204320WA	4.91785	4.248154	10.736106	11.504249	hypothetical protein CAA
C204330CA	14.876022	14.735667	10.813648	15.492519	hypothetical protein CAA
C204340CA	8.221545	6.194969	6.258911	6.062091	gluconokinase
C204360WA	7.338962	6.522533	13.178652	18.535299	non-specific serine/threo
C204370WA	54.219952	73.399361	46.542316	51.101387	hypothetical protein CAA
C204380CA	25.901484	18.221741	31.898226	30.988594	tetrahydrofolate synthas
C204390WA	4.765611	4.654414	2.587715	5.894542	hypothetical protein CAA
C204400WA	102.750114	114.275124	114.135475	114.176331	hypothetical protein CAA
C204410WA	9.662475	9.873306	13.879336	13.359344	hypothetical protein CAA
C204430WA	4.230759	1.33221	3.278385	2.355984	hypothetical protein CAA
C204440WA	4.449669	3.193789	3.293246	3.977091	hypothetical protein CAA
C204450WA	9.523415	10.058446	6.150566	7.423358	hypothetical protein CAA
C204480WA	22.469685	18.707207	19.911276	20.221794	hypothetical protein CAA
C204490WA	43.04221	42.944351	60.301804	57.966225	hypothetical protein CAA
C204500WA	19.24773	15.972542	32.04528	31.775345	DNA-binding ATPase
C204520CA	19.497574	19.423847	27.418837	22.881996	hypothetical protein ME
C204570WA	118.4953	121.727173	43.599293	49.736107	rRNA-processing protein
C204620WA	71.038216	59.915134	53.147449	61.524708	hypothetical protein CAA
C204670WA	7.97797	9.693067	2.341331	2.004908	hypothetical protein CAA
C204700CA	19.594448	29.079805	18.924103	15.477718	hypothetical protein CAA
C204730WA	10.362747	11.62488	12.647966	15.462833	hypothetical protein CAA
C204740CA	10.249372	10.482159	16.829178	14.102098	hypothetical protein CAA
C204750WA	31.678938	22.974699	20.355169	21.316862	hypothetical protein CAA
C204770WA	7.041311	6.507288	16.452415	16.347765	hypothetical protein CAA
C204780WA	18.240042	17.791626	37.464912	38.463692	hypothetical protein CAA
C204790CA	50.535889	63.207531	104.053497	96.206772	mitochondrial 37S ribos
C204820WA	27.47477	26.874949	51.863171	46.488621	hypothetical protein CAA
C204830WA	11.77837	18.007109	11.80517	14.234913	hypothetical protein CAA
C204850CA	160.723587	180.120056	263.111115	230.924896	hypothetical protein MG
C204870CA	31.231182	24.269587	33.912571	36.559055	hypothetical protein CAA
C204960CA	38.060558	46.125324	45.233585	48.784874	hypothetical protein CAA
C204990WA	6.384562	11.566843	15.85332	19.502443	hypothetical protein CAA
C205020WA	23.936237	29.559046	63.665306	59.404442	hypothetical protein CAA
C205040CA	95.801796	90.30426	82.997215	78.738747	hypothetical protein CAA
C205050CA	14.426431	13.757748	18.576239	19.775721	glucose N-acetyltransfer
C205060CA	31.958071	18.068176	889.357056	780.514771	sulfiredoxin
C205080CA	13.071632	10.285672	9.218744	15.40591	25S rRNA (adenine2142
C205130WA	23.671423	25.309792	25.146629	18.101675	hypothetical protein CAA
C205160CA	45.332111	51.875805	26.421623	26.673962	pumilio homology domai
C205170WA	77.685005	76.219124	112.802101	88.108559	hypothetical protein CAA
C205220CA	16.861809	14.747565	30.29402	33.485867	hypothetical protein CAA
C205270WA	47.427402	39.960648	25.471632	25.566002	hypothetical protein ME
C205290CA	80.727394	92.442963	139.135529	127.701836	hypothetical protein CAA

C205300CA	125.6213	138.447372	189.595383	184.539993	mitochondrial 37S ribos
C205330CA	66.527969	57.081436	21.420294	24.631983	hypothetical protein CAA
C205350CA	7.176032	6.669338	18.59898	12.397511	hypothetical protein CAA
C205380WA	60.059883	74.803329	29.449564	28.811872	hypothetical protein CAA
C205390CA	6.225351	6.179317	4.912626	6.694831	hypothetical protein CAA
C205400WA	3.04764	2.982761	4.820089	10.015747	hypothetical protein MEV
C205410WA	948.763062	1005.370361	1289.902832	1287.185669	ribosomal 60S subunit p
C205480CA	25.340298	29.199594	43.528835	30.924067	hypothetical protein CAA
C205490WA	8.979223	11.420178	22.089781	18.908991	hypothetical protein CAA
C205510CA	8.839539	9.096573	26.338539	28.646633	hypothetical protein CAA
C205520WA	28.918108	26.314924	30.679096	27.176872	hypothetical protein CAA
C205530CA	37.329235	32.59296	61.294888	65.467606	ran-binding protein 3
C205540CA	24.505804	22.619387	27.18117	27.850395	U1 snRNP complex sub
C205550WA	194.761978	222.089371	175.337296	192.465302	conserved hypothetical
C205560WA	26.645472	22.000477	33.496799	36.417358	hypothetical protein CAA
C205570CA	72.950844	61.241928	67.450676	56.99564	hypothetical protein CAA
C205580WA	10.743936	11.598941	6.405261	10.6061	hypothetical protein CAA
C205590CA	34.83202	40.689606	8.108428	8.385594	putative amidotransferas
C205640WA	32.250515	28.949839	56.963039	61.850113	hypothetical protein CAA
C205670CA	24.684029	26.974688	22.554247	19.832535	tRNA splicing endonucle
C205710CA	1279.484253	1262.23877	1338.847778	1206.505615	ribosomal 60S subunit p
C205720CA	41.323505	49.883945	59.664291	59.022984	oxysterol-binding protein
C205750WA	76.367531	79.974182	47.000774	45.78965	hypothetical protein CAA
C205760CA	309.165894	253.301376	407.052063	254.514755	hypothetical protein CAA
C205770WA	24.955032	28.593098	11.670064	17.665716	hypothetical protein CAA
C205800CA	16.613482	14.35614	41.058498	34.351486	hypothetical protein MG1
C205810WA	17.064373	19.996452	9.343355	8.090631	hypothetical protein CAA
C205820WA	20.878456	31.135176	22.078077	22.57584	hypothetical protein CAA
C205830CA	26.909576	22.168472	18.806482	22.032887	Hsp90 cochaperone
C205840WA	30.059971	37.519104	23.440109	20.919767	hypothetical protein CAA
C205850CA	11.183074	8.636999	21.951752	28.483999	Golgi transport complex
C205860CA	11.418478	8.609909	7.772805	7.767062	hypothetical protein CAA
C205870WA	36.01096	35.664543	113.757355	82.547562	hypothetical protein CAA
C205900WA	1.892219	0.843663	4.232457	2.142998	SUMO ligase
C205910WA	13.830553	10.366496	14.173198	16.028482	hypothetical protein MG
C205960CA	6.116969	7.624577	4.616589	5.172478	hypothetical protein CAA
C205980CA	15.499709	18.572296	16.952341	15.95037	hypothetical protein CAA
C205990CA	27.545218	28.98889	16.297915	16.363192	hypothetical protein CAA
C206030WA	18.105354	22.564419	33.760323	35.759804	Protein not essential for
C206040CA	8.96154	7.18596	7.529455	9.457156	N-acetyltransferase
C206080CA	25.733576	26.80302	40.924644	37.720051	hypothetical protein CAA
C206090WA	7.18295	6.646912	4.893104	8.255664	hypothetical protein CAA
C206110WA	30.042976	25.942196	35.732265	46.947136	exopolyphosphatase
C206120CA	6.243946	6.256769	7.642185	9.406105	putative polyadenylation
C206140CA	0.186928	0.606001	1.172917	1.018979	hypothetical protein CAA
C206160WA	19.380695	37.086533	57.648014	53.976025	hypothetical protein CAA
C206200CA	10.054768	6.743941	13.280721	13.530912	GTPase
C206230WA	12.893089	16.657757	26.258982	27.148674	cleavage polyadenylation
C206260WA	8.211738	9.523012	23.45853	12.306545	hypothetical protein CAA
C206270WA	3.085221	4.034085	15.629956	18.880955	hypothetical protein CAA
C206280CA	3.956838	4.117108	22.859921	21.082418	hypothetical protein CAA
C206300WA	32.170509	21.787016	58.643311	48.692951	RecName: Full=U1 smal
C206320WA	11.10568	7.960646	6.896779	7.362656	hypothetical protein CAA
C206350CA	0.114731	0.178502	0.761437	0	hypothetical protein CAA
C206430CA	10.424866	13.549353	2.555868	2.441253	ethanol metabolism prot
C206440CA	57.131805	52.044674	34.141918	42.200726	hypothetical protein CAA
C206480WA	36.268288	40.612228	22.829157	22.042795	tRNA (guanine(9)-N(1))-
C206490WA	19.332558	24.229044	33.074619	28.848309	peptide-N4-(N-acetyl-bet
C206510WA	127.019371	138.825592	55.920235	58.553341	hypothetical protein CAA
C206520CA	49.097084	46.808929	11.829724	11.081528	thiamine transporter
C206530WA	76.0382	86.060928	25.40271	35.798111	hypothetical protein CAA
C206550WA	10.969563	6.856331	2.879303	4.569131	hypothetical protein CAA
C206570CA	157.620224	158.231079	45.944973	23.645813	hypothetical protein MEU
C206600WA	210.384766	220.651611	56.735821	64.205215	hypothetical protein CAA

C206610CA	30.80055	26.192856	42.201782	37.423885	hypothetical protein CAA
C206620WA	1.796519	2.613118	8.775126	8.265098	Golgi transport complex
C206630CA	268.206909	240.676224	110.358971	69.365868	hypothetical protein CAA
C206650CA	8.374927	10.872727	8.764328	13.030943	U4/U6-U5 snRNP compl
C206660WA	22.691624	23.40782	13.900966	16.851038	exosome complex comp
C206710WA	11.69007	12.132173	24.027538	22.274481	hypothetical protein CAA
C206740WA	17.335569	13.352539	71.08223	80.810661	hypothetical protein CAA
C206750CA	11.853953	8.55735	17.045591	16.272104	hypothetical protein CAA
C206760CA	5.176709	5.141879	14.799359	23.351139	hypothetical protein CAA
C206770WA	6.706619	6.07376	14.421079	12.230753	hypothetical protein CAA
C206780CA	4.383613	6.320302	9.642168	8.18177	ubiquitin-protein ligase
C206790WA	8.238178	6.417352	28.001261	21.904549	U2 snRNP complex subu
C206800CA	44.858624	49.367222	14.625005	16.465469	hypothetical protein CAA
C206850WA	30.369226	29.164087	26.741577	30.65439	hypothetical protein CAA
C206890CA	11.769868	6.73159	15.367289	22.935753	hypothetical protein CAA
C206920CA	33.008553	19.237513	19.300631	31.054962	hypothetical protein CAA
C206930CA	2.171701	3.525398	4.793006	9.017116	hypothetical protein MEY
C206950CA	19.135626	26.803223	52.209949	57.923805	putative metalloprotease
C206980WA	0	0.266236	1.082016	0.134696	hypothetical protein CAA
C206990WA	22.832005	27.796459	15.826192	15.603358	hypothetical protein CAA
C207000WA	27.866337	28.098854	37.81953	42.55019	hypothetical protein CAA
C207010WA	56.08857	59.629162	126.604362	113.723175	hypothetical protein CAA
C207020CA	9.966271	8.187713	11.26364	6.421593	hypothetical protein CAA
C207030CA	71.261345	76.994087	114.522316	102.404053	mitochondrial 54S riboso
C207040WA	21.860229	19.650019	31.713743	28.264486	hypothetical protein CAA
C207060WA	25.677214	29.448971	30.592932	32.585045	U2 snRNP complex subu
C207070WA	24.662418	26.674393	22.145248	19.968992	NADPH2:quinone reduct
C207080CA	34.921406	31.796694	61.97332	53.626114	hypothetical protein CAA
C207100WA	41.730537	52.401508	141.067322	143.784317	hypothetical protein CAA
C207110CA	8.698885	11.139869	23.968664	27.069464	hypothetical protein CAA
C207140WA	28.352421	28.692556	37.22065	25.278765	putative phosphoric mon
C207180WA	2.775431	7.026807	12.590805	15.858319	hypothetical protein MGC
C207190CA	136.846268	143.970947	272.344391	271.213928	ribosomal protein L7/L12
C207200WA	56.519474	43.142372	126.65377	95.682358	DNA-directed RNA polyr
C207220WA	38.706665	34.576424	51.43795	65.2416	hypothetical protein CAA
C207240CA	3.826776	4.359831	4.747701	6.159381	hypothetical protein CAA
C207250CA	4.465165	2.712117	1.96588	3.88669	hypothetical protein CAA
C207270WA	9.936401	14.640747	18.312561	24.59832	hypothetical protein CAA
C207280WA	0.429864	1.507313	0.896721	0.837044	hypothetical protein CAA
C207290WA	122.615585	137.516724	55.935272	60.486931	hypothetical protein CAA
C207360WA	9.956217	11.507411	10.808445	12.899236	RNA methyltransferase
C207370WA	39.197189	41.554184	105.962784	122.05957	hypothetical protein CAA
C207390CA	56.798458	49.581989	101.790009	132.100204	hypothetical protein CAA
C207410WA	24.107857	29.271271	39.789139	33.260414	putative carboxylic ester
C207420WA	60.853462	51.256466	24.794985	21.675341	sedoheptulose-bisphosp
C207430CA	239.199478	273.437164	129.291946	126.349411	trifunctional uridine nucle
C207440CA	14.613158	18.962809	19.93891	23.498674	sterol esterase
C207510WA	10.461993	10.511278	22.525766	20.97163	hypothetical protein CAA
C207520CA	24.016209	23.838562	30.769697	27.269682	hypothetical protein MGC
C207530CA	0.244958	0	0.624105	1.041696	serine/threonine protein
C207540WA	199.208282	191.268463	295.277649	266.064117	hypothetical protein CAA
C207550WA	264.376038	262.398956	326.861908	345.628418	hypothetical protein CAA
C207580WA	24.672514	19.107023	17.078495	16.501329	hypothetical protein CAA
C207610CA	8.324162	10.937768	29.083624	30.523136	hypothetical protein CAA
C207620WA	1.116293	2.02573	2.922362	2.163791	hypothetical protein CAA
C207630CA	154.650513	158.599884	73.323616	60.691586	hypothetical protein CAA
C207640WA	61.312775	72.175972	107.161514	114.638756	hypothetical protein CAA
C207650CA	11.433172	16.467268	47.397415	47.079296	hypothetical protein CAA
C207680WA	71.205734	80.694588	147.87674	128.498718	mitochondrial 54S riboso
C207690WA	4.121923	4.638132	14.711761	11.438811	hypothetical protein CAA
C207700CA	6.223659	4.409619	7.843303	4.494361	hypothetical protein CAA
C207710WA	0.157511	0.21943	0.977539	0.391717	hypothetical protein CAA
C207720CA	20.556593	27.214823	19.06687	19.074877	hypothetical protein MG3
C207740WA	53.894951	47.707352	43.803349	46.613899	stress response protein

C207760WA	65.005516	68.689476	30.663198	48.572948	hypothetical protein CAA
C207770CA	21.714376	20.841177	21.214617	12.858103	hypothetical protein CAA
C207790CA	8.861159	10.390302	5.251618	3.132261	hypothetical protein CAA
C207800WA	48.953465	58.256577	138.267929	160.854416	hypothetical protein CAA
C207810WA	25.526512	27.124104	32.926289	32.64854	hypothetical protein CAA
C207840WA	0.503228	0	2.4831	1.237837	hypothetical protein CAA
C207860WA	21.134785	17.948538	38.556995	33.094639	hypothetical protein CAA
C207910CA	34.579525	32.245724	45.033028	63.943645	hypothetical protein CAA
C207920WA	28.876944	33.640884	27.605272	25.007723	diphthamide synthase
C207980WA	15.697836	15.828436	28.602871	30.021931	hypothetical protein MG
C208020CA	77.333565	81.179436	79.328865	105.721931	hypothetical protein CAA
C208030WA	9.375323	17.136347	14.007132	17.188793	hypothetical protein CAA
C208060WA	62.885353	80.238014	83.505272	76.014038	hypothetical protein CO
C208090WA	39.191696	47.435726	26.735933	12.379441	hypothetical protein MG1
C208100WA	359.898743	354.955383	183.910736	145.862885	hypothetical protein CAA
C208160CA	270.32132	250.041153	359.88739	389.941467	hypothetical protein CAA
C208170WA	15.042645	11.237076	16.327791	17.896395	hypothetical protein ME
C208180CA	54.455696	59.823662	25.40695	21.380217	hypothetical protein MG7
C208200WA	12.385995	20.775396	192.644333	160.18219	hypothetical protein CAA
C208240WA	111.048439	103.041595	59.907536	52.403156	hypothetical protein CAA
C208260WA	318.400909	324.892365	10.275381	6.013122	hypothetical protein CAA
C208270CA	98.423447	99.386269	100.674515	93.491508	casein kinase
C208320CA	20.070543	17.290173	78.740021	88.549248	hypothetical protein CAA
C208330WA	255.199936	174.674408	29.760811	43.117237	hypothetical protein ME
C208340CA	7.855094	3.452595	4.307535	5.447053	hypothetical protein CAA
C208350CA	0.137086	0	0.4892	0	hypothetical protein CAA
C208380CA	7.114381	5.009126	12.55564	13.885882	protein kinase activating
C208390WA	112.107887	112.953514	100.51152	106.90818	hypothetical protein MG
C208400CA	2.402121	0.30664	1.220837	3.125087	hypothetical protein CAA
C208420WA	38.7551	45.050838	14.753217	19.742334	hypothetical protein CAA
C208450WA	6.81323	6.590218	2.580098	3.606416	hypothetical protein CAA
C208460CA	10.014245	14.767152	17.531124	15.290986	hypothetical protein CAA
C208510WA	12.162343	9.748961	8.756116	12.205202	hypothetical protein MEY
C208520CA	3.003624	0	4.114673	0.694464	hypothetical protein ME
C208530CA	1.817075	4.010955	5.028234	5.336043	hypothetical protein ME
C208540CA	2.884546	3.473208	24.026077	19.849762	hypothetical protein CAA
C208580WA	90.129852	80.588379	14.143098	18.038317	hypothetical protein CAA
C208620WA	78.804626	87.437698	286.640564	357.28125	hypothetical protein CAA
C208630CA	33.100323	35.764111	67.321701	78.642097	RNA polymerase II-asso
C208650WA	170.636841	163.229721	347.191711	432.12796	hypothetical protein CAA
C208660CA	9.991618	7.044061	7.403018	8.818189	hypothetical protein CAA
C208690CA	7.882275	6.946941	5.868786	5.441049	hypothetical protein I503
C208700CA	106.435181	141.319489	98.176842	86.169395	hypothetical protein CAA
C208720WA	17.148684	17.544577	37.773708	39.082176	ino eighty subunit 2
C208740WA	0	5.903542	0	6.626554	hypothetical protein CAA
C208750WA	0.879898	0	0.895628	3.910069	hypothetical protein CAA
C208770CA	55.543419	52.978374	88.459839	98.474342	hypothetical protein ME
C208830WA	63.416355	56.644939	56.94791	60.429966	hypothetical protein MG
C208840WA	43.071705	59.708549	39.784386	40.771919	RNA methylation protein
C208850CA	66.965179	70.68988	59.100441	49.993725	hypothetical protein CAA
C208860WA	72.964722	88.736984	20.304291	22.711151	hypothetical protein L15
C208890WA	1.232576	1.434188	1.749866	0.837926	hypothetical protein CAA
C208900WA	356.390594	362.077728	397.299133	374.509552	hypothetical protein CAA
C208910CA	118.275711	146.651474	49.07814	52.988682	hypothetical protein MG
C208920WA	733.618164	718.396118	28.435247	27.496241	hypothetical protein CAA
C208930WA	48.250004	52.078217	123.745178	143.348083	proteasome regulatory p
C208950WA	278.617065	261.64798	122.500404	98.830353	conserved hypothetical
C208960CA	68.813507	51.286343	36.368279	44.994579	hypothetical protein CAA
C208990CA	390.468292	277.183563	16.249123	18.684652	hypothetical protein CAA
C209000CA	39.988659	32.011196	39.766979	43.83292	hypothetical protein CAA
C209030WA	8.899153	5.807228	26.763952	22.611412	hypothetical protein CAA
C209040WA	58.90398	60.102921	231.602478	220.803711	hypothetical protein CAA
C209050CA	33.048317	30.684776	32.535789	34.238968	hypothetical protein CAA
C209070CA	34.282566	39.301285	20.023857	19.933012	hypothetical protein CAA

C209100CA	9.261936	5.779367	11.190742	9.603716	hypothetical protein CAA
C209110CA	3.276626	2.761102	7.346027	5.701324	hypothetical protein CAA
C209160WA	28.094296	26.863541	17.761135	15.033704	exosome complex comp
C209180WA	5.897738	3.858512	14.011543	11.764805	hypothetical protein CAA
C209240CA	13.043097	8.340252	6.442673	14.255979	hypothetical protein CAA
C209250WA	26.518181	34.746742	52.539139	59.603878	hypothetical protein CAA
C209280CA	14.912217	22.987312	26.402838	25.707613	hypothetical protein CAA
C209290WA	38.724571	44.355148	45.796658	59.450447	hypothetical protein CAA
C209310CA	25.918844	28.032001	39.951778	52.929859	glutamyl-tRNA(Gln) amic
C209330CA	0	0.394165	0	0	hypothetical protein MEY
C209340WA	0	0.88035	0	1.667173	hypothetical protein MG3
C209360WA	5.703175	5.095801	11.268318	9.682024	hypothetical protein W5C
C209420WA	36.914524	29.575701	58.130199	75.222168	hypothetical protein CAA
C209460CA	13.218493	11.790133	13.189975	14.544107	Protein with a Gal4p-like
C209480WA	6.182496	4.847429	12.811666	14.200028	hypothetical protein CAA
C209500WA	89.157593	98.183777	23.783718	23.326118	tRNA dihydrouridine synt
C209510CA	121.375793	141.802429	46.740528	42.942833	Ca(2+)-binding ATP:ADF
C209560CA	16.682009	14.07338	28.147808	35.651154	hypothetical protein CAA
C209570CA	92.36631	101.097336	93.709137	90.454659	hypothetical protein CAA
C209590CA	11.308523	10.032131	52.686871	52.440216	Cu/Pi carrier
C209600CA	28.246235	32.155823	61.58284	54.989475	hypothetical protein CAA
C209610WA	38.408443	40.884212	10.745808	16.616987	NAD+ transporter
C209620WA	30.426178	28.625887	52.471844	54.329681	protein disulfide isomera
C209630CA	9.451472	9.002101	25.58687	37.429047	dynactin 5
C209650WA	768.395203	786.245117	1217.8125	1099.425049	hypothetical protein CAA
C209660WA	127.703804	117.995514	60.709248	52.130772	hypothetical protein CAA
C209670CA	91.75943	94.9021	139.429276	99.418968	iron-sulfur cluster assem
C209680WA	138.442078	143.042603	279.410034	271.937775	hypothetical protein CAA
C209690CA	10.726673	8.913756	8.813391	10.524126	hypothetical protein MEY
C209710CA	49.249996	57.568226	70.316727	64.639648	hypothetical protein CAA
C209760WA	28.703867	34.608253	58.135715	48.421585	conserved hypothetical p
C209780CA	102.020111	91.587463	142.92868	165.364548	increased recombination
C209790WA	13.85706	14.311642	42.816166	35.590584	hypothetical protein CAA
C209800CA	16.954718	17.819454	10.283858	5.314578	hypothetical protein CAA
C209810CA	10.169067	13.674704	7.904102	9.676993	hypothetical protein CAA
C209820WA	80.440834	87.075241	101.911804	117.73333	hypothetical protein CAA
C209830CA	184.651108	202.687668	334.4039	389.8685	hypothetical protein CAA
C209850CA	1.101847	0.527248	2.728475	1.990796	hypothetical protein CAA
C209860CA	5.099816	6.270447	6.023118	4.832482	hypothetical protein CAA
C209870WA	77.342796	90.189026	36.287567	40.920177	hypothetical protein CAA
C209880CA	971.015869	1069.662476	752.464355	727.930603	hypothetical protein CAA
C209910CA	100.167404	73.044861	183.005508	196.499115	dolichyl-diphosphooligos
C209920WA	17.828688	15.029507	27.140535	30.867426	hypothetical protein MEU
C209930WA	7.646034	6.038015	10.079574	13.787604	hypothetical protein CAA
C209960WA	8.37891	9.777375	21.339218	23.506361	thiosulfate sulfurtransfera
C209970CA	95.722603	100.576973	116.973526	123.59063	hypothetical protein CAA
C209980WA	1677.962402	1613.50293	995.386841	1053.539917	hypothetical protein CAA
C210000CA	0.800956	1.696139	1.821378	0.529276	hypothetical protein CAA
C210010CA	48.34473	55.163536	83.717224	94.358528	increased recombination
C210020CA	0	0.032909	0.286734	1.272063	hypothetical protein MEV
C210050WA	25.033648	27.760052	33.421009	39.817265	ubiquitin-specific proteas
C210060CA	3.708479	5.089551	16.011993	14.856796	putative pantetheine-phc
C210070WA	1.872685	1.902882	0.30334	0.76555	hypothetical protein CAA
C210090CA	11.755821	15.824993	15.247038	15.662452	hypothetical protein CAA
C210120WA	13.33991	14.683354	21.554356	20.685101	hypothetical protein MG1
C210130WA	2.468903	2.643144	2.561617	3.558712	hypothetical protein CAA
C210140WA	8.859248	9.976954	4.756096	3.169198	ubiquitin-specific proteas
C210150WA	57.316002	51.157066	4.051236	4.397408	conserved hypothetical p
C210160WA	5.270335	7.972695	6.346994	6.935523	hypothetical protein CAA
C210170CA	254.996155	288.535583	117.784195	105.984261	hypothetical protein CAA
C210200WA	33.281811	32.813049	47.671806	76.479851	dolichyl-diphosphooligos
C210230WA	5.577192	8.396003	15.343388	15.132534	hypothetical protein MGC
C210300CA	1.08027	4.15643	3.834361	4.755346	hypothetical protein CAA
C210320CA	2.02556	1.06651	2.066953	5.188839	hypothetical protein MGC

C210330CA	14.402015	12.276458	7.452693	8.158815	hypothetical protein MEC
C210460CA	18.082636	18.706409	28.804903	23.444384	methylenetetrahydrofolat
C210470CA	42.721596	47.123264	76.261307	77.195282	hypothetical protein CAA
C210540WA	273.902496	235.29985	106.485657	88.581436	hypothetical protein CAA
C210600WA	91.227615	92.590324	85.522308	64.905197	hypothetical protein MEV
C210630WA	21.352629	20.966555	31.834291	30.534206	hypothetical protein CAA
C210650WA	8.35501	13.03913	9.592293	12.362558	hypothetical protein CAA
C210670WA	148.621719	158.73941	182.624084	161.578247	hypothetical protein CAA
C210680WA	32.376598	30.450716	59.358685	62.565346	transcription initiation fac
C210700CA	25.723974	36.402122	51.641464	59.103283	hypothetical protein CAA
C210720CA	98.00248	80.055817	115.814117	101.939384	hypothetical protein CAA
C210730WA	12.428079	10.444456	8.169576	10.71039	hypothetical protein CAA
C210740CA	32.597588	33.624065	24.197302	19.52199	tetratricopeptide repeat-
C210760CA	14.735119	18.837475	30.449467	28.033562	origin recognition comple
C210790CA	76.516434	98.95977	93.654861	58.290771	N-acetylglucosaminyldipl
C210810WA	63.96933	63.119759	52.793179	44.531353	conserved hypothetical p
C210820CA	14.50411	11.724707	11.479501	14.432059	tRNA methylation protein
C210830WA	59.222336	79.996147	143.293945	132.943802	hypothetical protein CAA
C210850CA	24.077454	21.026546	30.707886	27.555899	hypothetical protein CAA
C210860CA	80.63121	69.418816	150.879074	127.14444	uroporphyrinogen decarb
C210870WA	31.990568	32.293724	43.835361	24.850677	hypothetical protein CAA
C300010CA	196.29184	154.767685	245.210907	147.131378	hypothetical protein MG1
C300030CA	70.374489	57.95005	93.795662	65.53994	hypothetical protein CAA
C300050CA	20.783991	24.864344	25.888662	17.044413	hypothetical protein CAA
C300100WA	84.495377	66.688072	74.718544	71.861397	mRNA splicing protein
C300120WA	8.72229	3.437047	21.298023	7.375347	hypothetical protein MEM
C300130CA	132.51088	134.737839	247.45665	195.849365	hypothetical protein MEC
C300140WA	0	0	0.193467	0	hypothetical protein CAA
C300150WA	0	0	0.592117	0	conserved hypothetical p
C300160CA	49.025223	53.346375	48.106441	37.368835	hypothetical protein CAA
C300170CA	785.303101	597.169006	241.715271	151.758316	hypothetical protein CAA
C300210CA	8.443751	8.835898	10.214145	8.76308	hypothetical protein CAA
C300230CA	0	2.277344	0.976117	1.092692	hypothetical protein CAA
C300270CA	32.048862	34.342812	82.569221	77.392349	hypothetical protein CAA
C300300WA	14.068029	13.044806	18.475548	15.213127	hypothetical protein CAA
C300310CA	28.590572	30.171904	49.4533	32.255173	SUMO-targeted ubiquitin
C300340WA	56.339516	44.550674	89.531517	70.573418	hypothetical protein CAA
C300360WA	5.024549	3.528544	3.267637	1.530175	hypothetical protein CAA
C300380CA	8.163987	9.622914	25.201139	26.338776	DNA-binding SCF ubiqui
C300390WA	15.223193	16.720734	12.959195	22.787897	solute carrier family 39 (
C300400CA	16.622368	12.434166	16.916094	19.570358	hypothetical protein CAA
C300410CA	0.782127	1.613869	2.960278	0	hypothetical protein CAA
C300420WA	15.112321	16.540766	22.241655	22.263311	ribonuclease Z
C300440WA	4.324685	3.356076	4.061706	10.577345	hypothetical protein CAA
C300450CA	133.164581	160.581467	263.829895	222.873016	mitochondrial 54S riboso
C300470WA	16.235275	15.111834	24.242216	24.598259	hypothetical protein CAA
C300500CA	19.290951	15.134402	30.501108	25.859875	mRNA splicing protein
C300510WA	10.99784	10.998219	12.040874	17.306921	hypothetical protein CAA
C300520WA	28.092083	28.221983	48.382713	63.263878	NEDD8-conjugating prot
C300530CA	9.298385	11.125443	32.143703	21.642458	nuclear distribution prote
C300570CA	28.729244	26.707767	53.251892	48.174892	dullard-like phosphatase
C300590WA	0.070445	0.285381	0.058678	0.123802	conserved hypothetical p
C300610WA	28.270149	28.630703	36.628468	34.73748	Golgi transport complex
C300620CA	227.102905	248.369049	367.785858	352.307953	hypothetical protein CAA
C300630WA	18.885254	18.788675	18.485743	21.105577	hypothetical protein MGM
C300640WA	76.908615	88.235466	39.106255	39.618111	hypothetical protein CAA
C300660WA	5.463698	5.615449	7.529497	12.416956	U2 snRNP complex subu
C300680CA	8.572983	8.947801	16.930134	6.228626	hypothetical protein MG1
C300730WA	18.510426	23.95915	26.644566	26.675297	hypothetical protein CAA
C300790WA	5.43909	6.766424	9.402853	7.575387	serine/threonine protein
C300830CA	10.168637	11.715267	42.96154	40.179825	DNA ligase (ATP)
C300840CA	35.419662	39.179306	154.124573	107.729744	hypothetical protein CAA
C300850CA	145.763626	149.389923	107.766411	113.722069	hypothetical protein W5C
C300890CA	7.565093	8.767962	14.949156	17.699627	hypothetical protein CAA

C300910WA	7.011737	6.073602	9.137368	5.885056	hypothetical protein CAA
C300940WA	52.465199	59.75967	57.439453	48.000179	hypothetical protein I503
C300950CA	11.920122	7.674965	22.933292	25.569233	peptidylprolyl isomerase
C300960WA	10.428068	9.017587	26.912893	19.263624	hypothetical protein CAA
C300990CA	0.125691	0.389259	1.086808	0.191433	hypothetical protein CAA
C301020WA	40.378174	40.459484	35.336227	40.184837	hypothetical protein CAA
C301050CA	0.041211	0.06601	0.067737	0.060892	hypothetical protein CAA
C301060WA	11.281264	17.020329	8.447032	9.538957	hypothetical protein CAA
C301070CA	4.559079	2.9689	9.101381	8.678012	hypothetical protein CAA
C301090WA	97.687187	97.351471	156.044708	156.680298	hypothetical protein CAA
C301100WA	11.677631	13.891496	53.646549	79.19413	hypothetical protein CAA
C301110CA	1.170923	1.470728	2.19308	2.084845	hypothetical protein CAA
C301120WA	10.686116	19.516558	22.499273	14.247299	hypothetical protein CAA
C301130CA	120.890816	133.872284	59.395687	63.402588	hypothetical protein CAA
C301140WA	20.007664	17.551645	32.034637	25.025396	hypothetical protein CAA
C301150CA	85.831512	127.228615	46.362846	39.853008	hypothetical protein CAA
C301170WA	40.116451	35.387466	47.828293	43.870068	hypothetical protein CAA
C301180CA	9.574441	8.073189	7.909422	9.101501	hypothetical protein CAA
C301190CA	23.7946	26.061745	31.905405	34.838692	hypothetical protein CAA
C301210CA	48.52726	51.30864	92.079308	92.781036	hypothetical protein CAA
C301220WA	18.44861	15.517512	31.491064	30.270149	hypothetical protein CAA
C301230CA	2.880965	15.301	7.095514	9.962758	hypothetical protein CAA
C301260CA	26.86014	23.923033	34.831421	38.552307	hypothetical protein L15
C301280WA	41.209366	40.529629	38.179905	37.873199	hypothetical protein CAA
C301310WA	2.552591	3.303536	6.68285	10.232302	putative ATPase
C301340WA	5.387969	3.70394	6.883725	8.373399	hypothetical protein ME
C301420CA	161.355301	144.25058	104.21627	93.53289	hypothetical protein CAA
C301430WA	34.803696	39.573963	12.988969	21.537849	hypothetical protein CAA
C301440CA	7.735427	13.364535	20.413351	17.989544	hypothetical protein ME
C301510WA	11.977913	14.120575	24.504179	29.401165	hypothetical protein MG
C301520CA	52.615517	58.333344	44.797375	38.286736	hypothetical protein CAA
C301540WA	43.454563	39.310204	6.803884	15.062071	hypothetical protein CAA
C301560WA	48.922935	57.110081	32.647327	30.289654	pre-mRNA-splicing facto
C301570WA	4.085977	5.101663	7.063722	9.004272	hypothetical protein CAA
C301590WA	11.256661	8.952362	16.070368	18.952301	hypothetical protein CAA
C301610WA	192.625717	188.249359	293.909485	265.31839	hypothetical protein CAA
C301620WA	12.032139	7.190255	23.15456	20.384556	hypothetical protein CAA
C301640CA	0.48797	0.752833	0.666866	0.520848	hypothetical protein CAA
C301660WA	53.832981	50.813511	34.253006	34.583702	hypothetical protein CAA
C301670WA	62.007881	68.611221	39.59766	44.457436	hypothetical protein CAA
C301680CA	22.026321	21.815435	20.037392	24.061575	hypothetical protein CAA
C301690WA	28.46715	20.922737	26.022203	33.304825	hypothetical protein CAA
C301720CA	38.536312	40.601021	74.722168	81.103371	coatomer subunit alpha
C301740CA	1297.739258	1509.293701	195.933334	197.892593	hypothetical protein CAA
C301770CA	13.03012	13.989016	12.092941	14.846392	hypothetical protein CAA
C301780CA	21.142	13.211711	56.976978	39.30743	hypothetical protein CAA
C301790CA	4.48545	4.182348	7.126918	7.934707	hypothetical protein CAA
C301800CA	34.017452	25.251581	29.290916	38.077374	hypothetical protein ME
C301820WA	6.412635	5.065463	4.535545	5.775184	hypothetical protein CAA
C301850WA	74.987495	77.963554	64.252342	58.040016	mitochondrial 37S ribos
C301890CA	172.111313	178.430161	286.994843	291.187592	hypothetical protein CAA
C301900CA	10.641693	11.503553	8.82916	10.581589	hypothetical protein CAA
C301910CA	551.127136	475.48233	787.192993	878.447144	hypothetical protein CAA
C301940CA	26.193651	41.508949	46.275547	56.193108	hypothetical protein CAA
C301950CA	41.263111	42.836288	103.645172	111.551346	hypothetical protein CAA
C301970CA	10.713408	10.218214	1.838193	4.322643	hypothetical protein CAA
C302010CA	2.050196	2.033608	3.435241	1.687425	hypothetical protein CAA
C302020WA	44.192116	51.060959	28.87575	17.752954	RNA-binding ribosome b
C302030WA	38.564091	43.752377	77.159645	76.515945	rhomboid protease
C302040CA	132.400345	142.001923	68.425865	52.557827	hypothetical protein CAA
C302060WA	2.579318	1.329922	0.725592	0.17771	hypothetical protein CAA
C302070CA	1.605171	0.999623	0.777277	0.864063	hypothetical protein CAA
C302080WA	6.072533	4.020344	5.683078	5.359536	hypothetical protein CAA
C302090CA	23.207134	20.014778	45.72826	36.468197	hypothetical protein CAA

C302120WA	23.576307	21.659391	51.341011	51.816765	hypothetical protein CAA
C302140CA	29.64625	30.903296	25.968351	25.063986	hypothetical protein CAA
C302160CA	40.351341	36.176556	57.978271	64.790466	hypothetical protein MG
C302180CA	49.280155	58.60717	45.328407	34.258083	deoxyhypusine synthase
C302190CA	217.415222	243.506836	306.603333	334.278442	hypothetical protein CAA
C302200WA	1.33893	3.50045	13.760284	8.257058	hypothetical protein CAA
C302210CA	10.74731	12.270169	21.384439	22.79781	hypothetical protein CAA
C302250CA	0	0	1.835	2.620216	hypothetical protein CAA
C302260CA	41.684597	39.937965	53.7314	47.139545	cyclin-dependent serine/
C302270WA	112.022408	121.051765	138.687119	130.549942	hypothetical protein CAA
C302290WA	34.590057	44.596104	127.024323	133.169205	hypothetical protein CAA
C302330CA	9.076777	7.514787	7.690098	12.916804	hypothetical protein CAA
C302340WA	4.339838	2.302394	7.029352	5.406509	hypothetical protein CAA
C302350WA	54.463615	53.714954	38.676296	35.934345	protein KRI1
C302360CA	3.918977	4.696203	5.365604	7.484057	hypothetical protein CAA
C302390WA	4.397846	4.904047	6.571198	7.153491	hypothetical protein CAA
C302410CA	14.704853	14.072238	34.435596	39.904251	ubiquitin-protein ligase
C302490CA	23.658686	24.72333	47.033623	47.434063	RSC chromatin remodeli
C302530WA	42.668804	52.298599	91.175232	74.46196	hypothetical protein CAA
C302570WA	7.114484	6.106661	5.707374	6.108389	putative metalloendopep
C302580CA	9.105532	10.208529	33.976608	24.339966	hypothetical protein CAA
C302620CA	31.818581	42.114971	47.016033	41.511868	pyruvate transporter
C302630CA	11.893305	12.021894	14.727011	10.760906	hypothetical protein CAA
C302660WA	5.824061	6.425661	5.373936	6.144495	hypothetical protein I503
C302670WA	19.011093	15.542508	25.159582	21.357519	hypothetical protein CAA
C302690CA	27.026649	30.707825	39.644283	44.513123	dolichol kinase
C302710WA	3709.116699	3556.87207	1500.50647	1795.888428	--
C302720WA	8.203917	15.499803	28.719906	33.689968	hypothetical protein CAA
C302750WA	3.287202	1.876534	1.304501	1.417344	hypothetical protein CAA
C302760CA	11.870712	10.851682	24.595751	21.151972	hypothetical protein CAA
C302770CA	12.411417	7.547621	20.471733	20.677353	hypothetical protein CAA
C302790WA	295.025665	333.479736	497.361298	395.156555	hypothetical protein CAA
C302820CA	46.964962	40.597778	70.537674	70.94725	hypothetical protein CAA
C302840WA	13.957541	13.513332	14.141222	19.457359	ribonuclease P/MRP pro
C302850CA	11.624181	11.781471	13.327964	16.412197	alcohol O-acetyltransfera
C302870CA	15.205332	16.031948	13.9131	15.32708	hypothetical protein CAA
C302880WA	9.081757	6.112245	3.675879	13.6561	D-tyrosyl-tRNA(Tyr) dea
C302890CA	34.096203	26.880806	28.952557	22.796917	hypothetical protein MG5
C302900WA	13.178008	12.463077	17.281853	13.355147	hypothetical protein CAA
C302910WA	47.903633	46.875935	60.107197	36.816891	hypothetical protein CAA
C302920WA	345.388245	391.316742	265.998535	228.19281	phosphatase regulator
C302930WA	11.342147	7.185056	23.820045	19.415726	hypothetical protein CAA
C302970CA	24.750053	31.578123	42.514565	36.460484	metalloendopeptidase
C302980CA	46.166569	48.348778	59.35741	39.528152	hypothetical protein CAA
C302990CA	13.095345	12.6954	17.281853	12.792555	hypothetical protein CAA
C303000WA	33.968407	26.546883	29.107019	22.35844	hypothetical protein MG5
C303020WA	3.261481	1.974023	1.072446	1.614089	hypothetical protein CAA
C303060WA	14.994823	10.181889	43.889481	39.774231	TRAPP subunit
C303070WA	16.002329	16.808397	31.782785	27.075853	hypothetical protein CAA
C303080WA	16.098448	18.658789	37.574661	43.218304	hypothetical protein CAA
C303100CA	45.725212	46.234921	71.768326	75.451164	hypothetical protein CAA
C303110WA	11.752359	10.483793	17.591663	18.963476	hypothetical protein CAA
C303130CA	4.708903	7.107379	3.646459	3.599363	hypothetical protein CAA
C303150WA	11.272591	10.905777	21.756031	22.07019	hypothetical protein CAA
C303160CA	24.825787	13.950723	51.212154	50.144741	hypothetical protein I503
C303190CA	24.314156	23.758211	26.249735	27.983198	hypothetical protein CAA
C303200CA	10.7478	19.407633	41.961773	31.189339	hypothetical protein CAA
C303210WA	31.083609	37.855892	131.466644	149.998993	hypothetical protein CAA
C303230CA	8.174725	11.804532	26.256142	23.089661	hypothetical protein CAA
C303250WA	8.40714	8.066283	11.498142	10.230204	hypothetical protein CAA
C303260WA	18.548141	19.550159	36.854355	33.903915	cleavage polyadenylatio
C303270WA	16.199665	9.746634	82.296738	67.37442	hypothetical protein CAA
C303300CA	60.25145	57.856056	54.609268	56.415291	branchpoint-bridging pro
C303310CA	11.659495	11.789273	30.471439	38.522411	hypothetical protein I503

C303330CA	12.653769	15.08954	21.141468	20.909098	hypothetical protein CAA
C303340CA	205.872498	178.914078	314.299225	296.952759	hypothetical protein CAA
C303370CA	1738.004272	2048.273926	864.604248	888.28833	hypothetical protein MG
C303380WA	4.265283	6.643098	11.052527	10.936952	hypothetical protein CAA
C303410CA	83.628647	94.941856	38.323189	40.901798	hypothetical protein CAA
C303430CA	11.663243	8.043928	19.21191	20.108202	ESCRT-I subunit protein
C303440CA	14.124852	11.176397	8.407474	15.159046	hypothetical protein CAA
C303460CA	10.594503	6.827507	3.852519	4.798694	hypothetical protein CAA
C303470WA	3.751019	6.414454	3.206766	4.275469	succinate-semialdehyde
C303510CA	6.70957	6.743874	10.50175	15.393453	hypothetical protein MG
C303530WA	12.959638	11.691867	20.871624	20.379843	hypothetical protein CAA
C303540WA	33.410225	37.184437	36.845051	43.439098	hypothetical protein CAA
C303560WA	9.75437	10.288755	10.593023	16.767553	aminopeptidase
C303570CA	0	0.386233	0.763983	0.615845	hypothetical protein CAA
C303590WA	93.04631	102.981979	205.651627	162.963028	prohibitin subunit
C303670WA	43.866383	47.096233	25.799145	27.591982	hypothetical protein CAA
C303680WA	34.141762	32.540707	50.057087	52.818684	sphinganine-1-phosphat
C303690WA	6.272196	6.464891	6.501206	5.463761	hypothetical protein ME
C303740WA	54.943817	64.073563	136.489609	139.000092	hypothetical protein L15
C303760WA	50.768124	49.2271	10.222225	11.631067	diacylglycerol O-acyltran
C303770CA	86.625687	83.705681	90.406593	96.474884	hypothetical protein CAA
C303780WA	18.548931	17.507772	18.130123	18.25038	hypothetical protein CAA
C303820CA	19.381544	28.465363	56.650917	61.46526	hypothetical protein ME
C303830WA	15.292484	21.121103	26.382328	18.889803	serine/threonine-protein
C303840CA	33.002831	29.637074	33.624519	40.548893	cleavage polyadenylatio
C303860WA	31.54813	33.681492	51.332973	56.342323	Mg-dependent acid phos
C303920WA	88.482407	68.404793	140.492371	107.135513	hypothetical protein CAA
C303930WA	26.454439	30.405792	85.207817	52.421928	hypothetical protein CAA
C303980CA	1.292826	2.609273	0.256763	1.139527	hypothetical protein MG
C304080WA	334.993103	340.300354	374.928741	446.277252	ubiquinol-cytochrome c
C304100WA	9.417645	6.563766	11.23679	10.970359	hypothetical protein CAA
C304120CA	12.55963	12.089028	16.504757	16.702827	hypothetical protein CAA
C304130WA	28.725983	28.553486	26.028015	25.527081	hypothetical protein MG
C304170WA	4.538118	0.879098	6.182562	5.437395	hypothetical protein CAA
C304190WA	17.229486	18.280529	14.134024	17.035843	hypothetical protein CAA
C304210WA	105.084648	69.88205	3.199111	0.985496	hypothetical protein CAA
C304230WA	7.222262	8.845321	15.391102	15.082134	pre-mRNA-splicing facto
C304260WA	73.232101	66.51049	46.238613	53.422241	hypothetical protein CAA
C304310CA	0.431043	0	0	0	hypothetical protein CAA
C304330CA	226.959335	219.963867	331.387451	310.613556	hypothetical protein CAA
C304350CA	6.856622	6.141711	7.871259	12.585411	hypothetical protein CAA
C304360WA	8.163863	6.333912	16.483156	15.939706	hypothetical protein CAA
C304370CA	10.759917	13.644866	17.616287	17.01932	hypothetical protein CAA
C304380CA	664.132568	662.991028	579.372192	556.705688	RNA binding protein
C304410CA	25.253077	25.712078	29.70265	30.783108	hypothetical protein CAA
C304420WA	9.774528	12.263031	22.741219	22.92041	putative E3 ubiquitin-pro
C304440CA	2.375178	2.803431	2.18087	2.228551	hypothetical protein CAA
C304450CA	0.469219	1.271552	4.406641	3.560367	hypothetical protein CAA
C304460WA	12.426239	14.029433	23.722736	21.833509	hypothetical protein CAA
C304510WA	86.671341	73.997459	67.16217	56.794769	hypothetical protein CAA
C304540CA	22.270761	18.756109	29.040937	25.080652	hypothetical protein CAA
C304590WA	216.195816	246.461105	461.456879	479.087189	THO complex subunit 4
C304620CA	63.446541	81.104599	170.845932	173.808578	hypothetical protein CAA
C304630WA	32.056499	38.813213	21.173477	19.231306	hypothetical protein CAA
C304650WA	7.801419	10.270465	8.742875	6.761837	hypothetical protein CAA
C304690CA	11.343241	16.405041	35.041492	44.455868	hypothetical protein CAA
C304700WA	21.525795	24.170839	39.959415	38.555042	FG-nucleoporin
C304720CA	24.483217	23.583326	15.131814	16.307703	hypothetical protein CAA
C304730CA	27.481646	33.02776	182.061203	251.260956	hypothetical protein CAA
C304740CA	6.832522	7.781382	35.910057	36.148495	DNA topoisomerase 3
C304750WA	9.892145	12.867864	16.755379	19.233578	hypothetical protein CAA
C304780CA	54.197197	61.31662	73.420776	85.300636	hypothetical protein CAA
C304790WA	7.57513	7.760472	8.456552	8.602437	hypothetical protein CAA
C304800CA	14.492127	15.921165	20.421215	16.388287	hypothetical protein W5

C304810CA	615.890442	675.221558	716.182007	730.889465	hypothetical protein MG5
C304840CA	11.022091	11.683416	29.898926	34.827599	hypothetical protein CAA
C304870WA	0.559713	1.139827	0.610021	0.491969	meiosis-specific APC/C
C304920CA	235.842072	212.001678	172.391983	168.632477	hypothetical protein CAA
C304940WA	74.736481	86.158661	59.318741	70.694435	ditrans,polycis-polypreny
C304970CA	10.734004	13.019208	28.046732	27.967339	ubiquitin-ubiquitin ligase
C305010CA	6.366401	6.492164	16.915836	14.411533	DNA helicase II/ATP-de
C305020WA	5.118421	6.994989	9.158595	7.169916	hypothetical protein CAA
C305060WA	12.635964	12.19072	16.231401	15.033511	hypothetical protein CAA
C305080WA	1.819121	2.495688	3.738877	4.644334	hypothetical protein CAA
C305090CA	5.775936	7.135078	12.443936	15.588126	hypothetical protein CAA
C305110WA	17.888109	11.850746	19.762455	32.69698	hypothetical protein CAA
C305120CA	42.832893	29.671329	78.805267	87.308296	tubulin-binding prefoldin
C305140CA	28.305641	23.503094	17.515875	26.068089	tRNA (guanine-N2-)-met
C305150WA	49.035233	52.237541	102.83416	99.022369	hypothetical protein CAA
C305160CA	75.157623	72.909943	32.346146	35.289688	putative ATP-dependent
C305250CA	13.686925	15.94609	9.931934	12.692609	hypothetical protein CAA
C305280CA	28.809942	31.596764	28.026379	31.927681	hypothetical protein CAA
C305290CA	5.980881	6.521325	25.529583	40.104549	hypothetical protein CAA
C305300CA	7.811736	8.656866	7.81362	10.4922	bifunctional choline kina
C305320WA	36.304115	38.754574	8.511303	8.52343	hypothetical protein CAA
C305330CA	2.439039	1.783365	2.636355	5.172041	hypothetical protein CAA
C305360CA	27.616352	28.153032	27.174217	26.06694	hypothetical protein CAA
C305380WA	9.112461	10.015288	6.027304	7.33994	hypothetical protein MEK
C305400CA	9.455766	15.980973	12.772965	16.256699	hypothetical protein MG7
C305410WA	70.501839	61.772102	30.687151	29.834824	hypothetical protein CAA
C305420WA	8.692657	11.032386	12.73893	13.199553	hypothetical protein ME
C305430WA	9.914089	11.844569	20.389622	23.079271	hypothetical protein ME
C305440CA	7.74985	8.829553	19.505951	17.166985	hypothetical protein CAA
C305450CA	235.085541	254.038376	19.060881	24.044256	hypothetical protein CAA
C305460WA	10.537395	11.563514	7.496763	10.410586	conserved hypothetical
C305510WA	6.110732	5.142806	7.928807	11.745025	hypothetical protein CAA
C305540CA	12.142218	13.082387	27.488295	23.674973	hypothetical protein CAA
C305550CA	26.684572	28.284517	18.102921	23.874825	peptidyl-prolyl cis-trans i
C305640WA	0.750303	0.119839	0.796696	0.470312	hypothetical protein CAA
C305660CA	0	0.199237	0.267186	0.526108	hypothetical protein CAA
C305680WA	18.161427	17.694668	39.542118	31.655027	E2 ubiquitin-conjugating
C305750CA	37.87822	57.138035	5.840222	6.747561	hypothetical protein CAA
C305760WA	69.722054	89.159195	34.900555	35.419647	phosphopantothenate--c
C305790CA	7.714013	7.520469	27.480614	33.420357	SAGA histone acetyltran
C305800WA	11.152519	13.309194	5.958787	10.961664	tRNA splicing endonucle
C305840WA	0.278566	0.435213	0.680517	0.36663	hypothetical protein CAA
C305850WA	12.334064	10.360492	21.700226	14.316501	protein FYV10
C305860CA	21.960192	30.300716	26.466419	18.758369	hypothetical protein MG
C305880CA	45.791229	48.421543	78.964996	87.710373	nucleolysin TIA-1/TIAR
C305900WA	82.06649	104.75106	29.302547	26.798567	cationic amino acid trans
C305940CA	11.166967	11.198344	24.170593	24.336725	hypothetical protein CAA
C305950WA	9.56116	5.568648	10.190711	10.290898	hypothetical protein CAA
C305970CA	30.219814	30.800903	45.481285	49.322392	hypothetical protein MG1
C305990CA	6.553189	3.620459	7.713054	10.414887	hypothetical protein CAA
C306040WA	6.600371	7.64769	0.215633	0	hypothetical protein CAA
C306050CA	66.781441	54.384712	96.514435	128.524567	hypothetical protein CAA
C306110CA	28.976757	30.084627	21.85841	21.971642	NADH/NAD(+) kinase
C306140WA	8.780217	8.050089	6.73384	6.837533	hypothetical protein CAA
C306150WA	8.017007	8.12609	11.237303	12.769216	hypothetical protein ME
C306160CA	136.764206	140.532104	48.169483	43.217785	rRNA-processing protein
C306170CA	10.206203	14.997387	27.592155	19.498915	hypothetical protein CAA
C306240CA	53.583881	51.20092	124.284683	144.96199	mitochondrial 54S ribos
C306260CA	9.438124	10.051373	16.856333	17.412086	hypothetical protein CAA
C306270CA	56.504154	76.608299	52.612026	50.388523	hypothetical protein CAA
C306280WA	56.603233	71.50119	66.80265	48.770962	L-serine/L-threonine am
C306290WA	37.913017	42.30238	40.49543	42.564999	hypothetical protein CAA
C306350WA	12.910951	19.873247	36.067108	25.719494	hypothetical protein MGI
C306370CA	80.408623	86.505836	35.072273	30.921844	U3 small nucleolar ribon

C306390WA	4.95617	3.435145	1.656345	44.834755	hypothetical protein CAA
C306400CA	11.036049	14.18201	18.526321	19.492781	uracil-DNA glycosylase
C306410CA	22.854067	23.922678	30.818087	34.160088	hypothetical protein L15
C306420CA	90.639236	112.583443	63.228321	63.306808	hypothetical protein CAA
C306440WA	73.825302	70.57032	89.442741	85.031937	nuclear pore complex pr
C306490WA	20.36223	19.410168	27.849358	20.344635	acetyltransferase
C306520CA	12.397371	11.619782	29.182884	19.637146	hypothetical protein CAA
C306530WA	11.329836	9.602509	20.676657	15.275883	hypothetical protein MG
C306540CA	12.85428	14.683267	34.302666	44.411774	hypothetical protein CAA
C306550CA	38.798927	44.474762	24.241833	26.655634	TFIIH complex subunit
C306560WA	314.020325	305.854614	195.859894	175.924774	hypothetical protein MG1
C306600CA	3.895477	4.524963	3.767439	8.499318	hypothetical protein CAA
C306610WA	33.621075	29.928194	69.91082	70.028282	hypothetical protein CAA
C306630WA	2.241807	1.738481	5.628772	6.964898	hypothetical protein CAA
C306640WA	6.146518	8.534396	8.471601	14.424065	hypothetical protein CAA
C306660CA	2.232487	5.81328	4.556662	2.920607	hypothetical protein CAA
C306670CA	8.990224	9.436172	11.675332	15.296789	hypothetical protein CAA
C306680CA	26.611469	23.420992	106.890167	103.768204	conserved hypothetical p
C306690CA	48.582016	59.716789	146.370392	154.455582	hypothetical protein ME
C306700CA	434.800323	483.148285	118.395363	114.075867	hypothetical protein CAA
C306710WA	11.793335	11.0794	8.277424	9.305712	hypothetical protein CAA
C306730WA	27.359083	18.903168	21.456446	21.315603	hypothetical protein CAA
C306740WA	16.62779	19.388643	11.381434	10.395753	hypothetical protein CAA
C306750WA	136.3181	127.868996	325.232239	318.82431	translocon subunit
C306760WA	95.721481	88.236328	55.288597	58.155052	ribosomal RNA-processi
C306800CA	13.116155	13.589405	27.727119	25.323378	NEDD8 ligase
C306810WA	9.737316	8.99449	24.724472	28.166613	anaphase promoting co
C306820CA	70.121178	69.80394	114.264221	113.048889	hypothetical protein CAA
C306830CA	9.492978	9.757708	10.146337	12.538086	putative helicase
C306860CA	41.007969	43.691669	29.783253	21.536968	aldo-keto reductase sup
C306880WA	0.903108	2.703978	15.76915	17.377142	hypothetical protein CAA
C306920WA	38.452496	31.194157	57.556999	53.780102	putative phosphomutase
C306940WA	119.441307	115.147408	120.94561	109.544846	hypothetical protein CAA
C306950WA	40.443279	43.14003	12.323473	13.404843	hypothetical protein MG1
C306970WA	16.992907	24.529064	23.524416	28.42325	signal recognition particl
C306990WA	5.478111	8.377037	9.669807	10.677842	palmitoyltransferase
C307030CA	6.162876	5.166025	9.85697	6.051639	hypothetical protein CAA
C307050WA	21.350632	17.939856	26.339561	28.383316	hypothetical protein CAA
C307070CA	42.398476	39.815727	18.599422	17.012468	hypothetical protein CAA
C307100CA	13.84218	16.743906	12.842623	17.843733	hypothetical protein CAA
C307110WA	4.228071	4.726148	13.951875	15.413422	hypothetical protein CAA
C307120WA	10.712153	7.991117	11.51028	14.167345	hypothetical protein MG5
C307130WA	77.249092	91.485313	141.575851	135.883423	cornichon family protein
C307140CA	4.148164	5.836868	21.569532	22.456533	hypothetical protein CAA
C307170CA	68.007057	69.510468	51.121727	53.818359	GTPase-activating prote
C307230WA	20.536699	20.13588	22.285902	21.621956	aminophospholipid-trans
C307240WA	2.619764	1.991865	7.232457	11.033927	hypothetical protein CAA
C307280CA	45.013229	39.214039	114.918167	131.634644	hypothetical protein ME
C307290WA	35.090633	40.852417	11.747509	13.793872	hypothetical protein CAA
C307330WA	7.337017	5.462258	11.317303	11.297011	hypothetical protein ME
C307350WA	74.800552	84.965286	79.567459	82.984932	hypothetical protein ME
C307370WA	139.525009	117.165154	90.365028	84.590347	hypothetical protein CAA
C307380WA	76.867584	56.110294	62.300655	39.571846	hypothetical protein CAA
C307390CA	84.393272	77.343254	150.273819	132.562805	mitochondrial 37S ribos
C307400WA	54.150982	58.296101	46.038857	42.343395	tRNA methyltransferase
C307420WA	135.645416	151.503067	130.729782	127.61248	hypothetical protein CAA
C307430WA	22.581192	26.362066	37.586037	34.956173	acid phosphatase
C307450CA	16.54414	20.51228	11.727325	19.054888	putative endodeoxyribon
C307460WA	15.499718	13.184693	54.666737	42.679272	FCP1-like phosphatase,
C307470WA	37.672195	40.336624	23.228191	34.337566	hypothetical protein ME
C307480WA	19.229376	23.199301	40.404167	42.627186	pre-mRNA-processing fa
C307490WA	48.635567	54.022247	53.573059	42.161381	phosphoribomutase
C307540CA	37.209892	31.536406	136.00296	185.044586	hypothetical protein CAA
C307550CA	24.883654	25.71203	30.435667	32.949005	hypothetical protein CAA

C307570CA	36.530403	43.885769	98.803329	87.44117	hypothetical protein CAA
C307580WA	125.025459	125.986053	268.624908	169.009354	hypothetical protein CAA
C307590WA	31.036467	35.261799	35.037663	30.57205	hypothetical protein CAA
C307600WA	56.417297	44.73156	39.873184	40.35091	hypothetical protein ME
C307630CA	31.165913	36.272114	39.938122	34.980747	hypothetical protein CAA
C307650CA	7.258827	9.046288	7.171201	11.191168	hypothetical protein CAA
C307660WA	9.933199	8.941719	14.632852	16.797712	hypothetical protein CAA
C307670WA	753.604004	574.177185	80.751556	72.527893	hypothetical protein CAA
C307680WA	12.787794	15.407188	25.65369	30.648886	hypothetical protein CAA
C307690CA	82.569862	85.605469	76.285309	76.698135	hypothetical protein CAA
C307700WA	62.877499	55.981262	61.879234	45.587547	putative serine hydrolase
C307740WA	42.402611	40.391331	86.336716	88.056229	hypothetical protein CAA
C307760CA	34.946136	37.322716	39.93301	43.905418	hypothetical protein CAA
C307770CA	13.220123	16.443007	27.681778	28.666822	hypothetical protein CAA
C307800CA	63.986977	81.454193	63.276154	72.613213	hypothetical protein ME
C307820WA	104.835716	81.102745	138.376495	91.449425	hypothetical protein CAA
C307840CA	1.620005	0	0	0	fructose 1,6-bisphospha
C307850WA	30.314222	28.054901	31.976908	21.503933	hypothetical protein CAA
C307880CA	39.978134	20.516373	57.602779	58.757088	hypothetical protein CAA
C307900CA	43.854671	37.082878	48.720467	39.142654	hypothetical protein CAA
C307910WA	5.032089	4.416678	5.232362	4.847691	hypothetical protein CAA
C307920WA	36.347466	37.032494	53.17524	26.335262	hypothetical protein CAA
C307940WA	62.190197	76.308853	72.692833	59.73848	hypothetical protein CAA
C400020WA	124.23275	108.621002	187.463242	189.08519	H(+)-transporting V0 se
C400030CA	47.013752	46.443913	54.352013	36.38826	hypothetical protein CAA
C400050WA	31.208345	32.953537	82.549591	83.76265	hypothetical protein CAA
C400060WA	36.153168	23.779337	34.371189	20.108124	gamma-glutamylcyclotra
C400070CA	107.805054	117.493919	128.78093	90.067863	putative zinc metalloprot
C400080CA	108.836853	89.020599	35.654709	28.581528	hypothetical protein CAA
C400100CA	36.17609	37.074501	19.166567	14.163536	hypothetical protein CAA
C400170WA	569.765564	550.391602	1110.056641	860.712402	hypothetical protein CAA
C400190WA	6.219852	6.516798	5.645149	11.70719	hypothetical protein CAA
C400210WA	5.934891	3.409748	30.806324	24.217548	hypothetical protein CAA
C400230WA	21.109161	23.433855	25.51129	15.377414	hypothetical protein CAA
C400250WA	11.851908	7.946636	3.276453	5.383115	hypothetical protein CAA
C400260WA	64.959373	68.843262	59.536617	47.097404	histone demethylase
C400290CA	6.690939	5.065523	4.405305	4.14124	hypothetical protein CAA
C400320CA	21.598726	22.284027	35.006737	41.885571	ubiquitin-protein ligase
C400330CA	422.010986	411.660126	695.206238	663.992432	F1F0 ATP synthase sub
C400380WA	17.684105	16.417501	19.636374	17.349951	D-arabinose 1-dehydrog
C400390WA	78.699585	63.323902	144.986191	119.575333	chromatin-binding trans
C400410WA	77.584236	87.61438	95.120857	84.542618	hypothetical protein CAA
C400420CA	47.731239	53.04747	94.539719	102.839233	conserved hypothetical
C400460CA	21.984039	24.808952	28.771397	31.583624	translocase
C400470CA	18.023443	19.607546	34.770283	32.918621	hypothetical protein CAA
C400490WA	12.574435	11.035933	10.193992	9.412279	hypothetical protein CAA
C400500WA	4.558387	6.402477	12.95451	13.894986	ubiquitin-ubiquitin ligase
C400530CA	17.741871	16.353548	2.472281	1.787422	hypothetical protein CAA
C400560CA	33.792046	43.63036	55.659081	40.914181	ERMES complex subuni
C400580WA	13.402044	11.092277	30.312103	32.724327	phosphatase
C400590CA	43.082767	34.615585	28.860302	37.496372	hypothetical protein CAA
C400610WA	13.803654	17.089499	26.910215	22.950979	hypothetical protein CAA
C400640WA	0.283296	1.717449	0	1.910756	hypothetical protein CAA
C400660WA	115.11673	115.878532	152.654099	168.900925	mitochondrial 37S ribos
C400680WA	41.427204	41.044666	21.111656	26.978062	nucleoside transmembra
C400690CA	12.887384	14.216837	14.450992	12.119135	hypothetical protein CAA
C400700CA	13.920409	21.510656	15.903744	19.957209	phosphoglycolate/pyrido
C400710WA	8.124225	10.710226	12.175615	14.940648	hypothetical protein CAA
C400730CA	3.660945	5.42552	10.577484	11.649499	hypothetical protein MG
C400740WA	27.602882	14.49143	43.376057	40.20863	ribonuclease P/MRP pro
C400750CA	5.093997	8.428333	5.656319	3.146425	hypothetical protein CAA
C400770CA	32.702118	46.562008	66.313889	55.344517	hypothetical protein CAA
C400780CA	14.974593	15.797848	19.851595	22.87718	hypothetical protein CAA
C400800WA	9.995094	10.883469	15.600682	15.444353	hypothetical protein ME

C400810CA	13.924547	18.587706	9.709852	16.41152	putative N(6)-L-threonylc
C400820WA	9.9954	12.348725	26.627781	29.422935	hypothetical protein CAA
C400840WA	18.429823	13.911633	30.61174	33.084602	hypothetical protein CAA
C400850CA	1.613993	1.627296	4.94499	3.153334	hypothetical protein CAA
C400860CA	166.871841	174.6763	452.592346	361.857483	hypothetical protein CAA
C400880WA	16.541929	15.53704	27.737331	27.279896	tRNA adenylyltransferas
C400910CA	11.950396	12.627267	40.035843	46.110806	hypothetical protein CAA
C400920CA	5.185499	6.209583	24.3624	26.417358	hypothetical protein MEV
C400940WA	10.199306	12.17629	12.549255	5.709033	Elongator subunit
C400950CA	15.108274	17.407791	11.380243	14.473395	TAG lipase/lysophospha
C400990WA	0.290793	0.497829	0	0.126758	hypothetical protein CAA
C401020CA	14.57053	17.48632	24.369648	25.437265	hypothetical protein MG(
C401090CA	5.807212	8.772689	7.284543	8.616261	hypothetical protein CAA
C401120CA	15.68816	12.408545	20.249817	14.376857	putative lipase
C401130CA	13.482916	10.954996	19.693085	21.406776	hypothetical protein CAA
C401140CA	22.113304	22.736368	100.699966	105.034782	hypothetical protein MG1
C401220CA	6.490996	8.476882	1.780812	3.221325	hypothetical protein CAA
C401230CA	62.072472	55.191673	33.176479	33.255695	hypothetical protein CAA
C401240CA	40.43499	36.094284	46.51329	27.883934	hypothetical protein CAA
C401280CA	36.863495	47.849312	30.028969	30.882448	hypothetical protein CAA
C401290WA	57.172329	56.338097	22.614847	25.948288	hypothetical protein CAA
C401300WA	66.349045	79.911499	31.70928	37.935604	Nem1-Spo7 phosphatas
C401310WA	6.748805	6.896631	4.542621	4.215604	hypothetical protein MG3
C401340WA	1.4414	3.848452	0	0.770224	hypothetical protein CAA
C401420WA	4.732376	4.920405	10.772797	10.643882	hypothetical protein CAA
C401430CA	14.689814	11.150063	16.30114	22.514551	hypothetical protein CAA
C401460CA	36.651058	43.64941	91.392784	75.148705	hypothetical protein CAA
C401470WA	5.034948	4.844037	6.763905	7.854784	SCF ubiquitin ligase com
C401500WA	48.22493	60.594791	25.809198	26.464159	hypothetical protein CAA
C401510WA	77.455627	85.281387	135.348053	122.137863	oxidoreductase
C401560CA	5.299284	6.115654	6.329144	5.368435	ubiquitin-ubiquitin ligase
C401650CA	29.6394	25.12516	26.219051	23.959003	protein MPE1
C401660WA	18.039917	17.844692	26.774113	28.561773	hypothetical protein CAA
C401670CA	13.162588	14.006436	11.780768	13.74915	hypothetical protein CAA
C401710CA	524.203857	508.176514	644.04541	772.991943	--
C401720CA	336.776306	315.260376	431.898712	444.855255	DNA damage-responsive
C401730CA	13.045918	20.061586	29.071835	36.32016	putative tubulin tyrosine l
C401760WA	50.993183	55.940727	71.856621	57.529926	peptide alpha-N-acetyltra
C401780CA	16.499611	18.004061	29.111292	27.145046	hypothetical protein MGI
C401790WA	5.85872	3.082753	8.015366	10.5599	autophagy protein
C401800WA	73.32943	86.55661	696.110962	577.287415	hypothetical protein CAA
C401820CA	86.127701	101.636887	111.816177	103.412071	ribose phosphate diphos
C401830CA	15.308818	17.540297	19.707609	18.325483	hypothetical protein CAA
C401840CA	96.871269	106.562027	127.722595	135.480225	hypothetical protein CAA
C401860CA	11.296674	8.064295	30.386219	27.434515	conserved hypothetical p
C401910WA	8.872837	8.257446	30.005415	29.97998	transcription factor TFIII(
C401930CA	49.923809	40.357723	32.728096	22.865812	hypothetical protein MG(
C401950WA	73.768402	68.354393	111.703827	95.410301	F-actin-capping protein s
C401960CA	26.417023	38.636974	38.609322	53.331059	hypothetical protein CAA
C401970WA	98.129539	106.323257	99.763962	78.734444	hypothetical protein CAA
C401990WA	4.953704	14.926043	17.828346	22.416239	hypothetical protein CAA
C402040WA	6.038048	9.289722	7.976307	7.548299	polyamine oxidase
C402080WA	2.962156	5.009977	4.120654	4.66971	hypothetical protein CAA
C402090CA	29.529964	37.567169	35.667698	40.652065	exosome non-catalytic c
C402100CA	2.623681	10.101297	15.056993	11.574397	glycosylphosphatidylinos
C402110WA	9.966673	15.375795	30.818142	34.453987	hypothetical protein CAA
C402150CA	5.901522	5.840044	7.860984	6.678553	hypothetical protein CAA
C402160CA	11.910358	11.653762	9.367891	14.602591	hypothetical protein CAA
C402170CA	2.860652	3.179933	1.852079	2.479872	putative hydrolase
C402190CA	1.020694	1.356752	0	0.909747	hypothetical protein CAA
C402200CA	13.867423	19.689493	30.097376	21.660658	hypothetical protein CAA
C402210WA	6.389095	5.490446	10.881577	6.001215	hypothetical protein CAA
C402230CA	5.157539	4.986727	1.463131	3.707615	hypothetical protein CAA
C402240CA	0.940027	1.409744	1.088685	0	hypothetical protein CAA

C402260CA	76.749794	64.057671	25.306118	30.004759	putative methyltransfera
C402330CA	102.48024	118.767036	7.269168	13.619206	hypothetical protein CAA
C402340WA	333.847961	366.153198	14.224027	18.503664	hypothetical protein CAA
C402400CA	4.711416	3.664244	16.917316	21.905373	hypothetical protein CAA
C402420CA	8.34916	13.839642	26.826294	32.981812	mannose-ethanolamine
C402430WA	9.281967	9.31522	15.430146	14.796331	hypothetical protein CAA
C402450WA	14.841881	15.084895	93.608528	108.358253	hypothetical protein CAA
C402460WA	37.021973	32.334805	167.774368	169.713272	hypothetical protein CAA
C402470CA	84.437782	92.764336	111.326134	119.30098	proteasome core particle
C402510WA	20.010345	22.312229	15.207626	14.539327	hypothetical protein CAA
C402520CA	11.144876	12.021711	9.903174	14.988139	hypothetical protein CAA
C402570CA	26.810865	30.030544	19.853188	17.107607	hypothetical protein CAA
C402580WA	20.398724	17.983322	29.716043	44.599331	hypothetical protein CAA
C402590CA	9.159951	6.063482	21.130278	17.22172	hypothetical protein CAA
C402600CA	20.953583	14.045792	23.075886	23.291807	hypothetical protein CAA
C402620CA	34.612923	36.870934	46.695248	38.918949	putative phosphotransfe
C402660WA	9.023378	4.454576	6.205923	5.326289	hypothetical protein CAA
C402670WA	10.556819	14.656544	25.800205	32.970272	beclin 1
C402680CA	13.417767	13.744186	38.877724	34.532677	hypothetical protein CAA
C402690WA	41.452888	40.236694	32.070946	27.304327	hypothetical protein CAA
C402700WA	3.554337	4.582612	10.642666	16.901367	hypothetical protein CAA
C402720CA	58.135624	72.993225	365.359314	369.342712	hypothetical protein CAA
C402740WA	218.024628	235.377304	47.640327	58.483578	hypothetical protein MG
C402770CA	12.294986	14.220152	15.367496	17.58539	cell proliferation protein
C402780WA	57.488995	65.481941	70.182091	60.867527	chaperonin-containing T
C402820WA	1.11554	1.111825	0.403022	0.571717	MutS family protein
C402850WA	21.752609	20.909222	22.593142	16.535288	Elongator subunit
C402860WA	46.965546	50.666046	107.212227	94.878296	hypothetical protein CAA
C402880CA	31.386679	37.266933	43.228451	35.914093	guanine nucleotide exch
C402920WA	40.26759	47.239544	57.282867	69.938347	hypothetical protein CAA
C402930WA	181.761124	174.589203	186.002441	174.848343	hypothetical protein CAA
C402950CA	32.158497	26.395575	64.644638	73.358322	hypothetical protein CAA
C402960WA	6.87316	6.693434	12.707895	14.498167	putative ubiquitin-protein
C403000CA	84.747101	69.650093	19.64653	14.749433	hypothetical protein CAA
C403020WA	107.214264	110.254395	107.580055	105.195808	dynamin-related GTPase
C403040WA	203.179199	226.553009	256.593231	245.174271	DNA-directed RNA poly
C403050CA	52.972672	49.597115	26.839508	36.502979	Gly-Xaa carboxypeptida
C403080WA	9.927543	10.655931	21.742746	19.685181	hypothetical protein CAA
C403090WA	60.673676	52.65979	50.163437	49.696941	transcription initiation fac
C403110WA	15.99856	14.059765	20.053085	23.921436	phospholipid-translocati
C403130WA	19.959538	21.515739	31.688118	34.972176	GPI-anchor transamidas
C403140CA	11.203356	15.565134	14.97125	22.234457	Elongator subunit
C403150WA	6.89889	7.692391	12.974695	15.545842	mRNA-binding U2 snRN
C403160CA	9.726987	13.15672	9.185347	12.091365	putative transcription fac
C403170WA	6.400986	11.25064	18.882282	18.626949	hypothetical protein L15
C403190WA	38.187195	45.01046	27.080061	23.195559	hypothetical protein CAA
C403200CA	39.219261	34.665943	53.920315	71.65107	hypothetical protein ME
C403230CA	7.135596	9.309109	7.756981	8.873598	hypothetical protein CAA
C403290WA	16.32299	14.607165	25.190351	29.819845	hypothetical protein CAA
C403300CA	17.99725	35.02523	20.800934	25.42193	hypothetical protein CAA
C403310CA	10.950185	14.843433	0.564866	3.342755	hypothetical protein CAA
C403320WA	39.825253	46.097679	61.91045	69.987762	hypothetical protein CAA
C403340CA	2.611807	5.874434	2.084599	3.036578	hypothetical protein CAA
C403350CA	19.430317	17.630354	13.066775	12.820455	hypothetical protein CAA
C403370CA	36.616562	56.574402	74.707794	59.955383	hypothetical protein CAA
C403400WA	135.126404	133.643204	254.021362	166.001663	hypothetical protein CAA
C403410WA	75.915436	85.079422	146.931107	136.40863	mitochondrial 54S ribos
C403460CA	23.784178	24.804308	31.707205	29.461849	hypothetical protein CAA
C403480CA	0.395899	2.181833	0	0	hypothetical protein CAA
C403490CA	7.954112	6.618701	38.950523	32.836235	hypothetical protein CAA
C403500CA	30.075991	21.284674	144.605087	129.798691	hypothetical protein CAA
C403530WA	6.213615	6.659837	11.60322	9.877348	hypothetical protein CAA
C403560WA	12.740143	9.14683	18.673117	20.360746	hypothetical protein CAA
C403580WA	12.042492	10.488654	15.759487	16.884396	hypothetical protein CAA

C403600CA	27.572018	27.121204	26.002102	24.46286	hypothetical protein MG
C403680CA	5.739605	3.635754	12.158116	11.408761	hypothetical protein CAA
C403690CA	11.877137	14.641397	20.92527	28.510761	hypothetical protein CAA
C403700WA	64.488792	62.318073	44.879402	49.573025	hypothetical protein ME
C403710CA	6.040983	3.746451	2.271911	5.733832	hypothetical protein ME
C403720CA	23.372213	27.360338	7.922763	8.737469	hypothetical protein CAA
C403730CA	13.535917	12.511673	17.975246	22.208183	tRNA (guanine) methyltr
C403740WA	34.165844	30.40592	26.555546	25.528946	exosome non-catalytic c
C403750CA	8.348605	7.616184	12.600895	9.015723	hypothetical protein CAA
C403760WA	3.294441	3.278369	1.155202	0	hypothetical protein MG
C403770WA	38.376209	41.733253	22.37215	24.748167	hypothetical protein ME
C403780CA	31.562862	30.157864	91.025078	74.111786	putative RNA methyltran
C403810WA	11.127161	13.024186	21.374104	20.673582	hypothetical protein CAA
C403830WA	12.436754	13.620393	5.430085	6.899579	tRNA (guanosine(18)-2
C403850WA	28.416498	25.561535	44.95755	45.5354	FG-nucleoporin
C403860CA	8.047891	7.350484	15.920899	22.050198	hypothetical protein MG
C403880WA	1.903057	2.249342	12.164267	7.854968	hypothetical protein CAA
C403920WA	12.117992	12.383893	14.897505	16.944796	hypothetical protein CAA
C403930CA	33.802441	29.526348	41.516773	33.147655	RNA-binding signal reco
C403950CA	33.634911	20.254204	41.081573	34.025322	hypothetical protein ME
C403960WA	185.648865	177.897583	168.893799	224.813385	hypothetical protein CAA
C403990CA	8.917408	12.215882	52.250374	47.294579	hypothetical protein CAA
C404010WA	11.996774	12.932956	17.255369	16.513906	hypothetical protein ME
C404020CA	29.948521	23.898378	12.584016	9.472389	hypothetical protein CAA
C404040WA	5.852516	4.636276	4.312454	9.547628	hypothetical protein MG
C404090CA	17.135624	20.33733	26.808777	29.54693	calnexin
C404110WA	69.30191	78.494225	32.476044	57.006428	hypothetical protein CAA
C404120CA	9.812112	9.020353	15.879256	12.517381	TFIIH/NER complex sub
C404130WA	52.01812	76.682274	168.860397	166.284805	hypothetical protein CAA
C404140WA	12.64667	19.530464	12.722646	14.198351	hypothetical protein CAA
C404160WA	45.316662	37.312397	21.735552	22.653465	conserved hypothetical
C404180CA	6.780735	6.808727	11.571965	10.124894	hypothetical protein CAA
C404190CA	14.71197	10.562155	2.804013	3.519727	hypothetical protein CAA
C404200CA	10.584641	10.209031	4.607267	3.107713	hypothetical protein CAA
C404230WA	4.776819	2.529789	17.872993	17.14588	hypothetical protein CAA
C404240CA	43.649101	45.396812	43.603378	49.197872	hypothetical protein ME
C404250WA	4.629993	5.098892	8.570762	7.082439	hypothetical protein MGI
C404270WA	6.791207	7.592045	10.772654	7.321077	ureidoglycolate hydrolas
C404280CA	8.15018	2.599179	9.468862	7.569908	hypothetical protein CAA
C404300CA	15.609785	20.126987	19.061049	24.259731	hypothetical protein CAA
C404330CA	158.83226	181.054596	53.609043	53.742764	hypothetical protein ME
C404350WA	37.371559	32.206097	58.619476	71.987267	hypothetical protein CAA
C404360WA	1.171329	1.440744	2.904144	1.952818	hypothetical protein CAA
C404380CA	36.676483	26.132933	31.827442	29.233273	hypothetical protein CAA
C404390WA	816.684143	860.237976	976.396362	834.503845	large subunit ribosomal
C404400CA	21.122465	20.225306	2.866313	2.419301	hypothetical protein CAA
C404440WA	83.232147	79.013641	101.672905	100.859894	translocation protein SE
C404460CA	22.415031	21.43996	20.901821	18.742638	calcium/calmodulin-depe
C404500CA	15.969685	17.777031	14.695444	10.647985	protein-lysine N-methyltr
C404510WA	20.24745	18.662691	24.794914	29.005524	transcription factor TFIII
C404520WA	163.309128	129.127121	39.157879	34.690598	telomerase inhibitor
C404550CA	39.981392	39.920082	91.363548	71.8461	metalloendopeptidase
C404560CA	202.28508	194.778702	24.579239	28.360136	hypothetical protein CAA
C404600CA	14.490397	11.220049	26.08358	22.372784	hypothetical protein CAA
C404620CA	25.437983	23.983015	64.06562	56.440971	hypothetical protein ME
C404630CA	5.035465	8.825597	18.445984	13.482275	hypothetical protein CAA
C404650WA	14.317016	11.499022	34.515785	28.82893	hypothetical protein CAA
C404660CA	79.828995	86.545052	45.880779	49.879318	ubiquitin-specific proteas
C404670CA	27.050787	25.320635	32.304672	31.531569	hypothetical protein CAA
C404720WA	67.561653	65.212021	84.850708	65.105988	methylenetetrahydrofola
C404750WA	17.169212	17.435749	29.486475	31.870335	glucose-induced degrada
C404760CA	24.910841	24.36161	30.121935	30.240374	hypothetical protein MG
C404800WA	191.418594	195.739609	263.354889	283.363007	hypothetical protein CAA
C404810CA	22.033228	32.245308	19.045313	16.874832	tRNA (guanine46-N7)-m

C404820CA	56.032631	63.50145	137.918472	136.128326	mitochondrial 54S ribosc
C404860WA	13.342655	9.761589	4.305113	5.568997	putative protein of unkno
C404870CA	63.511978	66.243729	82.164734	85.601501	hypothetical protein CAA
C404920WA	13.402716	9.321198	31.320641	30.526621	chromatin DNA-binding
C404930CA	19.226606	24.898397	17.621189	23.279472	U2-type spliceosomal co
C404950WA	13.05898	15.627378	13.183404	12.202056	hypothetical protein CAA
C404970CA	181.753906	140.338928	202.751465	195.428436	uncharacterized protein
C404980WA	4.099819	7.296065	9.563226	5.627789	hypothetical protein CAA
C404990CA	5.266698	6.61303	5.630143	6.149796	hypothetical protein MGC
C405000WA	3.137076	4.399118	4.263062	5.311124	Protein likely to be esser
C405010WA	37.313416	40.020737	17.240414	22.412485	ribosome assembly prote
C405040WA	11.897985	12.892793	44.780537	66.762375	ubiquitin-like protein
C405080CA	5.191377	8.862413	13.335755	14.312213	Zn(2+) transporter
C405160CA	8.368091	11.316086	7.56793	12.561586	charged multivesicular b
C405180CA	14.647316	13.047325	22.49094	20.082806	nucleocytoplasmic transp
C405200CA	2.439619	1.697381	3.039215	0.404372	hypothetical protein CAA
C405210WA	34.483971	23.546783	36.124805	31.461317	CDP-diacylglycerol-inosi
C405220CA	6.297858	7.660673	14.724918	15.431178	anaphase promoting cor
C405230CA	24.117437	19.659008	14.667488	14.581937	conserved hypothetical p
C405250WA	2.27072	3.579112	5.145449	5.482145	hypothetical protein CAA
C405260WA	30.94256	36.816959	16.462805	24.435656	Elongator subunit
C405310WA	4.707115	4.235499	17.249331	17.795637	hypothetical protein MG5
C405330CA	43.36731	48.274158	19.617762	21.861498	maintenance of killer 11
C405340WA	6.296883	8.73718	20.421843	25.357208	anaphase-promoting cor
C405350WA	16.963419	19.763939	29.147833	36.144745	hypothetical protein CAA
C405360CA	3.178437	5.465672	12.260227	8.863551	hypothetical protein CAA
C405380CA	37.395771	51.834339	76.765663	52.620277	signal peptidase comple:
C405390WA	18.866228	20.145412	17.892233	19.009281	glyoxylate reductase
C405400CA	55.667297	67.509186	7.732999	9.711066	hypothetical protein MGK
C405440CA	69.938469	70.885597	81.886116	65.592346	hypothetical protein CAA
C405580CA	27.867472	38.939049	13.828734	11.360499	hypothetical protein MG7
C405590WA	5.838002	5.437212	8.872488	9.453314	hypothetical protein CAA
C405610CA	57.039608	55.934834	62.162521	74.23745	hypothetical protein MEK
C405620CA	20.531401	24.51833	47.068298	45.667763	hypothetical protein CAA
C405630WA	63.312183	76.485817	173.098663	188.234512	DNA-directed RNA polyr
C405640CA	29.410725	33.910423	43.297577	29.757776	1-(5-phosphoribosyl)-5- (
C405650WA	23.278099	28.572767	45.276123	38.102631	hypothetical protein CAA
C405730WA	12.853057	18.232683	43.503872	36.774483	hypothetical protein CAA
C405740CA	15.775977	13.040892	16.654058	21.550262	DNA-binding E3 ubiquitir
C405790WA	5.633174	5.188747	9.327261	10.929708	transport protein particle
C405800CA	104.925034	109.425987	111.459778	111.598068	hypothetical protein CAA
C405810WA	135.491699	158.28566	361.597748	368.667084	hypothetical protein CAA
C405820WA	102.077744	118.354141	223.102295	171.914917	hypothetical protein CAA
C405830WA	4.521408	1.23296	3.80173	4.763779	hypothetical protein CAA
C405850CA	16.95503	19.759365	27.652605	19.233116	hypothetical protein CAA
C405860WA	66.076637	61.199059	91.847046	106.357666	tubulin-binding prefolding
C405870CA	4.931592	5.006346	6.708833	5.964817	hypothetical protein MG9
C405890WA	9.683572	6.602604	30.622066	24.963715	hypothetical protein CAA
C405900CA	240.796234	200.785583	33.335384	27.773252	hypothetical protein MEU
C405970WA	14.678769	13.907832	20.440069	22.964909	hypothetical protein MEQ
C405980CA	7.280565	6.643479	7.770782	7.695302	nucleotide diphosphatas
C406020CA	8.000825	6.001281	11.710467	10.789126	DNA repair protein REV1
C406040WA	11.953681	10.026701	14.424663	13.116463	hypothetical protein CAA
C406080WA	26.588678	41.758183	94.997688	60.330074	hypothetical protein CAA
C406090CA	11.233208	14.325828	30.610857	26.942333	hypothetical protein CAA
C406130WA	21.378578	16.246	29.830498	36.643539	hypothetical protein CAA
C406140CA	8.030218	8.529943	21.040634	14.664713	hypothetical protein CAA
C406150CA	0.962779	0.872208	2.967149	2.759313	hypothetical protein CAA
C406160WA	8.09873	8.93609	16.836876	11.227396	hypothetical protein CAA
C406170CA	63.170235	64.053612	106.696777	95.284187	hypothetical protein CAA
C406200WA	33.347565	39.036884	81.604256	63.335102	hypothetical protein CAA
C406210CA	85.157616	85.91346	65.215576	57.810493	RNA-binding GTPase
C406220CA	1.00082	1.169754	1.441341	2.809978	hypothetical protein CAA
C406230CA	22.034534	28.514526	45.260441	39.06509	apyrase

C406240WA	11.063568	11.330769	14.275546	18.619225	hypothetical protein CAA
C406280CA	5.922542	9.090947	13.026799	9.833724	hypothetical protein CAA
C406290WA	12.956753	29.808512	29.587837	39.359966	chromatin DNA-binding
C406360CA	2.5052	5.553626	1.65254	2.158647	hypothetical protein CAA
C406370CA	34.989922	31.041573	25.231361	18.743725	hypothetical protein L15
C406410WA	5.827447	5.9459	9.415071	8.95415	mRNA splicing protein
C406420WA	8.177969	10.448578	6.558818	8.921371	hypothetical protein CAA
C406430CA	12.795897	13.884139	12.145536	11.559505	hypothetical protein CAA
C406440CA	13.120366	16.620443	31.591892	32.295956	conserved hypothetical p
C406450WA	36.427143	35.482868	73.468452	78.894623	hypothetical protein CAA
C406460CA	28.481201	25.599424	41.244404	47.570774	hypothetical protein CAA
C406470WA	239.712234	229.395416	134.136505	139.080002	hypothetical protein CAA
C406590WA	7.114302	15.425151	27.283123	30.533684	hypothetical protein MG
C406620CA	43.525314	53.657497	21.260092	16.983017	hypothetical protein CAA
C406630CA	0	0	0	1.02944	hypothetical protein CAA
C406640CA	0.334069	1.612218	0	0.483105	hypothetical protein CAA
C406650WA	24.888763	23.440193	32.671154	40.047241	sorting nexin 1
C406660WA	26.218231	25.384048	66.070435	56.265003	hypothetical protein ME
C406670WA	10.685587	13.681143	14.631735	9.667805	hypothetical protein ME
C406680CA	55.202435	56.298187	52.397293	53.855022	hypothetical protein MG
C406690CA	112.280136	126.198898	243.660156	217.362549	hypothetical protein CAA
C406710WA	17.222406	16.193005	32.634212	28.459055	hypothetical protein CAA
C406730CA	62.870132	65.114044	71.813957	72.443626	Imp2'p
C406740CA	23.917694	24.650677	42.498425	36.247738	hypothetical protein CAA
C406770WA	32.410275	38.36451	23.664513	28.315187	hypothetical protein L15
C406790WA	48.867477	52.018196	62.175072	44.742229	putative signal sequence
C406800WA	54.709709	57.954582	102.320709	74.736557	RuvB family ATP-depen
C406810CA	33.694786	35.480164	56.836552	64.464882	syntaxin-binding protein
C406840WA	19.908751	22.128807	22.754396	29.806976	hypothetical protein CAA
C406850CA	81.874985	85.166946	47.670635	47.27861	methionine aminopeptid
C406860CA	31.11628	27.65365	36.0037	41.141117	cytidine deaminase
C406880CA	79.49752	81.750824	176.917511	190.659882	proteasome regulatory p
C406910WA	12.069287	11.231104	0.366251	0.176011	hypothetical protein CAA
C406940CA	13.958287	7.154166	29.753071	36.78516	hypothetical protein MG
C406950WA	10.642709	9.890295	25.711426	15.199798	pseudouridine synthase,
C406960WA	16.970438	14.25928	25.925007	24.325661	hypothetical protein CAA
C406990WA	19.772863	21.895485	12.095627	14.320686	hypothetical protein CAA
C407000WA	4.606742	2.425208	1.388288	2.870894	hypothetical protein CAA
C407010CA	71.980865	66.496559	48.05891	50.178959	methylated-DNA--protei
C407020CA	4.993471	4.267272	3.162706	7.091455	hypothetical protein CAA
C407040WA	5.411372	6.999182	7.71397	12.663948	hypothetical protein CAA
C407060WA	21.288582	21.353937	23.919649	23.182341	DNA-directed RNA poly
C407080CA	26.627789	25.075245	53.151661	50.348293	hypothetical protein CAA
C407100CA	9.959295	8.561224	16.561136	23.862762	ATP-dependent RNA he
C407130WA	16.619463	17.90349	17.576368	22.106937	hypothetical protein CAA
C407140WA	587.816284	657.109314	260.51416	203.999634	hypothetical protein CAA
C407150WA	16.521488	19.582638	9.404969	12.160833	hypothetical protein CAA
C407160WA	13.707731	16.260239	49.348957	63.109406	hypothetical protein CAA
C407170CA	13.221479	7.129368	28.229979	15.711173	hypothetical protein CAA
C407200CA	48.274143	54.941483	98.232719	102.249565	putative lipid phosphatas
C407210WA	61.882626	42.679329	69.71962	50.219524	hypothetical protein CAA
C407220CA	18.46871	19.038496	15.341394	14.331463	cohesin-loading factor c
C407240WA	71.00576	78.237282	105.836494	40.291954	hypothetical protein CAA
C407260WA	3.454553	4.132648	10.678052	3.748062	hypothetical protein CAA
C500030WA	107.747612	95.88427	190.262207	198.289993	mitochondrial 54S ribos
C500040CA	63.775753	65.433189	104.547928	62.720982	GPI-anchor transamidas
C500050WA	15.063923	18.353451	30.993456	23.975298	hypothetical protein CAA
C500060CA	17.588064	17.062231	32.805672	27.986412	anaphase promoting co
C500080CA	83.968422	90.275383	151.354767	138.316757	coatomer subunit epsilo
C500090CA	65.361717	58.719589	145.631348	85.233658	hypothetical protein CAA
C500100CA	249.713547	244.494431	237.974197	145.913406	hypothetical protein CAA
C500120WA	33.106358	22.116968	58.427547	35.964809	hypothetical protein CAA
C500130CA	107.228996	93.845352	204.500961	127.259193	mitochondrial 54S ribos
C500140CA	63.136223	47.772255	32.198486	24.810844	hypothetical protein CAA

C500150CA	106.23597	127.058403	150.859436	144.745926	karyopherin alpha
C500160WA	37.850807	43.702965	71.290253	70.743195	hypothetical protein CAA
C500170WA	51.00164	53.672318	49.64851	52.170395	hypothetical protein CAA
C500230CA	15.404487	18.243988	33.143906	42.74939	endonuclease
C500250CA	16.104563	17.056953	13.619823	20.247889	hypothetical protein CAA
C500260WA	190.625168	220.262283	183.735519	171.488846	ribose phosphate diphos
C500280CA	37.493885	34.75415	37.541695	37.078094	ribonuclease
C500310CA	84.147804	105.773773	62.598774	46.228661	hypothetical protein MG5
C500320WA	99.137695	66.057114	153.156937	104.414062	putative mitochondrial 54
C500330CA	5.232913	4.034445	10.475563	10.783845	hypothetical protein CAA
C500340WA	19.451042	20.744381	80.160828	77.43911	hypothetical protein CAA
C500350CA	54.748363	58.454586	98.357872	94.276619	hypothetical protein CAA
C500380WA	18.010025	18.728046	15.984872	25.228664	hypothetical protein ME
C500390CA	272.702972	298.416046	614.493103	661.31073	Hap43p-repressed prote
C500400CA	28.598518	29.36499	47.366581	48.359741	hypothetical protein CAA
C500510WA	17.643585	19.928026	10.00732	10.100703	hypothetical protein CAA
C500530WA	1.645723	1.546731	1.155726	0.877713	hypothetical protein CAA
C500550CA	36.250992	44.378471	111.906319	105.593872	hypothetical protein CAA
C500560WA	67.496674	101.198219	167.745438	179.778305	E2 ubiquitin-conjugating
C500570WA	11.722745	11.255474	16.460327	15.371635	aminophospholipid-trans
C500580WA	14.002102	18.279427	21.799412	27.77356	hypothetical protein MG
C500600CA	2.840499	3.187298	2.96249	0.667386	hypothetical protein CAA
C500610CA	8.939824	9.529253	12.114664	10.974429	hypothetical protein CAA
C500620WA	5.306005	9.127717	7.947411	13.896084	hypothetical protein CAA
C500750CA	23.762377	34.227089	37.519047	32.821033	conserved hypothetical p
C500760WA	26.02623	29.002981	17.023113	16.603998	Rab GTPase-activating p
C500780CA	24.886143	24.760748	58.011219	60.351082	hypothetical protein W5
C500790CA	251.416946	257.754517	134.853317	125.431694	protein NRD1
C500800CA	347.976349	399.365295	244.470123	220.019852	dioxygenase
C500810CA	3.059373	1.61097	2.228446	1.222447	hypothetical protein CAA
C500820WA	107.557373	107.982536	126.197601	133.772324	mitochondrial 54S ribos
C500840WA	6.875168	8.58577	25.919786	28.318596	hypothetical protein CAA
C500850CA	10.8696	12.149909	10.726477	10.675743	hypothetical protein CAA
C500920WA	10.428761	7.709121	28.835794	24.273609	U4/U6-U5 snRNP compl
C500950CA	23.76206	27.147606	21.946743	16.116982	S-adenosylmethionine-d
C501000CA	47.560238	50.495716	90.144547	75.200096	hypothetical protein CAA
C501020CA	16.926594	11.692699	12.305686	18.274965	hypothetical protein CAA
C501040WA	7.187428	6.740568	15.746541	17.503061	hypothetical protein CAA
C501050CA	44.615074	53.124786	156.433548	153.378662	mitochondrial 54S ribos
C501070CA	22.358458	19.524288	23.942385	19.302214	hypothetical protein CAA
C501090CA	29.851068	27.452347	30.782269	30.536789	hypothetical protein CAA
C501110WA	41.563103	39.372162	31.506897	29.627243	hypothetical protein CAA
C501140CA	30.164581	32.920834	60.840553	61.288277	hypothetical protein CAA
C501170WA	8.884877	5.959492	9.222245	6.023443	hypothetical protein CAA
C501190WA	13.003804	12.679332	14.452608	12.527492	hypothetical protein CAA
C501200WA	31.950962	36.374573	81.184387	83.481636	ADP-ribose 1'&ap
C501220WA	20.951715	15.11701	52.436932	69.072754	hypothetical protein CAA
C501230CA	89.389717	87.979881	101.423096	106.886101	glucose-6-phosphate 1-e
C501260WA	2.520468	2.677592	1.419422	2.792781	hypothetical protein CAA
C501290CA	98.328156	103.839729	109.809456	79.797272	putative monooxygenase
C501300CA	6.598806	5.765433	20.678419	12.648755	mRNA-binding phosphat
C501310WA	9.570475	7.109424	4.994161	8.066215	hypothetical protein CAA
C501350WA	8.780306	10.817646	7.720757	9.402275	hypothetical protein MG
C501410CA	11.780115	11.000758	17.689865	14.342854	hypothetical protein CAA
C501420WA	261.048492	268.06778	136.995392	95.290359	hypothetical protein CAA
C501430CA	15.044417	11.893131	22.34141	20.620756	hypothetical protein CAA
C501440CA	25.945211	25.754375	25.486231	22.642773	palmitoyltransferase
C501470CA	9.445362	17.750257	10.210051	9.746655	hypothetical protein CAA
C501490CA	16.609341	25.38196	21.671885	21.822145	hypothetical protein CAA
C501530CA	20.142677	24.904703	34.469658	39.889893	hypothetical protein CAA
C501540WA	792.661804	893.653015	903.621765	761.554016	ribosomal 40S subunit p
C501550CA	567.493713	559.326721	655.553467	619.829285	hypothetical protein CAA
C501560CA	289.815948	313.185638	1049.544922	1036.724365	glutathione-disulfide redu
C501590WA	12.13008	16.164202	18.573952	23.860815	amyloid beta protein bind

C501610WA	18.082153	19.208927	19.378094	22.507715	pseudouridine synthase
C501710CA	5.505194	5.217029	5.381156	3.106293	hypothetical protein CAA
C501730WA	2.160025	3.188875	2.864346	2.472502	hypothetical protein CAA
C501870WA	46.728527	47.634022	42.690845	47.312679	peptide alpha-N-acetyltr
C501880CA	43.063614	36.655674	59.937836	50.374348	hypothetical protein CAA
C501890WA	34.616688	45.971409	56.297783	65.734856	hypothetical protein CAA
C501900CA	45.809013	58.181847	57.23877	47.602337	hypothetical protein CAA
C501920CA	18.278223	25.944117	28.496866	33.312275	phosphoinositide 5-phos
C501930WA	10.063451	15.080175	19.997347	27.988649	SF3a splicing factor com
C501940WA	11.702342	13.968088	22.046114	19.353765	bifunctional DRAP deam
C501960CA	41.312145	46.760445	44.195736	39.441235	putative electron-transfe
C501980CA	51.044262	44.507607	46.468903	48.341721	hypothetical protein MG
C501990WA	4.933646	3.478311	3.203938	4.361129	hypothetical protein CAA
C502010CA	43.312672	36.188885	39.494949	51.83139	hypothetical protein CAA
C502020CA	80.778435	77.7164	66.686081	63.595573	hypothetical protein W5
C502040WA	47.146847	52.200298	137.342438	126.575806	protoheme IX farnesyltr
C502050WA	10.516309	10.791923	22.750463	22.202881	hypothetical protein CAA
C502060WA	13.844758	20.566305	36.756233	34.945885	hypothetical protein CAA
C502070CA	78.745529	80.740166	89.220009	57.168869	pre-rRNA-processing pr
C502110WA	40.790752	49.248962	10.860365	10.222996	Hsp12p
C502140CA	81.895607	77.941116	121.148193	94.197983	pyridoxal 5'-phosp
C502190CA	251.105759	283.763458	391.548279	310.850525	mitochondrial 37S ribos
C502200WA	7.010943	7.00789	8.456667	10.20196	hypothetical protein CAA
C502210WA	46.274521	51.809525	72.478531	62.739937	hypothetical protein CAA
C502220CA	24.783587	27.293203	24.372463	23.093622	polyphosphatase
C502230WA	181.340973	185.681091	273.431091	227.477966	proteasome core particle
C502280CA	33.289673	48.654545	19.013315	15.4159	hypothetical protein CAA
C502310CA	5.871001	4.128348	8.355026	10.372745	hypothetical protein CAA
C502320CA	19.720493	26.367523	15.283648	17.266657	hypothetical protein MG
C502330WA	116.142189	129.592545	74.370308	73.96701	hypothetical protein CAA
C502350CA	6.101687	7.902904	14.900047	13.830021	hypothetical protein CAA
C502360CA	2.646266	6.085901	4.371468	5.605938	hypothetical protein CAA
C502370CA	27.125887	41.079834	8.542235	10.003991	hypothetical protein CAA
C502380WA	89.647926	101.728844	148.60257	118.157578	TIGR01456 family HAD
C502390CA	21.680878	36.897579	60.490685	59.254688	hypothetical protein CAA
C502400WA	118.619591	123.689156	148.019104	160.456787	palmitoyl-(protein) hydro
C502410CA	6.753903	6.727794	5.687831	9.206663	hypothetical protein CAA
C502440CA	21.612511	15.371932	15.083028	18.732988	serine/threonine protein
C502450WA	9.464621	8.824263	20.540874	17.695507	glucose-induced degrad
C502480WA	50.035461	55.193783	97.14431	81.927612	cleavage polyadenylatio
C502500CA	56.117588	60.031048	65.448044	73.802307	hypothetical protein CAA
C502510CA	27.409492	33.824448	33.545757	35.793526	hypothetical protein CAA
C502520WA	14.629874	11.533462	8.556641	8.387606	Biofilm-induced protein
C502560CA	23.688526	19.088926	34.618214	35.316158	hypothetical protein CAA
C502580WA	126.976143	119.880699	166.560501	179.889969	hypothetical protein CAA
C502590CA	21.40851	24.388039	19.681295	17.968023	hypothetical protein CAA
C502620CA	26.630814	25.454014	30.696466	31.752028	hypothetical protein CAA
C502640WA	19.277384	24.248627	29.208202	39.197205	hypothetical protein CAA
C502660CA	114.804413	124.073013	85.088005	96.298981	hypothetical protein CAA
C502680WA	112.632378	144.493637	42.550247	46.17757	hypothetical protein ME
C502690WA	20.900354	23.391813	17.902279	20.039837	hypothetical protein W5
C502730CA	22.543226	28.511877	42.634991	31.637894	iron-sulfur cluster assem
C502740WA	12.154953	10.984923	32.325108	32.243233	oxidoreductase
C502750CA	6.598482	6.286188	19.466238	15.571886	protein HIR2
C502780WA	5.859029	6.100068	24.31838	27.140757	hypothetical protein CAA
C502800CA	0.149945	0.59423	0	0	hypothetical protein MG
C502810WA	16.45911	10.610362	36.578056	17.241127	U4/U6-U5 snRNP compl
C502820CA	34.857155	26.522713	39.541313	39.419147	methylthioribulose 1-pho
C502830WA	38.507935	38.126278	52.072392	65.61261	hypothetical protein CAA
C502900WA	8.734193	7.341229	23.009588	25.197058	SAGA complex subunit
C502920WA	23.096321	27.212498	47.472221	45.357933	hypothetical protein CAA
C502980CA	17.368105	28.527046	29.932314	30.240181	hypothetical protein CAA
C502990WA	17.216682	18.62332	31.741768	30.543272	hypothetical protein CAA
C503000CA	6.09872	6.881302	17.42041	18.861008	hypothetical protein MG

C503010WA	8.525284	7.555719	11.469954	15.214838	U4/U6-U5 snRNP compl
C503030WA	4.901568	4.856024	3.526426	2.498565	hypothetical protein CAA
C503040WA	18.158524	17.381071	19.971821	18.309647	hypothetical protein CAA
C503080CA	12.892683	16.03154	10.652654	15.089603	hypothetical protein MEQ
C503100CA	16.605947	20.243607	36.102077	31.323864	hypothetical protein CAA
C503110CA	31.514706	36.431698	65.429253	76.800652	mRNA splicing protein
C503120WA	8.544857	8.508585	17.796085	17.18762	GPI-anchor transamidas
C503140CA	10.960048	8.744589	10.150885	15.314556	hypothetical protein CAA
C503150WA	190.032379	195.512894	100.528961	123.83213	
C503170CA	21.133047	21.18737	25.228643	37.355518	hypothetical protein CAA
C503210CA	6.269111	7.308993	15.071938	15.386348	hypothetical protein CAA
C503260CA	8.576762	9.5036	5.797303	8.012678	hypothetical protein CAA
C503290CA	50.044186	35.636608	117.840469	130.096222	mitochondrial 37S riboso
C503300CA	9.552238	10.559202	8.033726	10.784136	hypothetical protein CAA
C503370CA	5.785025	7.699743	21.456923	25.953568	hypothetical protein CAA
C503400CA	49.992039	44.632645	146.904129	146.744705	Sm-like protein
C503410CA	85.72805	69.015564	102.349197	93.173897	mitochondrial 54S riboso
C503430WA	4.162378	3.4976	2.024408	1.605319	hypothetical protein CAA
C503440WA	67.900574	79.427277	53.236416	74.900826	hypothetical protein CAA
C503460CA	18.103241	11.953736	41.76371	54.922226	hypothetical protein CAA
C503470CA	19.212814	24.575756	22.237671	19.602947	hypothetical protein CAA
C503480CA	18.74622	22.784187	22.73439	17.477341	hypothetical protein CAA
C503490CA	27.403376	26.904175	47.639587	48.454811	Stationary phase enriche
C503510CA	41.560719	40.63818	21.313982	16.033468	hypothetical protein CAA
C503520WA	0.1222	0.23256	0.89279	0	hypothetical protein CAA
C503530CA	7.206439	11.325756	5.444577	6.511552	ubiquinone-binding prote
C503550WA	45.150856	43.491314	62.340191	71.064758	hypothetical protein MGN
C503560WA	15.528193	20.631668	61.935219	61.986034	hypothetical protein MEV
C503570WA	27.203987	32.586777	62.813278	72.463219	hypothetical protein CAA
C503630CA	12.941794	10.518549	18.402281	19.164829	hypothetical protein CAA
C503640WA	36.281597	31.349165	48.056225	24.637838	diphthine synthase
C503650CA	5.22661	3.941699	9.06488	13.357289	hypothetical protein CAA
C503670CA	15.312511	14.186494	12.097775	7.02207	hypothetical protein CAA
C503690WA	12.608582	11.088986	16.269005	16.237066	hypothetical protein MGE
C503700CA	33.339291	33.056408	45.603699	24.58807	diphthine synthase
C503710CA	44.794331	50.877331	69.845688	62.455841	hypothetical protein CAA
C503730WA	14.658512	15.253873	1.442413	1.82513	hypothetical protein CAA
C503740WA	16.84874	24.937761	15.227793	18.86838	hypothetical protein CAA
C503770CA	1.133055	2.392931	0.242026	1.146779	hypothetical protein CAA
C503780CA	6.472495	4.825039	14.696777	14.935956	hypothetical protein CAA
C503800WA	245.279602	276.184753	794.960754	484.522064	hypothetical protein CAA
C503810CA	2.28591	2.114629	4.62106	4.53843	hypothetical protein CAA
C503830CA	32.256084	37.735657	71.073425	99.558273	transcription initiation fac
C503840WA	3.845587	10.107305	8.898049	8.068098	thiamine pyrophosphokir
C503850WA	78.539246	93.810387	186.191666	212.442322	hypothetical protein MG7
C503870CA	190.101135	179.895264	113.084816	118.602791	hypothetical protein CAA
C503880CA	1.397799	0.876267	1.462413	1.944941	hypothetical protein CAA
C503890CA	4.390886	2.123934	1.74135	0.25033	hypothetical protein CAA
C503910CA	0.723375	0.4469	1.586573	1.980101	hypothetical protein CAA
C503920CA	150.15007	188.172455	55.689121	57.645657	rRNA-processing protein
C503930CA	18.982811	22.643551	76.572052	69.436584	hypothetical protein CAA
C503940CA	9.047993	11.756141	25.980318	26.349779	hypothetical protein CAA
C503950WA	11.705773	10.396501	8.474707	9.712098	hypothetical protein CAA
C503960WA	345.407654	296.598572	397.99295	417.826843	hypothetical protein CAA
C503970WA	8.043996	7.364731	4.219082	7.442688	hypothetical protein CAA
C503980WA	42.151878	38.978127	20.241364	20.98315	hypothetical protein CAA
C504010CA	3.478618	1.590594	7.689937	5.245974	hypothetical protein MG5
C504030WA	137.867706	137.695694	33.281975	33.886555	hypothetical protein CAA
C504050WA	25.186518	25.051622	20.612764	23.596867	hypothetical protein MEN
C504080CA	91.911903	123.390923	87.953445	90.345993	pre-mRNA-splicing facto
C504120CA	27.419128	35.124775	26.444313	26.703255	hypothetical protein CAA
C504140WA	25.372126	25.779306	72.21402	76.911469	hypothetical protein MGE
C504150CA	18.516888	19.004738	55.803329	32.202717	hypothetical protein CAA
C504170WA	138.818878	141.298965	137.199936	145.449356	hypothetical protein MG5

C504180WA	14.182034	17.415718	25.089895	16.095503	hypothetical protein CAA
C504260WA	9.035231	9.040273	9.94658	10.537733	hypothetical protein CAA
C504290CA	100.570175	98.893112	43.70805	52.780857	hypothetical protein MG
C504300CA	92.847557	100.545341	186.961182	167.776077	RecName: Full=Cys-Gly
C504310WA	4.458217	3.906466	20.260195	21.068033	hypothetical protein CAA
C504320CA	25.507019	32.980347	32.946423	29.022964	hypothetical protein MG
C504330WA	138.891922	134.667709	237.240341	243.309265	hypothetical protein ME
C504340WA	21.521511	27.262835	28.10639	22.813137	protein disulfide isomera
C504350CA	18.051662	17.045574	19.496141	19.71397	hypothetical protein ME
C504360CA	35.374287	50.682026	90.802597	76.858826	nucleotidase
C504380CA	23.394602	15.069444	1.808767	7.600724	hypothetical protein CAA
C504390CA	9.281173	13.085658	6.98501	3.470035	hypothetical protein CAA
C504410CA	38.396294	37.049194	87.514709	83.835091	hypothetical protein CAA
C504420WA	17.423969	19.746485	36.635704	34.496391	hypothetical protein CAA
C504460CA	0.592408	1.266234	1.981359	3.677243	hypothetical protein CAA
C504470CA	565.012512	648.890747	484.542664	401.019531	hypothetical protein CAA
C504480CA	4.986327	7.484609	13.899459	11.138429	hypothetical protein CAA
C504530WA	62.936745	65.708244	81.036362	94.435204	mitochondrial 37S ribos
C504540CA	5.737561	7.117961	16.669905	23.43873	hypothetical protein CAA
C504550WA	15.480227	23.164753	43.74868	45.208908	hypothetical protein CAA
C504580CA	14.005115	15.281126	31.471161	45.133106	ESCRT-II subunit protei
C504610WA	54.094593	58.355709	35.668755	35.453327	hypothetical protein CAA
C504620CA	21.404837	25.674089	80.452492	61.573048	membrane insertase
C504630WA	55.123775	37.744438	85.923172	78.511284	transcription elongation
C504640CA	20.008364	23.676146	38.17894	43.336922	hypothetical protein MG
C504690CA	109.899895	91.138237	49.158016	50.172813	hypothetical protein CAA
C504710WA	16.233917	12.292084	21.901981	21.81094	glutamyl-tRNA(Gln) ami
C504720CA	66.731461	53.850826	71.324097	76.611183	GTP cyclohydrolase I
C504770WA	36.505253	56.564461	45.006531	44.551521	hypothetical protein CAA
C504790CA	14.954397	10.544734	19.245737	23.604628	hypothetical protein CAA
C504840CA	28.854599	28.089205	23.377142	16.991871	hypothetical protein CAA
C504850WA	4.421194	5.140267	4.846354	5.451405	hypothetical protein CAA
C504860CA	27.530294	28.297688	37.938313	42.204685	hypothetical protein CAA
C504870WA	30.556702	27.719753	44.788887	40.549271	conserved hypothetical
C504890CA	2.733147	4.501886	9.524055	16.729338	hypothetical protein CAA
C504900CA	38.196201	30.483971	51.810795	41.465118	ribosome-interacting GT
C504910WA	37.177349	47.889694	24.722809	18.899338	hypothetical protein CAA
C504920CA	7.524486	6.104987	12.817526	11.409537	putative RNA helicase
C504940WA	3.40097	5.301778	2.111511	2.880893	hypothetical protein CAA
C504950CA	12.627196	13.570917	18.042736	16.705345	hypothetical protein CAA
C504960WA	57.23938	61.407551	126.173454	140.452637	hypothetical protein ME
C504980WA	3.372268	5.095713	4.730745	4.202952	hypothetical protein CAA
C504990WA	28.03186	34.646141	42.041965	40.931023	hypothetical protein ME
C505000CA	12.933338	10.560684	34.212276	35.093132	putative lipase
C505010WA	2.499833	1.922719	18.921041	19.762457	hypothetical protein CAA
C505020CA	45.853241	46.801254	54.774696	65.73616	dolichyl-diphosphooligos
C505040WA	15.951794	14.51614	34.787544	38.191196	putative glycosylphosph
C505060CA	9.137103	16.178183	25.72048	41.747131	hypothetical protein CAA
C505070WA	8.699371	12.105914	11.959331	13.396008	hypothetical protein CAA
C505090WA	5.600623	8.404631	11.245975	18.14657	hypothetical protein CAA
C505130CA	27.110172	25.187405	46.492714	30.249353	putative dephospho-Co
C505140WA	31.247314	36.997242	68.411537	57.806545	2-dehydropantoate 2-re
C505150CA	8.960602	4.734721	14.735628	12.890141	protein-lysine N-methyltr
C505180WA	0	0.996135	1.569933	1.574458	hypothetical protein ME
C505200CA	19.587255	25.861834	27.786444	28.535278	hypothetical protein CAA
C505210WA	24.960054	22.60331	23.268368	31.680059	hypothetical protein MG
C505230CA	304.742096	306.428131	359.026031	369.068848	ubiquinol--cytochrome-c
C505240CA	3.214834	1.534387	0.425032	1.363575	hypothetical protein CAA
C505250CA	75.710884	91.736969	137.261841	145.012039	mitochondrial 37S ribos
C505260WA	15.254269	18.509735	31.653303	37.022972	hypothetical protein CAA
C505270CA	42.625946	37.552567	73.915543	67.827873	hypothetical protein MG1
C505340WA	173.802933	180.725906	81.952614	81.8591	hypothetical protein CAA
C505350WA	9.653635	14.466025	42.099258	48.41148	DNA primase subunit
C505360CA	38.267792	42.946293	13.052627	12.424562	hydrolase

C505440CA	55.668636	57.387936	39.504543	51.675766	hypothetical protein CAA
C505460CA	44.07962	41.956699	50.189095	33.6021	hypothetical protein CAA
C505510CA	27.493216	27.443058	34.312572	22.900612	hypothetical protein CAA
C600080CA	51.983597	61.583614	71.711258	69.59314	hypothetical protein MG5
C600090WA	47.633614	35.125877	75.880501	69.149963	hypothetical protein CAA
C600110CA	19.675442	17.049646	73.495651	66.391541	hypothetical protein CAA
C600120WA	9.968554	3.779947	40.530804	38.775642	hypothetical protein CAA
C600170CA	94.239555	97.35862	45.662373	48.154022	mRNA-binding ubiquitin-
C600180CA	6.180903	5.978547	17.639688	10.401487	hypothetical protein CAA
C600190WA	26.873419	20.388262	46.596287	45.224838	hypothetical protein CAA
C600200CA	405.323944	326.480011	452.358765	396.15094	hypothetical protein CAA
C600210WA	31.048046	27.065334	50.063133	48.599949	2-aminoadipate transam
C600230WA	8.034428	7.443756	15.967349	15.757091	hypothetical protein CAA
C600240CA	14.811958	18.712137	38.159977	26.552019	hypothetical protein CAA
C600250WA	34.03614	34.879101	25.690954	23.372063	hypothetical protein CAA
C600260WA	324.625336	251.753494	110.726631	107.713219	ubiquitin-conjugating pro
C600270WA	71.736504	73.039795	108.684479	98.050171	hypothetical protein CAA
C600290WA	645.476013	602.380737	728.265381	724.230469	hypothetical protein CAA
C600310WA	55.860569	47.752914	50.96151	51.706142	ubiquitin ligase complex
C600340CA	8.24992	7.64741	17.815296	18.523315	metalloendopeptidase
C600360CA	22.081074	26.824448	40.233967	44.296875	hypothetical protein CAA
C600380CA	14.854522	15.415903	13.724615	15.829382	hypothetical protein CAA
C600390WA	30.944584	32.745461	56.481121	51.949947	putative serine--tRNA lig
C600400CA	8.338453	11.931142	29.529629	28.53076	hypothetical protein CAA
C600430CA	14.447209	14.334772	17.720783	22.616102	hypothetical protein MG3
C600490WA	8.213746	8.316161	9.41676	7.008247	carboxylic ester hydrolas
C600500CA	9.611353	11.851244	13.969762	12.511856	NEDD8-activating protei
C600520WA	14.62816	17.026642	20.878256	33.552525	hypothetical protein CAA
C600530CA	27.761921	16.41132	53.917973	56.431175	mRNA splicing protein
C600540WA	3.632589	4.884688	11.037825	14.475901	hypothetical protein CAA
C600550WA	80.498627	86.769356	143.813553	142.025909	mitochondrial 37S ribos
C600560WA	17.027975	16.683666	24.282938	27.725657	hypothetical protein CAA
C600630WA	5.185578	3.863385	12.682634	8.816558	hypothetical protein CAA
C600640CA	14.131209	14.455913	28.158634	27.862499	TFIIH/NER complex sub
C600660CA	61.352722	36.288727	155.015152	131.842957	hypothetical protein CAA
C600680CA	31.061977	21.203382	42.256725	37.238941	hypothetical protein CAA
C600690WA	6.770468	7.29633	10.447873	10.376027	hypothetical protein CAA
C600700CA	32.875881	36.109386	45.710388	39.770874	RNA polymerase II subu
C600710WA	8.285904	8.35153	13.450562	11.831071	hypothetical protein CAA
C600730WA	3.24978	6.695952	4.73178	4.47	hypothetical protein CAA
C600760WA	46.642258	47.239803	42.849243	47.202827	hypothetical protein CAA
C600770CA	3.423502	3.672471	15.610661	18.247982	hypothetical protein CAA
C600800CA	29.101904	29.019972	30.739182	31.992378	hypothetical protein MG1
C600810CA	2.8794	2.229805	1.718331	0.399628	hypothetical protein L15
C600850WA	145.775192	141.449615	164.368408	174.953445	peroxiredoxin
C600890WA	15.141158	10.734122	30.409897	38.745102	hypothetical protein CAA
C600900CA	8.173281	9.882113	36.146278	23.453201	hypothetical protein CAA
C600910CA	22.198408	22.053658	36.562511	33.985764	hypothetical protein CAA
C600920WA	254.874725	268.842651	328.68634	320.063324	hypothetical protein CAA
C600930CA	118.482727	129.169937	86.88707	92.642899	hypothetical protein CAA
C600940CA	0.73381	0.932004	0.411056	0.232658	pheromone-regulated pr
C600980CA	104.764099	88.539719	15.872044	19.093798	hypothetical protein CAA
C601000CA	4.996	9.187492	16.216351	21.8906	hypothetical protein CAA
C601020WA	3.214131	4.977202	2.351718	6.759449	hypothetical protein CAA
C601040CA	12.933488	9.810824	8.505753	9.885259	RNA helicase
C601050WA	18.665522	24.343042	54.876881	50.417797	tyrosine--tRNA ligase
C601080CA	4.024461	2.160247	3.65518	5.460821	hypothetical protein CAA
C601090CA	0.804376	3.113763	2.931463	2.682367	hypothetical protein CAA
C601120CA	5.890117	3.03338	8.928328	8.616835	protein-S-isoprenylcystei
C601130WA	0.273616	0	0.583604	1.524859	hypothetical protein CAA
C601200WA	9.810801	6.426745	14.10022	13.78125	hypothetical protein CAA
C601210WA	270.526611	264.311035	361.795837	355.299072	hypothetical protein CAA
C601220CA	25.561222	23.819128	69.321228	75.536964	hypothetical protein CAA
C601300WA	10.803302	16.311726	13.896116	16.061573	putative acyltransferase

C601330CA	9.425126	6.343768	11.888366	7.956346	hypothetical protein CAA
C601340CA	34.63694	39.019226	45.500881	41.467243	phosphatidylglycerophos
C601350WA	21.517443	18.905056	14.926519	20.755934	hypothetical protein ME
C601360WA	345.745209	337.412201	634.553406	725.757324	hypothetical protein MG
C601370WA	11.983435	16.738167	18.13357	22.675253	hypothetical protein CAA
C601380CA	20.336124	15.101998	21.899637	23.569429	Ran GTPase-binding pro
C601400WA	21.622616	27.380119	12.710292	10.674433	hypothetical protein CAA
C601420CA	20.212042	30.946716	30.201469	23.957327	hypothetical protein CAA
C601450CA	159.145966	189.492737	63.314613	70.287163	hypothetical protein ME
C601460CA	33.468712	35.190155	38.882874	46.552528	hypothetical protein CAA
C601470WA	6.0468	6.263155	6.508135	5.815335	hypothetical protein CAA
C601480WA	55.139584	46.705544	10.853378	11.038922	hypothetical protein CAA
C601490CA	37.647297	22.629583	6.841089	11.285037	hypothetical protein MG
C601520WA	22.541563	20.316853	5.607221	5.841367	hypothetical protein CAA
C601530CA	44.885559	58.013081	102.028603	139.613953	hypothetical protein L15
C601550CA	7.348418	5.180729	27.805826	33.481144	DNA-directed DNA polyr
C601560WA	21.751947	22.103106	115.084267	132.267181	hypothetical protein CAA
C601590WA	367.064819	396.579987	110.804581	118.514336	hypothetical protein CAA
C601620WA	27.587275	31.676802	10.379829	11.794311	hypothetical protein CAA
C601680CA	4.411672	3.775658	5.67813	6.113967	hypothetical protein CAA
C601750CA	7.968584	9.95854	12.182251	8.575221	putative pyridoxal kinase
C601780CA	10.207413	10.512481	10.937102	6.526921	formate/nitrite transporte
C601810WA	0.775747	0.311371	1.516573	0.70571	hypothetical protein CAA
C601850WA	19.620136	17.598276	27.924994	31.563154	hypothetical protein CAA
C601870CA	23.822624	24.303541	18.537136	16.676643	hypothetical protein CAA
C601880WA	31.81885	25.325277	29.534573	24.09128	hypothetical protein CAA
C601890CA	49.654263	52.27029	25.958895	26.067757	ATP-dependent DNA/R
C601920CA	51.281296	42.61488	39.837311	45.818466	hypothetical protein CAA
C601940WA	69.971626	68.638191	30.056599	37.48769	hypothetical protein CAA
C601950CA	15.901104	17.671246	18.20241	14.156227	hypothetical protein CAA
C601960WA	4.662034	4.722447	11.419103	10.572657	hypothetical protein CAA
C601980CA	72.581093	77.227997	172.168198	186.891144	mitochondrial 37S ribos
C602020CA	56.528126	71.402992	16.204998	15.752832	hypothetical protein CAA
C602030CA	28.786766	32.090927	27.448383	33.958916	NADHX dehydratase
C602090CA	10.889212	8.809558	14.789716	18.24229	hypothetical protein CAA
C602100WA	114.481766	98.14669	200.738129	270.063751	hypothetical protein CAA
C602110WA	4.582908	8.410531	8.311086	9.591805	hypothetical protein CAA
C602140WA	9.076236	6.904155	11.408325	17.203014	hypothetical protein ME
C602150CA	6.816926	6.570191	10.581487	9.581765	hypothetical protein CAA
C602160WA	6.596903	8.249494	11.123428	12.335149	hypothetical protein CAA
C602180WA	64.797928	71.256821	105.193245	79.483673	hypothetical protein MG
C602190CA	32.673431	32.064598	89.754036	99.011436	serine/threonine/tyrosine
C602200CA	24.411093	21.057882	14.394948	16.783741	hypothetical protein CAA
C602210WA	19.785101	11.665629	7.48982	3.839639	hypothetical protein CAA
C602230WA	74.224419	73.300949	30.124088	30.038855	putative GTPase
C602250WA	4.495361	3.410995	12.754536	13.096126	hypothetical protein CAA
C602280WA	32.137222	41.576042	48.095646	48.183689	hypothetical protein I503
C602290CA	44.849495	42.65955	21.467159	17.655912	putative tRNA 4-demeth
C602300CA	9.848806	12.963525	47.61623	51.003494	hypothetical protein CAA
C602310WA	16.131456	12.848466	37.247375	43.955143	deubiquitination module
C602330WA	2607.786377	2607.119385	1872.368286	1768.346436	hypothetical protein CAA
C602350CA	36.880375	44.3452	20.577648	21.759489	pseudouridine synthase
C602370CA	62.170502	77.523834	88.90419	90.835579	mitochondrial 37S ribos
C602380WA	102.611481	106.76136	54.97208	60.41711	ATP-dependent RNA he
C602410WA	40.862862	44.940136	40.151684	35.140022	NAD(+) diphosphatase
C602420WA	254.138596	302.673157	148.636429	137.508972	phosphatidylglycerol pho
C602430WA	11.720599	10.707323	24.739937	21.366081	hypothetical protein CAA
C602450WA	2.155335	1.556087	2.125837	2.343815	hypothetical protein CAA
C602460CA	33.261024	41.311195	61.944115	66.364838	hypothetical protein CAA
C602470WA	19.515774	18.963972	34.693409	29.033722	signal recognition particl
C602480WA	70.131866	84.277107	22.498602	19.049896	NADP-dependent alcoho
C602490CA	36.833225	41.479523	51.991848	63.542034	hypothetical protein CAA
C602530CA	24.504946	29.42037	60.395061	72.753143	hypothetical protein CAA
C602540CA	5.900022	13.733292	23.439718	15.403637	hypothetical protein CAA

C602550WA	0	0.176989	0	2.273192	hypothetical protein MG3
C602560WA	25.80574	29.869495	51.999275	57.89719	hypothetical protein CAA
C602580WA	6.655074	5.109013	11.338099	9.173756	RNA exonuclease
C602620CA	2.041281	3.896523	5.77396	2.143161	hypothetical protein CAA
C602630CA	13.580123	15.78882	27.544277	31.917685	hypothetical protein MG
C602640CA	35.044273	37.083042	46.431232	50.270473	hypothetical protein CAA
C602650CA	10.836332	12.894525	10.610734	12.579655	hypothetical protein CAA
C602660CA	7.722906	5.164047	2.872056	4.870943	putative amidase
C602680WA	16.762983	16.426521	20.736856	29.709957	SNAP receptor
C602690CA	42.015701	44.104336	23.930935	32.809917	hypothetical protein CAA
C602720CA	16.808565	19.215353	28.730423	35.158184	hypothetical protein CAA
C602740WA	172.804428	175.392883	319.068054	293.221313	hypothetical protein CAA
C602760WA	1.38454	2.445204	12.838598	5.025644	hypothetical protein CAA
C602790CA	77.824959	84.74865	52.185814	53.769993	hypothetical protein CAA
C602800WA	324.582397	358.358856	169.96228	130.681534	L-methionine (R)-S-oxid
C602810CA	6.042113	6.922036	9.854055	14.120868	hypothetical protein CAA
C602880WA	33.808052	28.227581	25.211426	17.986023	hypothetical protein CAA
C602900CA	6.705861	5.956107	18.496311	12.249485	putative lipoate--protein
C602930WA	74.209122	80.083107	94.169792	102.833878	hypothetical protein I503
C602940CA	33.686207	35.311611	45.463268	46.0327	hypothetical protein CAA
C602950CA	6.110885	3.472979	9.297752	8.117147	hypothetical protein MEU
C602960WA	7.091731	12.39108	16.800026	13.175669	putative cysteine synthas
C602970CA	17.491053	16.144213	20.977301	22.150183	hypothetical protein CAA
C602980CA	132.676987	153.127045	65.237442	59.685726	pantothenate kinase
C602990WA	3.600971	10.070883	17.430843	11.842825	hypothetical protein CAA
C603000CA	5.567207	7.875977	4.514223	6.179179	hypothetical protein CAA
C603040CA	4.959141	5.249422	11.087305	11.751842	phosphatidylinositol-3,5-
C603050CA	5.21691	4.018502	2.849492	0.292954	hypothetical protein MG5
C603070CA	16.237207	10.614245	21.658558	24.740276	hypothetical protein CAA
C603090WA	1.068154	1.921637	0	0.120552	hypothetical protein CAA
C603110CA	3.94851	3.227334	4.782152	7.55551	hypothetical protein CAA
C603130WA	397.66748	358.546722	395.481354	403.461884	hypothetical protein CAA
C603150CA	6.748541	7.670889	15.136787	19.356476	hypothetical protein CAA
C603180CA	43.824863	40.854042	35.949188	40.501804	hypothetical protein CAA
C603200WA	58.45454	70.176308	130.645142	114.021454	hypothetical protein CAA
C603210CA	26.195185	33.546936	19.691996	18.629883	DNA-directed RNA poly
C603220WA	14.161304	13.8279	14.183521	21.203215	hypothetical protein MG9
C603240WA	14.210934	15.218315	14.769528	12.793075	methylglyoxal reductase
C603260WA	410.187805	465.322906	97.869034	86.812836	RNA-DNA hybrid ribonu
C603280WA	1.165136	1.182362	0.670707	1.135576	hypothetical protein CAA
C603290WA	21.071083	21.100878	34.069839	34.665321	hypothetical protein CAA
C603300CA	42.091251	40.538338	46.745792	45.669239	hypothetical protein CAA
C603310WA	24.175362	31.774076	10.079112	8.708833	hypothetical protein CAA
C603320WA	45.609005	45.435997	18.904579	16.721272	hypothetical protein CAA
C603330CA	10.51945	7.770648	8.576764	14.422053	hypothetical protein CAA
C603360CA	25.088133	36.622787	6.524774	3.582891	hypothetical protein CAA
C603370WA	2114.286621	1936.060303	1039.283081	1114.146118	hypothetical protein CAA
C603380WA	281.230011	310.176605	249.295639	268.435699	hypothetical protein CAA
C603390WA	43.529606	55.647644	26.904364	31.268795	solute carrier family 25 (
C603420WA	2.263212	2.57243	8.980011	15.561959	hypothetical protein W5
C603430CA	9.790402	8.740216	11.211979	13.673042	hypothetical protein CAA
C603440WA	20.569027	22.046482	17.678062	19.96335	hypothetical protein CAA
C603460WA	43.610954	43.269176	42.183678	44.466904	FG-nucleoporin
C603470WA	31.070639	24.576017	17.845423	22.575098	hypothetical protein CAA
C603520CA	12.496484	12.290423	21.643238	18.989851	hypothetical protein CAA
C603530CA	20.652325	16.995731	47.697681	46.534264	hypothetical protein CAA
C603540WA	13.966863	19.017336	12.318405	9.536211	hypothetical protein ME
C603550CA	25.500713	15.788153	24.625496	32.954884	hypothetical protein CAA
C603580WA	5.193317	5.317905	10.945316	9.513854	hypothetical protein CAA
C603590CA	19.184084	15.002688	52.867565	59.335896	hypothetical protein CAA
C603600CA	20.616983	21.389828	4.528141	5.081314	hypothetical protein CAA
C603620CA	15.819212	14.439098	21.83177	14.537127	putative phenylacrylic ac
C603730CA	49.107342	50.272736	76.979843	72.303329	mitochondrial 37S ribos
C603740WA	9.230717	5.498772	9.602735	4.475245	hypothetical protein CAA

C603780CA	11.956489	13.777133	8.187391	10.852358	SCF ubiquitin ligase com
C603800CA	292.093719	306.579346	77.167336	81.050789	hypothetical protein MG
C603810WA	143.649918	170.149658	258.458008	208.354736	phosphate system cyclin
C603820CA	25.628868	29.976477	84.091431	56.724773	hypothetical protein CAA
C603880WA	8.137745	12.479004	15.382862	14.554471	hypothetical protein CAA
C603910CA	11.084891	11.358659	19.563488	25.563116	U2 snRNP complex sub
C603950CA	18.012653	22.313402	40.630955	32.927624	SWR1-complex protein
C603960WA	54.567146	65.102814	123.317917	121.328087	dipeptidyl-peptidase III
C603990CA	6.152773	6.973201	33.612896	29.237654	hypothetical protein CAA
C604050WA	3.047906	3.501866	4.856964	3.284416	hypothetical protein CAA
C604060WA	10.967166	10.637524	11.675501	15.070813	ubiquitin-protein ligase
C604070CA	0.286384	2.120734	2.864062	1.072699	hypothetical protein CAA
C604080WA	68.03228	76.95475	60.797878	51.545685	methionine aminopeptid
C604100WA	115.404778	131.255615	189.429962	198.361389	phosphatidylinositol-bind
C604110WA	45.940346	54.131058	49.595619	50.147491	aspartate/glutamate tran
C604120CA	6.420265	4.588447	22.76869	32.894455	hypothetical protein CAA
C604140CA	24.126598	21.338511	25.070908	26.242258	hypothetical protein CAA
C604150WA	0	1.373371	0.140493	0	hypothetical protein CAA
C604180WA	28.65498	34.05722	22.779964	21.096346	hypothetical protein I503
C604190CA	11.480173	10.551978	7.751348	7.432417	hypothetical protein CAA
C604230WA	3.376203	4.572396	2.12204	3.620022	hypothetical protein MGI
C604240WA	13.477219	15.46887	19.072033	37.719074	hypothetical protein CAA
C604250WA	1598.579346	1431.707642	2983.891113	2858.636475	cytochrome c oxidase s
C604260CA	9.144794	12.33396	15.399684	20.265854	hypothetical protein CAA
C604280WA	69.384659	70.162033	142.294785	123.610092	E2 ubiquitin-conjugating
C604290WA	50.059765	54.75499	28.855267	36.933662	hypothetical protein ME
C604300WA	5.816097	5.644594	7.670449	4.586731	hypothetical protein CAA
C604320CA	6.756947	23.796797	14.372904	8.662837	hypothetical protein CAA
C604340WA	10.085784	12.919705	31.695597	36.192253	dolichyl-P-Man:Man(5)G
C604370WA	7.455616	9.160039	8.145851	9.568213	hypothetical protein CAA
C604400WA	58.173813	71.800461	32.745567	29.964462	hypothetical protein CAA
C604410CA	79.61911	93.490448	67.290817	58.330097	hypothetical protein CAA
C604420WA	345.421448	310.710236	81.635468	60.681065	hypothetical protein CAA
C604440CA	5.835711	7.054671	13.92108	12.834235	hypothetical protein CAA
C604450WA	10.982254	17.737514	36.574894	41.007477	hypothetical protein CAA
C604470CA	16.85976	18.715219	33.509392	27.715096	ubiquitin-protein ligase
C604480CA	60.961956	48.624737	84.241257	78.357193	hypothetical protein CAA
C604510CA	16.879034	18.789526	36.655388	34.054554	hypothetical protein CAA
C604530CA	43.794952	40.891006	26.841248	26.554817	hypothetical protein CAA
C604550CA	24.453785	20.812986	17.199633	19.346041	hypothetical protein CAA
C604560WA	98.884453	109.421211	138.405945	129.67218	hypothetical protein CAA
C604650WA	74.750946	67.90519	67.493271	47.472366	hypothetical protein CAA
C700010CA	51.759743	50.056683	50.194157	38.238956	hypothetical protein MG
C700030WA	472.053986	431.140747	490.817108	462.117493	hypothetical protein CAA
C700040CA	47.871532	57.25396	34.443336	24.67626	hypothetical protein CAA
C700060CA	106.891853	84.849991	100.061211	61.749668	adenylate kinase
C700070CA	55.499352	55.143181	95.953453	85.117683	hypothetical protein CAA
C700120WA	69.338684	89.450287	121.629524	77.546967	hypothetical protein
C700130WA	34.89962	35.089813	38.414276	43.448891	tRNA-specific adenosine
C700140CA	58.781555	57.801445	71.496002	65.966217	hypothetical protein CAA
C700150WA	181.341583	201.238312	222.655716	146.540878	ribulose-phosphate 3-ep
C700160CA	162.135681	189.484299	101.329498	98.938553	ribosome biogenesis pro
C700190WA	73.714897	47.520233	157.246338	176.121368	hypothetical protein MG
C700200WA	24.357773	20.245083	50.120712	41.076817	hypothetical protein CAA
C700210CA	9.602649	8.531308	13.807073	13.178735	hypothetical protein
C700220WA	5.713138	5.438307	13.86456	11.271678	hypothetical protein CAA
C700230WA	10.109913	13.198784	28.389475	22.492846	hypothetical protein CAA
C700240WA	21.042379	21.149912	31.724733	27.628361	hypothetical protein CAA
C700250CA	82.960419	94.005882	216.157455	161.243073	hypothetical protein CAA
C700260CA	39.225471	33.750229	10.867992	9.786467	hypothetical protein CAA
C700270WA	25.721876	30.873898	27.659822	24.73428	hypothetical protein ME
C700300WA	60.153614	54.655838	72.137611	40.792599	ubiquinone biosynthesis
C700310CA	39.992428	41.774174	65.9748	48.561447	hypothetical protein CAA
C700330CA	20.911066	27.270693	25.626957	19.848431	Sua5/YciO/YrdC/YwlC fa

C700340CA	35.329041	38.680843	50.220123	49.281933	hypothetical protein CAA
C700350CA	2156.180176	1939.922119	3266.291992	3370.211914	hypothetical protein CAA
C700380WA	8.666608	15.546656	18.460135	27.748028	hypothetical protein CAA
C700410CA	9.60741	7.18854	14.478124	19.499434	hypothetical protein CAA
C700420CA	90.027466	96.140274	280.729187	309.618225	hypothetical protein CAA
C700430WA	673.415161	673.71814	1334.971436	1255.0354	putative ferric-chelate re
C700450CA	21.982889	19.719465	37.624119	48.209106	hypothetical protein CAA
C700460WA	2.679259	5.517261	3.753695	8.73699	hypothetical protein MG
C700490CA	64.524185	57.095177	93.829353	76.839653	N-terminal protein methy
C700500WA	0.017882	0.016084	0	0.00169	N-terminal protein methy
C700520WA	22.059013	23.902847	49.139446	53.657829	RNA polymerase-associ
C700580CA	14.299008	12.399977	26.26862	21.211739	hypothetical protein CAA
C700590WA	12.680872	9.179072	10.619406	15.395729	hypothetical protein CAA
C700600CA	20.397484	18.729204	46.32159	34.419746	mRNA-processing endor
C700610CA	11.832591	17.565235	11.440152	14.216307	hypothetical protein ME
C700630CA	2.262438	1.032482	0.435062	0.888282	hypothetical protein CAA
C700670CA	6.860732	7.736831	15.855453	18.703726	hypothetical protein MEY
C700680WA	4.869563	3.132242	10.293447	9.036142	hypothetical protein CAA
C700760CA	8.270447	7.817628	14.164106	15.680585	hypothetical protein CAA
C700770WA	114.063454	120.513023	65.216774	67.992851	hypothetical protein CAA
C700780WA	10.369597	13.563036	17.80933	18.014854	RNA-processing protein
C700790WA	8.568616	7.968094	19.708466	15.56135	hypothetical protein CAA
C700810WA	46.377708	48.338932	48.251186	50.605598	hypothetical protein CAA
C700830CA	60.576355	58.119129	44.073971	56.138237	hypothetical protein CAA
C700840CA	5.849972	6.876616	9.7172	10.068206	hypothetical protein
C700850WA	6.518341	8.992523	8.059877	6.552101	hypothetical protein CAA
C700870WA	0.657001	1.432897	5.370219	3.468341	guanine deaminase
C700880CA	47.175049	46.105297	58.180843	65.828987	hypothetical protein CAA
C700910CA	26.543453	31.160471	33.727951	39.442657	hypothetical protein MG
C700920CA	49.471249	46.637589	41.863213	39.247334	hypothetical protein CAA
C700940WA	56.862949	59.105675	26.057842	26.598606	hypothetical protein L15
C701000CA	0.422851	0	0	0.036075	ribosomal protein P0
C701010WA	1.861161	0.481893	0.89925	1.767495	hypothetical protein CAA
C701020CA	61.752724	75.428444	132.091324	96.985466	mitochondrial 37S ribos
C701030CA	41.181282	42.96806	19.22702	16.723864	mRNA-binding protein
C701040CA	7.74417	5.657259	4.271266	4.421525	hypothetical protein MG
C701050WA	0.854077	3.713218	1.246564	2.01605	hypothetical protein CAA
C701060WA	0.466232	0	0	0	hypothetical protein CAA
C701070CA	37.480724	37.875847	16.885464	18.259983	hypothetical protein CAA
C701100CA	7.750352	12.347076	60.180599	56.783176	hypothetical protein
C701130CA	0	0.056378	0.080282	0.26692	hypothetical protein CAA
C701150WA	33.394386	29.123672	32.37796	33.928398	hypothetical protein
C701160CA	166.469955	131.613953	222.358658	279.72702	NADH-ubiquinone oxido
C701170CA	201.191956	215.259659	42.88525	37.969498	hypothetical protein CAA
C701180WA	17.946651	19.167694	27.213194	23.963051	ERMES complex subuni
C701190WA	9.787009	16.043447	20.666937	18.992899	5'-(N(7)-methyl 5&
C701210CA	30.965994	32.514656	33.618969	26.407051	DNA-directed RNA poly
C701230CA	36.641453	41.421272	40.007538	46.260303	hypothetical protein CAA
C701270CA	8.016012	10.979742	16.397959	18.433954	hypothetical protein CAA
C701280CA	12.896413	10.903461	25.127722	19.641563	dihydrofolate synthase
C701320WA	13.557496	13.306006	23.788559	23.234791	ethanolamine kinase
C701350CA	18.223379	14.852385	19.582993	19.895306	hypothetical protein CAA
C701360CA	7.30157	6.751916	6.955472	18.923203	hypothetical protein CAA
C701370WA	9.333051	12.681546	8.189468	11.056066	hypothetical protein CAA
C701380WA	0.100579	0	3.385442	4.768484	hypothetical protein CAA
C701390WA	19.58349	27.312332	26.960934	37.827091	Hap43p-induced protein
C701400CA	13.113235	14.434762	21.965593	26.103935	hypothetical protein CAA
C701430CA	183.209961	181.508636	206.392776	236.985779	hypothetical protein CAA
C701440WA	14.815044	19.954884	30.01473	32.233532	hypothetical protein MG
C701460CA	3.848946	5.201673	8.8833	10.741776	hypothetical protein CAA
C701480WA	14.313615	13.649484	25.569304	32.966156	palmitoyltransferase
C701490WA	154.211365	141.366806	254.078629	301.228973	hypothetical protein MG
C701500WA	1.179498	2.799193	5.794089	3.608192	hypothetical protein CAA
C701510WA	27.533068	33.32637	22.093145	16.234993	hypothetical protein CAA

C701570CA	1.418393	2.434231	1.746968	1.488792	hypothetical protein CAA
C701590CA	18.48295	29.128988	59.442493	75.526077	hypothetical protein CAA
C701600WA	52.263432	49.393112	110.515617	94.409134	membrane insertase
C701610WA	373.45517	324.754089	522.326294	388.443298	mitochondrial membrane
C701650WA	27.015324	27.536604	61.187565	76.619644	transcription factor TFIII
C701660CA	19.120296	14.808774	10.429482	13.789703	hypothetical protein CAA
C701670WA	7.371302	7.782898	4.600592	4.280176	hypothetical protein CAA
C701680CA	1950.902466	2248.278564	363.963989	384.083832	hypothetical protein CAA
C701690WA	90.97187	88.614456	109.936905	79.898354	hypothetical protein CAA
C701700WA	1153.286011	1294.49646	1355.284302	1613.05603	hypothetical protein CAA
C701710WA	66.644806	68.401588	78.179031	94.908882	hypothetical protein CAA
C701720WA	57.385056	66.301964	92.004852	97.103752	flavin-linked sulfhydryl ox
C701740CA	23.989151	19.614683	34.818279	35.834335	hypothetical protein L15
C701750WA	14.178414	14.55468	24.160162	25.553915	hypothetical protein ME
C701830WA	7.987969	9.544713	32.442913	35.595028	kinetochor protein Mis14
C701880CA	2.584803	2.410458	1.810074	3.031981	flavin adenine dinucleoti
C701910CA	36.117413	45.414806	18.657333	16.405502	hypothetical protein CAA
C701930CA	44.002502	37.351002	77.058372	96.790894	hypothetical protein CAA
C701940CA	182.188553	207.724014	48.33456	49.511318	pheromone-regulated pr
C701950WA	70.260719	66.418152	60.082329	73.637527	putative rhomboid protea
C701960WA	16.683931	18.194452	10.566926	14.338603	hypothetical protein CAA
C701990CA	15.458653	19.185251	10.278026	5.41775	hypothetical protein CAA
C702000CA	1.294916	2.141429	0.56128	0.3727	hypothetical protein CAA
C702010CA	14.410653	19.714434	11.393866	13.784374	hypothetical protein MG
C702080WA	62.187237	65.886818	82.762924	95.632538	hypothetical protein CAA
C702090CA	12.655194	18.59771	25.601004	21.334606	hypothetical protein
C702100WA	113.551857	121.261017	163.950882	167.627106	hypothetical protein CAA
C702110WA	18.106855	22.085627	31.425192	32.357578	hypothetical protein CAA
C702120CA	66.945786	77.929115	86.737595	111.019516	mitochondrial 54S riboso
C702130WA	2.529273	1.992853	2.449908	1.622758	short-chain dehydrogena
C702140WA	3.491526	4.085124	10.135886	9.307433	hypothetical protein CAA
C702160WA	2.870018	4.706586	4.532488	3.460355	hypothetical protein CAA
C702170CA	19.105244	19.504576	45.535213	39.274666	hypothetical protein CAA
C702210WA	5.737334	6.032855	4.765304	9.255983	hypothetical protein CAA
C702220CA	27.365143	37.272644	13.092908	15.192457	hypothetical protein CAA
C702250WA	0.114019	0.523427	0.142074	0.460844	hypothetical protein CAA
C702260WA	0.428435	0	0	2.383473	hypothetical protein CAA
C702280WA	12.170124	12.064121	46.269466	67.710258	hypothetical protein CAA
C702290WA	4.14563	8.669533	12.219432	13.075925	hypothetical protein CAA
C702310CA	12.010341	13.124024	8.584813	12.563614	hypothetical protein CAA
C702340CA	47.889893	48.873062	27.078571	26.762878	hypothetical protein
C702350CA	13.539068	13.513319	21.662231	24.572735	hypothetical protein CAA
C702360WA	2.090831	0.72066	2.518346	0.603881	hypothetical protein CAA
C702370WA	360.991791	317.959076	1036.122681	1123.665283	hypothetical protein CAA
C702420CA	3.168018	3.297232	3.008387	5.123536	hypothetical protein CAA
C702430CA	1.929491	0.121102	0.796473	3.361871	hypothetical protein MG1
C702450WA	37.000828	30.020899	35.692039	37.759579	hypothetical protein CAA
C702460CA	44.987286	47.065689	36.524818	50.912685	GTPase
C702470CA	41.33532	45.489342	67.250122	63.805862	hypothetical protein CAA
C702480WA	75.51152	64.805046	124.809319	103.630562	hypothetical protein CAA
C702510WA	166.705582	176.792496	259.5755	233.591675	U6 snRNA-associated S
C702520WA	9.065728	6.919595	13.315073	14.994504	hypothetical protein CAA
C702530CA	18.960735	19.712219	21.119495	23.740524	hypothetical protein MG
C702540WA	33.421753	34.0891	44.154709	48.565884	conserved hypothetical p
C702550CA	36.419506	26.671896	63.036449	48.519043	hypothetical protein ME
C702560WA	5.243817	5.225088	8.395038	9.725066	hypothetical protein CAA
C702600CA	24.111712	21.759588	10.549946	10.913656	hypothetical protein CAA
C702610CA	36.425224	42.144054	27.50663	27.149675	hypothetical protein CAA
C702630WA	8.42365	11.052705	12.797458	13.437916	hypothetical protein CAA
C702660CA	14.886419	11.941422	11.08972	12.794044	hypothetical protein MG
C702670WA	2.986464	4.843817	8.106572	10.532051	hypothetical protein CAA
C702690CA	19.401312	22.936247	20.006989	19.139112	bifunctional diacylglycero
C702780WA	65.8097	63.975433	122.143982	94.286507	Ran guanyl-nucleotide ex
C702850WA	32.237186	40.993343	19.370619	23.030359	hypothetical protein CAA

C702860CA	20.876865	22.458187	24.347136	25.562418	E3 ubiquitin-protein ligas
C702920WA	4.324457	4.76175	3.364038	5.473439	hypothetical protein CAA
C702930CA	36.35775	49.686634	44.793972	45.744411	hypothetical protein CAA
C702960CA	12.261679	10.330384	14.568875	16.155521	hypothetical protein CAA
C703000CA	42.211002	55.439301	144.728622	123.385948	mitochondrial 54S ribosc
C703010WA	28.532713	25.716507	34.742874	32.945545	hypothetical protein CAA
C703030WA	94.298805	120.226494	133.073624	141.520081	hypothetical protein CAA
C703040WA	8.254245	11.976371	24.881542	23.363262	hypothetical protein CAA
C703050WA	72.300209	59.889954	85.007126	108.376137	enoyl-CoA hydratase
C703140WA	5.854113	8.054524	11.790186	12.743702	hypothetical protein CAA
C703150WA	13.416089	19.289112	7.449564	7.455508	hypothetical protein W5C
C703160WA	33.723457	34.218609	42.922958	37.21944	hypothetical protein CAA
C703200CA	22.655113	15.39681	14.232439	12.736893	hypothetical protein MGK
C703210WA	11.719769	17.868544	18.091166	16.664434	hypothetical protein CAA
C703230CA	11.458892	14.643575	25.403671	10.654825	hypothetical protein MEV
C703240WA	107.133499	98.658333	58.439331	64.105469	glucose-induced degrada
C703260CA	19.303331	22.572626	33.040798	28.315321	hypothetical protein CAA
C703270WA	90.734909	78.353889	41.11993	58.568848	hypothetical protein
C703280CA	161.165283	164.703262	117.55397	114.464546	hypothetical protein CAA
C703310WA	19.523731	15.379971	3.927118	8.017984	hypothetical protein MGC
C703350CA	6.386077	10.641257	6.421866	8.14427	aldo-keto reductase supe
C703370CA	39.897522	35.093033	95.339027	93.850601	hypothetical protein MGK
C703380WA	37.800838	43.615894	177.464966	165.258072	hypothetical protein CAA
C703400CA	32.163643	36.715477	30.975349	28.273108	hypothetical protein
C703410CA	11.261683	9.08977	16.172211	21.481264	hypothetical protein
C703460WA	5.790565	5.60253	6.788793	6.320868	hypothetical protein CAA
C703470WA	1.176509	5.630695	4.712288	4.826391	hypothetical protein CAA
C703480WA	68.919922	81.223701	72.070251	75.690613	Arf family guanine nucle
C703500WA	51.553417	43.712425	46.166901	59.70425	putative serine/threonine
C703550CA	0.903295	1.39152	0.887605	0.672632	hypothetical protein CAA
C703560WA	165.324249	216.99884	17.203726	33.011585	hypothetical protein CAA
C703580CA	9.409644	11.271113	9.391463	10.009604	hypothetical protein CAA
C703590CA	133.326416	126.149315	29.576427	28.693678	hypothetical protein CAA
C703610CA	7.930834	9.189654	16.100327	15.907106	hypothetical protein CAA
C703620CA	12.148336	13.744329	23.963556	23.040415	hypothetical protein CAA
C703640CA	7.727606	8.967504	24.932487	22.918159	asparagine--tRNA ligase
C703650WA	17.603451	10.050059	21.203278	23.511629	histidinol-phosphatase
C703660CA	69.644875	75.532944	89.544533	93.415428	proline--tRNA ligase
C703680WA	13.88422	11.583197	14.68359	13.609431	hypothetical protein CAA
C703690WA	11.825716	10.295254	8.27628	15.173095	hypothetical protein CAA
C703730CA	29.900436	25.153336	15.618459	14.357203	hypothetical protein CAA
C703760WA	48.123268	31.403877	42.790512	52.729858	hypothetical protein CAA
C703780CA	11.294698	13.146224	33.616051	42.331703	putative nitronate monoc
C703800WA	22.634562	35.713421	38.171513	60.984089	protein retreival receptor
C703820CA	70.764221	63.800186	77.547585	68.990021	hypothetical protein MGC
C703830CA	40.178036	40.313942	78.008377	73.689194	hypothetical protein CAA
C703840WA	47.909107	35.931168	68.336243	63.606197	cell differentiation protein
C703850WA	37.174023	38.769894	15.782514	17.176983	hypothetical protein CAA
C703860WA	263.696594	258.818237	80.313293	61.421391	proteinase B
C703880CA	11.717442	13.072389	20.164227	21.858755	hypothetical protein L15C
C703890CA	134.850052	125.795982	78.345787	79.091949	hypothetical protein CAA
C703970CA	57.82983	68.274719	81.672707	68.695915	hypothetical protein CAA
C703980WA	71.870155	100.718964	95.131042	102.509926	chaperone
C703990CA	22.058472	24.260128	36.619068	32.349365	putative tRNA acetyltrans
C704000WA	14.460925	15.807854	20.224396	22.087215	hypothetical protein CAA
C704010WA	14.20118	16.626009	37.786732	28.582241	Hsp70 family ATPase
C704060WA	2.268864	1.894305	3.345605	3.775391	hypothetical protein CAA
C704080CA	0.621114	0.371234	0	0	hypothetical protein MGC
C704090CA	102.337761	105.403267	19.468904	21.034658	hypothetical protein CAA
C704110WA	38.655739	37.798645	41.509583	44.344845	putative serine/threonine
C704120WA	15.357755	21.389277	53.438564	27.293451	hypothetical protein CAA
C704140CA	90.69133	87.121567	72.237648	73.653923	hypothetical protein MEC
C704150WA	5.79448	7.314649	8.785069	0	hypothetical protein CAA
C704160WA	6.525934	7.135698	5.277073	7.215403	hypothetical protein MG1

C704170WA	5.69891	6.917542	8.003798	13.386063	hypothetical protein CAA
C704200CA	19.509495	20.012655	18.590996	22.594782	Ran GTPase-binding pro
C704210CA	75.869499	81.958305	115.587051	112.139786	hypothetical protein CAA
C704240CA	26.34334	31.251154	64.445412	73.164688	hypothetical protein CAA
C704260WA	29.639482	34.657486	50.127029	43.952106	hypothetical protein
C704280CA	70.681824	77.334793	114.583832	85.636604	hypothetical protein CAA
C704290WA	48.521584	43.267418	100.647171	82.837013	hypothetical protein CAA
C704310CA	106.318764	88.173393	114.378639	101.238274	hypothetical protein CAA
C704320WA	14.980721	22.376474	18.777206	9.28975	hypothetical protein CAA
C704340CA	22.598192	20.041107	25.199509	23.242081	hypothetical protein MEK
CAC2	5.210674	5.963465	19.842358	22.726742	Cac2p
CAF16	63.997219	57.405842	29.412922	31.07239	putative ATP-binding cas
CAG1	45.702351	62.234741	86.193962	75.377594	guanine nucleotide-bindi
CAK1	23.474953	21.534065	27.797985	21.321062	cyclin-dependent protein
CAM1	259.63916	295.147125	189.520462	167.001724	elongation factor 1-gamr
CAM1-1	90.410027	111.354256	102.490112	81.279617	Cam1-1p
CAN1	275.129028	320.817596	44.596848	36.246883	lysine/arginine permease
CAN2	191.163879	159.08548	30.809156	28.045233	arginine permease
CAN3	61.822437	63.196114	96.766968	91.58165	Can3p
CAP1	148.447998	161.015793	175.190155	188.001785	DNA-binding transcriptio
CAP4	31.816204	24.28215	51.449902	53.538456	Cap4p
CAR1	184.02211	191.530731	245.755569	244.583389	arginase
CAR2	206.099945	220.336685	220.654007	212.216721	ornithine-oxo-acid transa
CAS1	9.149097	9.064085	18.85482	20.385336	ATP-dependent DNA he
CAS4	10.049974	9.544274	18.283092	22.928713	Cas4p
CAS5	51.570297	49.042332	88.364159	104.704781	Cas5p
CAT1	412.928253	394.994415	580.324768	641.135925	catalase A
CAT2	226.20665	222.862411	90.838913	103.503639	carnitine O-acetyltransfe
CAT8	4.893144	5.396887	7.327333	7.076371	DNA-binding transcriptio
CBF1	335.704437	397.720459	408.051971	449.612976	Cbf1p
CBK1	26.590254	30.125196	49.17437	53.656094	hypothetical protein L15C
CBP1	50.500145	58.09021	93.89402	98.690399	Cbp1p
CBR1	78.491684	80.921646	102.940727	93.699654	Cbr1p
CCC1	61.884727	54.764774	43.574398	33.880074	Ccc1p
CCC2	18.938231	22.240437	11.136468	11.204785	Cu(2+)-transporting P-ty
CCE1	3.268192	2.692842	12.137494	16.774534	cruciform cutting endonu
CCH1	8.626039	8.524708	14.971634	22.269192	Cch1p
CCN1	8.941175	7.63413	14.521631	17.082911	Ccn1p
CCP1	169.74855	203.264832	12.786083	13.801287	cytochrome c peroxidase
CCR4	37.474953	36.478405	32.85054	41.201622	CCR4-NOT core exoribo
CCS1	120.964722	139.296646	214.198944	174.933777	copper chaperone
CCT2	64.975975	67.323479	90.74118	73.602631	chaperonin-containing T-
CCT3	77.522217	86.28907	77.930878	74.362015	chaperonin-containing T-
CCT5	53.997368	62.603409	95.898369	83.583595	chaperonin-containing T-
CCT6	92.389114	89.699471	108.857994	102.464424	chaperonin-containing T-
CCT7	68.327454	84.062607	50.021774	53.062721	chaperonin-containing T-
CCT8	96.420906	85.256378	112.267159	93.244049	T-complex protein 1 sub
CCW14	43.763222	40.68716	29.588846	21.192636	Ccw14p
CDA2	6.436917	8.389376	5.390925	2.719354	chitin deacetylase
CDC10	67.12809	84.076843	239.573975	262.977753	septin
CDC11	51.472355	53.508404	130.146179	148.62265	septin
CDC12	90.401985	106.07357	207.126205	196.604813	septin, putative
CDC13	5.119889	6.510932	24.174215	22.391031	Cdc13p
CDC14	39.802296	37.89822	85.865555	117.544708	phosphoprotein phospha
CDC15	10.284551	6.663305	13.900431	12.934157	serine/threonine protein
CDC19	223.53157	237.288773	205.521301	209.615311	pyruvate kinase
CDC20	21.903133	17.756571	42.332611	57.937973	ubiquitin-protein transfer
CDC21	12.348801	13.403854	49.621628	46.00713	thymidylate synthase
CDC23	10.914526	12.489089	27.593435	26.354483	anaphase promoting cor
CDC24	25.104025	25.266048	33.258305	34.070641	Rho family guanine nucle
CDC27	7.093128	4.793553	19.388458	15.892203	anaphase promoting cor
CDC28	35.011059	27.532499	74.038536	73.972404	cyclin-dependent serine/
CDC3	91.963844	94.917366	173.107529	166.539398	septin
CDC34	682.277222	770.683044	271.698608	253.742935	SCF E2 ubiquitin-protein

CDC37	22.951458	22.747381	27.160629	35.860394	Cdc37p
CDC39	24.455675	25.545315	26.973223	29.92461	CCR4-NOT transcription
CDC4	33.38765	32.889957	26.520269	36.211456	SCF ubiquitin ligase com
CDC42	93.42215	82.502892	129.366364	104.628937	Rho family GTPase
CDC43	14.646836	13.000097	11.411393	15.302557	protein geranylgeranyltra
CDC45	7.006167	10.546379	15.038049	14.833986	DNA replication initiation
CDC46	10.128128	18.761543	65.614281	56.764561	MCM DNA helicase com
CDC47	24.018166	28.874279	114.43763	113.597679	mini-chromosome maint
CDC48	176.118896	176.726959	227.812363	219.918289	AAA family ATPase
CDC5	55.978603	52.556965	265.234039	372.436554	polo kinase
CDC50	39.250053	43.653229	53.727097	45.008953	aminophospholipid trans
CDC53	24.355377	29.093929	31.507763	43.752144	cullin
CDC54	13.426332	11.396379	61.743881	60.095844	MCM DNA helicase com
CDC55	52.370975	51.639294	62.29948	77.999641	protein phosphatase PP2
CDC6	21.102213	21.574539	36.764427	37.402351	AAA family ATPase
CDC60	59.55304	69.033615	65.970428	72.660965	leucine--tRNA ligase
CDC68	34.937923	30.85574	73.561684	75.814377	FACT complex subunit S
CDC7	6.917566	7.4505	20.10882	23.34276	hypothetical protein L15
CDC73	30.577286	33.102974	71.132141	68.171638	Cdc73p
CDG1	542.27417	645.650085	199.701721	186.13591	Cdg1p
CDH1	20.804626	22.672499	33.367512	37.374466	Cdh1p
CDL1	9.564344	8.483829	14.467103	15.360118	Cdl1p
CDR1	480.499695	511.279694	170.694427	184.161926	ATP-binding cassette mu
CDR11	307.968628	280.088318	18.879271	18.399391	Cdr11p
CDR2	37.556286	40.60569	17.138809	14.667105	Cdr2p
CDR3	21.905949	23.974939	16.88175	13.580436	RecName: Full=Opaque-
CDR4	651.972961	627.802673	199.818298	179.741547	Cdr4p
CDS1	52.370811	60.343872	40.040943	53.533634	phosphatidate cytidylyltra
CEF1	64.043571	56.178696	51.024738	56.986385	Cef1p
CEF3	589.086365	624.787903	318.097992	328.257385	translation elongation fac
CEK1	39.761971	44.6469	72.803757	79.922592	extracellular signal-regul
CEK2	63.504807	71.051918	28.632399	25.749155	Cek2p
CEM1	10.55814	11.370113	14.064487	13.733729	fatty acid synthase
CET1	66.334526	67.94928	72.30278	60.300388	polynucleotide 5'-
CEX1	8.334453	8.068507	20.772236	24.830805	Cex1p
CFL1	10.028754	11.572559	16.758572	12.867658	Cfl1p
CFL11	0.196848	0	0.303009	0.649417	Cfl11p
CFL2	4.926359	3.352265	28.091923	30.414042	Cfl2p
CFL4	0.826208	0.748796	4.026531	5.138153	ferric/cupric-chelate redu
CFL5	11.171741	12.996702	15.431314	12.393395	ferric-chelate reductase
CGR1	24.395197	29.027441	42.710209	33.992073	Cgr1p
CGT1	46.61998	49.80727	83.043167	79.481392	mRNA guanylyltransfera
CHA1	158.749451	196.145096	500.014526	489.466553	Cha1p
CHC1	37.96463	41.704117	75.692894	78.842575	clathrin heavy chain, par
CHK1	4.925519	5.834432	4.623576	4.529606	Chk1p
CHL4	3.782366	2.196743	18.952669	16.498734	Chl4p
CHO1	129.338593	144.288635	139.237839	138.470764	CDP-diacylglycerol-serin
CHO2	15.506764	13.706116	19.757698	19.474672	phosphatidylethanolami
CHR1	173.728683	165.934219	91.741196	96.418343	ATP-dependent RNA he
CHS1	17.025511	14.128757	60.496628	82.450203	chitin synthase
CHS2	31.125023	32.524418	18.343182	25.442131	chitin synthase
CHS3	49.74651	53.702995	22.473866	25.07678	chitin synthase
CHS4	64.965744	64.430229	36.592648	40.454365	Chs4p
CHS5	44.644775	43.660107	93.332245	86.616173	Chs5p
CHS6	11.493448	7.780323	26.035452	23.775393	Chs6p
CHS7	72.585388	84.484314	84.071602	67.367462	Chs7p
CHS8	14.331751	14.408405	22.984709	37.810921	Chs8p
CHT1	12.315719	14.997527	15.514292	17.28751	chitinase 1
CHT2	656.073853	551.995056	1477.774048	1725.005981	Cht2p
CHT3	1334.829346	888.095093	1061.997314	1321.656372	hypothetical protein CA
CHT4	20.199657	16.452452	24.222164	17.480316	putative chitinase
CIC1	66.434608	65.336044	29.574728	26.117344	proteasome-interacting
CIP1	9.432935	12.852385	28.800907	21.674219	Cip1p
CIRT4B	18.010994	22.157658	18.88492	23.374453	Cirt4bp

CIS2	13.160867	11.138407	8.709406	11.330009	gamma-glutamyltransfer
CIT1	1074.750244	1011.806274	572.343079	615.919678	citrate (Si)-synthase
CKA1	77.958878	77.814491	101.536598	88.080132	casein kinase 2 catalytic
CKA2	64.241615	69.509216	50.42551	45.912479	casein kinase 2 catalytic
CKB1	74.646866	72.428185	48.346264	54.524837	casein kinase 2 regulato
CKB2	56.635536	64.776741	72.002075	80.309044	casein kinase 2 beta&ap
CKS1	107.613708	99.100189	99.832092	95.030296	cyclin-dependent protein
CLA4	15.684167	17.547283	18.469593	20.395699	serine/threonine protein
CLB2	31.287703	37.003975	139.952194	157.515808	G2/mitotic-specific cyclin
CLB4	12.302169	16.060553	62.143211	65.714539	B-type cyclin
CLC1	103.295113	104.580498	309.134705	296.53302	hypothetical protein ME
CLG1	839.966309	704.96814	157.444443	175.656631	Clg1p
CLN3	106.417816	100.190834	68.507492	70.533531	cyclin
CMD1	302.604675	282.953583	599.545044	519.664978	CaM, putative
CMK1	79.823112	86.424355	23.47764	30.128212	protein kinase
CMK2	41.993237	47.439651	62.790543	80.541832	calmodulin-dependent p
CMP1	31.582211	28.461464	46.136974	50.692451	calcineurin catalytic subu
CNB1	90.989357	72.774506	107.412636	118.006966	Ca++/calmodulin-regulat
CNH1	71.486496	54.933125	47.879887	40.923088	Cnh1p
CNS1	44.69339	43.218369	27.639008	27.424219	HSP70/90 family co-cha
CNT	204.818344	236.709167	34.708664	33.749916	Cntp
COF1	437.761475	427.622925	817.700195	921.389648	cofilin
COG4	5.768175	9.339827	27.119963	28.882282	Golgi transport complex
COI1	42.791428	35.665962	84.765526	80.595779	Coi1p
COQ3	35.339172	46.139606	61.430202	52.266872	hexaprenyldihydroxyben
COQ4	32.622261	35.623306	110.649048	95.376244	ubiquinone biosynthesis
COQ5	72.982727	71.68895	193.954056	165.60022	ubiquinone/menaquinon
COQ6	62.848873	67.180077	125.319832	117.848778	putative N,N-dimethylani
COX11	66.612839	71.062706	145.391037	121.147186	Cox11p
COX13	1214.028564	1280.786499	3149.645752	3401.445312	cytochrome c oxidase su
COX15	124.770226	145.677063	407.305237	315.983215	Cox15p
COX17	257.295563	241.195404	309.744812	366.760925	copper metallochaperon
COX19	62.555511	81.04882	242.034821	202.352661	Cox19p
COX4	652.637146	750.693481	1783.851929	1383.477539	cytochrome c oxidase su
COX5	647.382141	637.51886	1267.145874	1187.949463	cytochrome c oxidase su
COX6	975.443054	919.761475	1906.815796	2050.227539	cytochrome c oxidase su
COX7	175.422958	165.923462	409.169159	466.727051	cytochrome c oxidase su
COX8	1270.738525	1170.414795	3087.48877	2752.810303	cytochrome c oxidase su
COX9	1101.650146	1069.991089	2524.94751	2397.098877	cytochrome c oxidase su
CPA1	61.035347	71.883911	17.88673	23.331408	carbamoyl-phosphate sy
CPA2	26.408533	30.432295	8.882386	10.809784	carbamoyl-phosphate sy
CPH1	8.259806	6.950469	15.376604	19.239397	transcription factor CPH
CPH2	1054.682007	1079.48938	708.755188	687.451294	Cph2p
CPP1	107.372978	126.159744	23.747803	36.322311	hypothetical protein L15
CPR3	206.425842	172.87796	281.437225	253.591125	peptidylprolyl isomerase
CPR6	40.117748	54.143452	62.56736	53.077682	peptidylprolyl isomerase
CPY1	180.115799	166.28038	156.415573	197.314102	hypothetical protein
CR00010CA	20.90596	19.295574	26.991636	33.670074	hypothetical protein W5
CR00040CA	30.148529	31.298588	26.492691	28.091507	hypothetical protein CAA
CR00060CA	17.484865	21.493092	64.824684	38.212341	hypothetical protein CAA
CR00090CA	72.177513	88.361496	42.61076	40.40572	hypothetical protein CAA
CR00110WA	36.484039	35.473137	28.862923	28.644962	hypothetical protein CAA
CR00130CA	29.073412	28.363459	43.602524	49.201256	hypothetical protein CAA
CR00160CA	141.008652	142.817062	234.721878	175.812744	hypothetical protein CAA
CR00220WA	13.302832	22.682455	6.248393	9.761791	hypothetical protein CAA
CR00230WA	16.170424	18.313047	28.645416	32.150707	hypothetical protein CAA
CR00270CA	26.82445	14.880603	40.519257	37.349064	hypothetical protein CAA
CR00280CA	13.068595	15.706135	27.76528	33.668118	hypothetical protein MG
CR00290WA	354.572266	375.7034	212.965225	235.522949	hypothetical protein MG5
CR00310CA	1861.404907	1991.030762	847.113403	840.766479	hypothetical protein CAA
CR00340CA	37.90519	48.896744	48.426548	71.692543	hypothetical protein CAA
CR00350WA	39.06221	48.121586	31.842997	30.462259	nicotinamide-nucleotide
CR00370WA	5.858641	8.928232	13.419746	14.236104	cullin
CR00380WA	10.747832	8.016562	15.984604	21.25733	hypothetical protein CAA

CR00420WA	5.458849	5.283413	6.396728	6.644577	hypothetical protein CAA
CR00430CA	65.989464	64.536331	119.162766	99.975784	hypothetical protein CAA
CR00460CA	137.490891	146.711853	94.566231	86.966492	snoRNA-binding rRNA-p
CR00470WA	107.892448	94.495857	95.186943	77.586029	hypothetical protein CAA
CR00490WA	78.615738	95.709755	185.974197	157.839355	50S ribosomal protein L
CR00530WA	0	0.707805	0.721504	0.163293	hypothetical protein CAA
CR00570WA	22.155546	19.051386	40.493889	49.961983	hexaprenyl-diphosphate
CR00600CA	23.551308	25.764544	24.097309	39.462589	hypothetical protein MG
CR00630WA	51.193108	43.279057	65.465317	70.490662	hypothetical protein CAA
CR00650WA	0	0	0	0.241235	hypothetical protein CAA
CR00660WA	3.123923	4.435231	9.260427	3.737269	hypothetical protein CAA
CR00670CA	6.841733	8.489227	14.965899	13.203262	tRNA guanosine-2&apos
CR00690CA	13.890688	11.491858	28.421549	34.105801	hypothetical protein CAA
CR00700WA	3.129946	0	6.788596	8.966401	hypothetical protein CAA
CR00710CA	5.379135	3.586593	10.379118	12.481552	3-oxoacyl-
CR00720WA	0.110201	0.011018	0.048489	0.123623	hypothetical protein CAA
CR00750CA	40.031792	47.24926	58.046268	63.215057	
CR00810WA	58.466679	53.650803	31.276247	38.947849	hypothetical protein CAA
CR00820CA	32.381981	31.755117	33.78746	31.821409	hypothetical protein CAA
CR00830WA	13.786017	15.129333	28.236435	25.352161	hypothetical protein CAA
CR00840CA	0.445711	0	4.178935	1.677891	hypothetical protein CAA
CR00870CA	4.903871	5.156094	5.530554	9.723475	palmitoyltransferase
CR00880WA	12.48439	14.023873	25.602734	21.618546	hypothetical protein CAA
CR00890CA	30.328176	27.297586	46.49472	57.903919	hypothetical protein CAA
CR00910WA	4824.819336	4064.050049	8011.208008	8584.949219	--
CR00980CA	45.402988	58.079208	51.532562	50.471012	phosphopantothenoylcys
CR00990WA	52.337479	47.607452	141.25647	153.798782	signal peptidase comple
CR01020CA	4.350103	4.746451	6.944894	7.588762	hypothetical protein CAA
CR01050CA	23.471518	21.559811	32.280315	30.446424	hypothetical protein CAA
CR01070WA	7.36056	7.41714	25.302523	36.38242	hypothetical protein CAA
CR01080WA	7.454217	9.216955	14.687777	19.010628	hypothetical protein CAA
CR01090WA	11.48503	8.884212	11.386811	10.842715	hypothetical protein CAA
CR01100CA	27.422796	25.16584	160.429657	134.192734	cytochrome c oxidase-a
CR01120CA	62.96767	60.8153	148.869064	106.845398	hypothetical protein CAA
CR01130WA	6.858857	7.361805	10.370229	10.97478	hypothetical protein MG
CR01170WA	13.230286	13.748288	19.335154	21.798943	E3 ubiquitin-protein ligas
CR01180WA	28.723867	21.879221	47.742992	52.629734	hypothetical protein CAA
CR01220WA	40.651154	47.418945	11.711774	16.03187	hypothetical protein CAA
CR01250CA	0	0	0.051866	0.292764	hypothetical protein CAA
CR01260WA	25.578766	25.260374	23.764076	23.848476	hypothetical protein CAA
CR01280CA	104.062035	96.184067	23.628157	30.029263	sterol transporter
CR01300WA	99.87085	122.642838	227.778656	197.85556	hypothetical protein CAA
CR01320CA	11.415257	7.981631	8.431396	6.92135	hypothetical protein ME
CR01340WA	1.538423	2.422571	2.303061	0.733678	hypothetical protein ME
CR01350CA	80.142159	87.104195	109.569466	102.555077	hypothetical protein CAA
CR01360WA	16.489319	19.698364	46.544682	60.365475	MIND complex subunit
CR01370CA	78.323158	75.624069	142.055756	143.483597	mitochondrial 37S ribos
CR01380WA	5.794238	7.255449	12.182574	15.678338	hypothetical protein CAA
CR01410CA	40.780243	41.196827	26.201048	28.396124	hypothetical protein CAA
CR01420WA	21.525278	19.485195	53.285347	47.856205	transcription factor TFIII
CR01430WA	28.22793	42.012413	50.364475	48.784397	phosphatidylinositol N-a
CR01440CA	519.744812	529.163513	12.686373	16.689178	hypothetical protein CAA
CR01490CA	186.248993	216.364624	251.356827	212.16954	Arf family guanine nucle
CR01510CA	1.410483	0.735705	1.277953	0.292406	hypothetical protein CAA
CR01530CA	0	0	0.828425	0	hypothetical protein CAA
CR01550CA	3.345329	6.879094	7.859755	10.380054	3'-5'-exode
CR01560WA	7.80541	6.339835	9.400611	13.820946	hypothetical protein CAA
CR01570WA	12.545351	10.070039	9.063235	9.919664	peptidyl-tRNA hydrolase
CR01600CA	5.019081	4.301147	5.80444	5.356589	hypothetical protein CAA
CR01630CA	23.359053	21.754211	8.827928	9.204032	HAD ATPase, P-type, fa
CR01640CA	13.455718	10.123889	8.112624	7.699574	HAD ATPase, P-type, fa
CR01670WA	10.24536	10.892939	21.299356	19.716734	hypothetical protein MG
CR01700CA	15.069871	14.945517	19.651571	28.187954	U6 snRNP complex subu
CR01710WA	28.481903	17.131126	22.158762	11.467093	nucleolar protein TMA23

CR01720WA	10.50097	10.727807	17.185087	16.99386	hypothetical protein MG
CR01770CA	17.142023	12.450564	15.259793	18.68927	hypothetical protein ME
CR01780WA	33.447609	31.797386	34.230495	23.759344	25S rRNA (uracil2843-N
CR01790CA	8.076057	6.341033	6.791033	9.124339	MutS family protein
CR01810CA	14.670581	12.553192	3.9334	1.118045	hypothetical protein CAA
CR01820WA	8.82563	11.099018	18.813354	15.98187	hypothetical protein CAA
CR01910CA	1.190227	3.447324	0.896045	1.432943	dethiobiotin synthase
CR01920WA	2.282356	2.199075	0.432263	0.65846	adenosylmethionine-8-a
CR01950WA	64.443138	69.701897	23.437363	29.753145	DNA-directed RNA poly
CR02030CA	33.816662	28.083448	18.836124	18.104769	rRNA (cytosine-C5-)-me
CR02060WA	13.499936	18.51037	6.264057	9.123857	hypothetical protein CAA
CR02100CA	51.586914	48.171238	80.822098	54.811413	hypothetical protein CAA
CR02120CA	37.747337	34.70219	66.700188	52.396053	hypothetical protein CAA
CR02210WA	45.891045	41.006794	88.424606	118.902687	protein-serine/threonine
CR02260CA	8.779627	6.948895	19.460388	10.496616	hypothetical protein ME
CR02270CA	18.407598	15.634081	37.368385	45.087059	hypothetical protein CAA
CR02300CA	24.610226	21.839558	13.768503	16.604158	hypothetical protein CAA
CR02340WA	0	0	0.785726	0.198892	hypothetical protein CAA
CR02380CA	9.011559	11.183362	37.442001	49.023529	hypothetical protein CAA
CR02390WA	19.96262	23.668592	22.182203	25.807526	protein phosphatase reg
CR02410WA	8.051019	6.817265	11.275703	8.64597	hypothetical protein CAA
CR02420WA	36.79258	51.681374	51.406296	36.937763	U3 small nucleolar RNA-
CR02430CA	11.009467	11.423215	16.897346	21.379683	hypothetical protein CAA
CR02440WA	7.687191	10.270631	30.47694	29.323893	hypothetical protein CAA
CR02460WA	27.502474	26.039541	26.388912	22.19495	hypothetical protein CAA
CR02500WA	35.577145	35.427258	36.875427	28.178173	hypothetical protein CAA
CR02510WA	726.656067	683.354248	447.314728	487.342987	hypothetical protein MG
CR02550CA	63.022697	69.673599	44.869946	44.123428	exosome non-catalytic c
CR02570CA	16.161175	19.80444	30.180799	31.45904	hypothetical protein ME
CR02590CA	2.776459	3.102698	7.24827	7.023746	DEAH-box RNA helicase
CR02600WA	2.783318	2.305317	5.801778	8.531075	hypothetical protein MG
CR02610CA	51.451813	54.604977	94.673073	83.62632	hypothetical protein MG
CR02620CA	137.496445	151.144791	194.973267	188.499588	hypothetical protein CAA
CR02630CA	7.23969	5.887124	14.328242	13.475554	Golgi transport complex
CR02670CA	20.810656	18.283796	51.40675	42.43293	hypothetical protein CAA
CR02680WA	5.513144	6.235119	21.699133	23.286982	kinetochore-associated
CR02690WA	24.856405	23.895182	47.885868	61.788879	hypothetical protein CAA
CR02700WA	18.127522	21.741957	21.876514	15.880435	hypothetical protein CAA
CR02770CA	18.53388	16.746017	30.405109	36.750492	E1 ubiquitin-activating pr
CR02780WA	8.011056	8.049063	7.865963	9.129659	hypothetical protein CAA
CR02800CA	11.531992	11.052005	6.002075	5.310481	hypothetical protein CAA
CR02880WA	12.9733	13.570018	7.51965	10.771739	hypothetical protein CAA
CR02890CA	33.971493	34.45966	19.365429	20.080029	DNA-directed RNA poly
CR02910WA	53.924061	51.240326	82.400642	77.280983	serine/threonine protein
CR02930WA	7.212162	5.814524	17.615938	18.800825	hypothetical protein CAA
CR02940CA	3.889148	4.629997	1.899081	2.77689	hypothetical protein CAA
CR02950CA	93.534775	96.482849	172.100296	183.048492	mitochondrial 37S ribos
CR02960WA	64.468002	71.990326	22.321257	24.168789	hypothetical protein CAA
CR02970CA	31.141312	29.083527	28.308287	28.221643	TFIIH/NER complex AT
CR03000CA	67.41925	63.072975	79.537186	91.883392	hypothetical protein CAA
CR03020CA	24.990667	23.410994	60.443138	82.395081	hypothetical protein CAA
CR03070WA	34.34161	45.167751	52.659191	37.684357	ribosome dissociation fa
CR03080CA	18.665169	20.796654	43.57711	38.33115	hypothetical protein CAA
CR03110WA	14.238331	10.764759	38.785919	24.500275	glutamate--tRNA ligase
CR03120WA	109.79303	139.593689	214.782959	159.789032	hypothetical protein CAA
CR03130WA	36.89225	41.511078	87.656113	92.624718	hypothetical protein CAA
CR03160WA	20.484051	17.872353	15.404962	10.496218	tRNA methyltransferase
CR03180WA	43.820232	40.804161	60.652332	78.521759	hypothetical protein MG3
CR03200CA	18.803236	11.743293	17.582666	13.030101	ribonuclease P/MRP pro
CR03220CA	7.85494	6.65454	14.443389	11.386411	cysteine protease ATG4
CR03230WA	9.67443	10.317924	17.708481	14.653581	hypothetical protein CAA
CR03240CA	31.654774	29.258154	7.923924	8.26686	hypothetical protein CAA
CR03250CA	1521.419189	1489.589478	1002.727112	1170.223389	hypothetical protein CAA
CR03260WA	393.486176	399.960236	386.717316	390.814148	hypothetical protein CAA

CR03270WA	13.793928	19.587091	10.175264	9.601448	hypothetical protein CAA
CR03300CA	1.836327	0.74634	1.527733	1.439765	hypothetical protein CAA
CR03310CA	77.113724	91.348167	156.858276	167.094757	hypothetical protein CAA
CR03320CA	0.076382	0.047984	0.151011	0.052288	hypothetical protein CAA
CR03330WA	11.564391	13.552746	16.535866	19.648672	conserved hypothetical p
CR03340CA	5.890636	8.486486	28.183573	31.534529	hypothetical protein CAA
CR03350CA	25.450432	25.158306	57.312115	58.334366	hypothetical protein CAA
CR03360WA	178.922211	169.039978	83.578133	81.592499	U3 small nucleolar RNA-
CR03400WA	6.989176	10.35012	29.398281	26.590336	isoleucine--tRNA ligase
CR03410WA	121.830009	126.213806	125.674736	123.430412	hypothetical protein CAA
CR03430WA	44.858902	58.353012	50.964783	61.939701	hypothetical protein CAA
CR03440WA	7.12825	11.696968	1.583958	6.310273	hypothetical protein CAA
CR03460WA	18.444881	14.819561	44.711636	47.426174	transcription initiation fac
CR03470WA	15.697966	14.066349	48.333763	51.477135	hypothetical protein MG1
CR03480WA	8.629528	12.326406	4.014931	2.041763	hypothetical protein CAA
CR03510WA	3.131075	4.288025	2.455239	2.509817	hypothetical protein CAA
CR03520CA	34.999916	34.000149	46.622463	38.135002	hypothetical protein CAA
CR03530WA	115.225464	124.375031	157.523117	164.743805	hypothetical protein CAA
CR03540WA	24.632542	23.321514	19.792589	15.206622	hypothetical protein CAA
CR03560WA	20.727613	14.430144	20.954714	24.599852	hypothetical protein CAA
CR03580CA	1.741343	3.079376	2.191786	1.189523	sugar porter (SP) family
CR03590CA	5.212586	6.021885	8.325171	8.241417	DNA 5'-adenosine
CR03600CA	43.566601	48.841488	105.820068	142.598297	coatomer subunit zeta
CR03620CA	18.416336	22.059484	29.844643	27.643343	hypothetical protein CAA
CR03640CA	46.507759	41.300838	63.507736	52.268723	hypothetical protein CAA
CR03660CA	8.945159	16.601057	9.770844	7.792379	hypothetical protein CAA
CR03670WA	0.230062	0.688038	0	0.40876	hypothetical protein CAA
CR03690WA	13.233421	13.013642	6.14339	4.488102	hypothetical protein CAA
CR03700CA	12.586923	9.265267	16.056456	22.199051	hypothetical protein CAA
CR03710CA	52.555687	36.93454	105.03392	110.811989	hypothetical protein CAA
CR03730CA	69.233849	75.642349	59.370762	63.374371	hypothetical protein ME
CR03740CA	60.601616	38.394451	84.249268	87.374931	riboflavin kinase
CR03760WA	56.183788	61.601639	48.166599	43.797436	S-adenosylmethionine-d
CR03780CA	27.697643	21.954683	29.801332	27.851952	hypothetical protein MGI
CR03840CA	177.697906	174.423096	24.093094	28.127817	hypothetical protein CAA
CR03860CA	9.02879	13.123948	16.427412	10.833636	hypothetical protein ME
CR03870WA	24.776314	41.49371	85.639923	61.766026	hypothetical protein CAA
CR03910CA	22.882317	17.450054	28.106352	37.836258	hypothetical protein CAA
CR03930CA	17.104757	18.464888	25.029037	26.286415	hypothetical protein CAA
CR03940WA	66.095589	57.7421	40.709	46.943489	hypothetical protein CAA
CR03950WA	22.261841	27.967747	45.986431	43.356277	hypothetical protein CAA
CR03960CA	6.788468	7.331144	6.826048	9.284467	hypothetical protein CAA
CR03980WA	73.116425	85.727028	50.988808	54.37109	hypothetical protein CAA
CR04020CA	32.560345	34.005352	111.25132	87.51619	cell division control prote
CR04080CA	50.877388	53.989796	61.201271	74.707932	translocation protein SE
CR04110WA	67.208755	60.708969	21.663919	32.114777	RNA-binding snoRNP as
CR04120CA	3.284866	3.359521	7.138728	5.881147	mismatch repair ATPase
CR04140WA	82.929619	88.77903	157.633362	162.312881	mitochondrial 37S riboso
CR04150WA	23.053755	18.095547	15.216061	16.282576	S-adenosylmethionine-d
CR04160CA	51.71497	47.847469	34.763386	31.615694	tRNA 1-methyladenosine
CR04170WA	72.250198	80.79203	52.184387	51.122189	rRNA (cytosine-C5-)-me
CR04180CA	27.819468	23.527349	36.755009	37.144875	hypothetical protein CAA
CR04220CA	43.525455	60.920727	13.504389	7.24376	hypothetical protein CAA
CR04230WA	23.596691	23.834135	30.130733	27.321293	ribosylnicotinamide kinas
CR04240CA	49.705341	46.766441	24.566183	28.308891	ribosome biosynthesis p
CR04250WA	0.721151	1.170726	1.612864	1.296993	hypothetical protein CAA
CR04270CA	15.832086	19.774508	37.135849	36.135422	hypothetical protein CAA
CR04280CA	19.760679	22.31513	45.588791	32.09362	glycolipid translocation p
CR04300WA	66.925354	62.971241	66.875893	68.232536	tRNA (cytosine-5-)-meth
CR04310CA	40.234489	29.223034	74.228149	49.5709	hypothetical protein CAA
CR04330WA	15.825986	19.724449	30.150612	27.742092	hypothetical protein CAA
CR04350CA	20.407116	21.124664	36.391285	35.856915	hypothetical protein CAA
CR04370WA	12.845383	19.339804	33.389744	42.293377	hypothetical protein CAA
CR04390CA	16.610415	17.759584	20.713335	26.184166	hypothetical protein CAA

CR04400WA	3.335423	1.710557	15.333716	3.976963	hypothetical protein CAA
CR04410WA	4.144921	4.860049	6.727495	8.646231	hypothetical protein CAA
CR04450CA	25.16794	23.021019	63.69083	63.814621	chromatin modification p
CR04460CA	15.179714	17.432589	47.728931	34.257168	hypothetical protein CAA
CR04490CA	24.922796	31.034777	28.750658	26.677708	hypothetical protein CAA
CR04500CA	13.296473	17.317947	26.113077	24.010996	hypothetical protein CAA
CR04560CA	26.29624	25.108934	59.286434	45.237892	multifunctional nuclease
CR04580WA	154.752029	154.394485	269.97525	248.958603	mitochondrial 54S ribos
CR04600WA	578.959778	616.357056	58.926926	63.935883	hypothetical protein CAA
CR04610CA	9.338809	8.622395	4.16693	3.328159	hypothetical protein CAA
CR04620CA	0.125118	0.263368	0.210712	0	hypothetical protein CAA
CR04650WA	28.865137	24.389666	74.356621	76.734634	hypothetical protein CAA
CR04680CA	13.202201	13.949398	4.424024	2.36874	hypothetical protein CAA
CR04710WA	13.566628	15.514356	18.879269	25.337643	putative peptidylprolyl iso
CR04720CA	11.399988	11.182983	17.648781	18.451574	chromatin-remodeling A
CR04730WA	115.113548	117.976357	215.937897	178.083054	hypothetical protein CAA
CR04750WA	78.691559	66.710388	63.858479	80.88163	hypothetical protein CAA
CR04760CA	8.294761	9.651348	11.721776	14.627607	hypothetical protein CAA
CR04770CA	20.507044	17.983185	55.993599	86.658119	hypothetical protein MG
CR04820WA	1512.461548	1321.80127	227.865707	202.946854	hypothetical protein CAA
CR04830CA	7.369486	5.7058	6.102674	8.761259	hypothetical protein CAA
CR04850CA	69.1763	84.646866	51.437115	54.573513	hypothetical protein CAA
CR04860CA	37.738255	50.147438	24.297148	15.270452	hypothetical protein CAA
CR04870CA	23.879749	27.902411	13.562157	10.14927	hypothetical protein CAA
CR04880WA	12.697493	18.611673	24.096691	25.866901	threonine aldolase
CR04920WA	70.291199	77.26767	41.746136	37.517307	hypothetical protein CAA
CR04940WA	6.121405	6.510614	23.921137	23.683544	hypothetical protein L15
CR04970CA	0	0	0.825118	0	hypothetical protein I503
CR04980CA	0.245475	0.487003	0	0.524427	hypothetical protein W5
CR04990CA	0.076123	0.540494	2.105502	2.546367	hypothetical protein CAA
CR05010WA	6.483492	7.383572	15.41166	13.341817	crossover junction endo
CR05030WA	38.000267	39.840828	21.942799	27.865808	hypothetical protein CAA
CR05100WA	15.861881	11.418593	7.888511	9.089116	hypothetical protein CAA
CR05120WA	26.580017	23.660021	27.4695	26.844969	SIT4-associating protein
CR05130CA	14.97164	15.226026	23.656935	16.749037	hypothetical protein CAA
CR05140WA	13.02961	16.420557	21.692944	26.459656	hypothetical protein ME
CR05150WA	43.02747	62.347851	97.773148	126.384865	mitochondrial 54S ribos
CR05160CA	1.979872	3.993826	3.193351	4.979601	hypothetical protein CAA
CR05190WA	0.076123	0.813144	0.56471	0.95363	hypothetical protein CAA
CR05200CA	102.994064	98.598564	283.085999	346.190247	hypothetical protein CAA
CR05210WA	3.804699	1.831992	10.769784	19.177965	Hap43p-repressed prote
CR05310WA	36.891762	38.16378	170.948944	142.042664	hypothetical protein CAA
CR05330WA	113.303848	99.119499	64.953796	61.073616	hypothetical protein ME
CR05360CA	13.5788	12.456238	44.501087	50.659801	hypothetical protein CAA
CR05440WA	124.433418	147.378296	295.622467	227.148224	3-hydroxyanthranilate 3,
CR05450CA	39.851189	36.365608	33.305496	28.731834	hypothetical protein CAA
CR05460WA	32.944374	26.940565	41.039024	30.686621	hypothetical protein CAA
CR05480WA	166.700226	159.629822	164.233093	164.55043	mitochondrial 2-oxodica
CR05500CA	7.826132	7.633628	13.62921	15.747896	hypothetical protein CAA
CR05540CA	39.979424	47.65387	50.513618	52.099861	hypothetical protein CAA
CR05550CA	22.918951	26.881252	27.615383	28.676918	DNA-directed RNA poly
CR05560WA	14.05181	21.720499	27.050797	26.764919	TFIIH/NER complex sub
CR05580CA	2.875504	1.748904	4.773364	6.430361	hypothetical protein CAA
CR05640CA	25.325569	38.941277	55.505711	37.877213	hypothetical protein CAA
CR05680CA	77.128624	82.728767	186.641235	213.602448	Biofilm-induced protein,
CR05700CA	67.266739	84.793266	86.624023	91.755745	hypothetical protein CAA
CR05710CA	9.717402	10.025079	8.884508	13.639172	hypothetical protein CAA
CR05730CA	163.630859	168.44931	294.496674	326.159149	hypothetical protein CAA
CR05750WA	86.986717	91.771332	218.064804	174.52504	hypothetical protein CAA
CR05760CA	12.227032	8.747893	24.241467	29.25638	hypothetical protein CAA
CR05770WA	13.340323	14.525755	15.066664	17.554808	hypothetical protein CAA
CR05800CA	34.003719	44.279026	78.401863	63.916393	hypothetical protein CAA
CR05840WA	24.932804	20.369499	138.012268	122.535255	hypothetical protein CAA
CR05860WA	53.177948	65.690239	191.113922	143.568924	hypothetical protein CAA

CR05880WA	16.16046	24.846888	55.114864	57.303238	hypothetical protein CAA
CR05890CA	29.968914	23.907877	46.788441	50.565018	hypothetical protein CAA
CR05900WA	5.016735	7.107221	7.632458	4.850202	hypothetical protein MG7
CR05910WA	72.260696	67.410812	166.854065	171.965958	hypothetical protein CAA
CR05960WA	19.045845	28.084097	115.090446	106.320908	hypothetical protein CAA
CR05970CA	21.728703	22.559362	69.701118	59.315014	bifunctional AAA family A
CR05980WA	8.129158	7.683765	13.714229	14.115444	ubiquitin-specific proteas
CR06010WA	15.923253	11.091133	20.089525	18.525751	hypothetical protein CAA
CR06020WA	22.34564	29.173174	13.589391	15.542322	hypothetical protein CAA
CR06030CA	6.554214	6.573011	8.400669	11.329533	hypothetical protein CAA
CR06040WA	433.759125	487.280487	193.504333	221.879013	serine/threonine protein
CR06060WA	80.67437	70.984451	120.522705	81.691734	hypothetical protein MEK
CR06070WA	85.668633	74.088165	118.613243	117.192894	ketoreductase
CR06090WA	41.141754	40.098804	79.768784	69.823166	G protein beta subunit-lik
CR06100CA	2.305862	2.407734	3.755381	3.268712	hypothetical protein CAA
CR06140WA	53.362747	52.670498	4.12163	3.241425	hypothetical protein MG0
CR06170WA	32.139412	31.76886	35.224796	39.793045	hypothetical protein CAA
CR06230WA	62.8923	56.252407	13.20826	13.830748	hypothetical protein CAA
CR06250WA	7.425333	7.583691	12.703491	12.072097	hypothetical protein CAA
CR06260WA	11.384341	15.229653	20.028811	21.181149	hypothetical protein CAA
CR06270WA	3.546625	4.626983	3.598387	2.209658	hypothetical protein CAA
CR06290CA	15.771359	14.561283	53.721363	50.315838	hypothetical protein CAA
CR06310WA	4.076173	4.569814	3.432694	1.717986	hypothetical protein CAA
CR06320CA	21.080435	23.677698	16.673473	15.957829	hypothetical protein CAA
CR06330CA	45.154331	47.932861	33.692455	37.623711	hypothetical protein CAA
CR06380CA	9.582941	10.808439	53.918331	41.845509	hypothetical protein CAA
CR06430WA	1.964098	7.555513	13.685093	12.418802	hypothetical protein CAA
CR06450WA	10.860672	12.67578	14.549942	14.791473	polynucleotide 5'-k
CR06470WA	39.958393	37.38615	39.901863	34.651997	E3 ubiquitin-protein ligas
CR06500CA	89.645187	129.228729	31.018042	39.54285	hypothetical protein CAA
CR06510WA	59.422516	67.861404	13.590978	24.097034	hypothetical protein MG7
CR06520CA	39.429668	33.733482	25.926147	35.359261	Rab family GTPase
CR06530WA	54.407833	52.790115	83.362404	109.805222	hypothetical protein CAA
CR06550CA	1187.461426	1062.383789	526.972595	560.662781	hypothetical protein MG0
CR06560CA	129.436615	131.893539	153.756363	144.565125	hypothetical protein CAA
CR06570CA	28.769743	33.604858	7.015491	7.407942	hypothetical protein CAA
CR06580WA	0	1.170932	0	0	hypothetical protein CAA
CR06620WA	31.777679	36.373817	37.867706	41.835648	hypothetical protein CAA
CR06640CA	90.97728	86.997482	36.621826	39.631535	hypothetical protein CAA
CR06650CA	68.921043	99.777237	5.190174	6.308046	hypothetical protein CAA
CR06680CA	11.797911	11.791747	11.837853	9.940377	hypothetical protein CAA
CR06690CA	65.008476	74.5802	146.452698	134.956528	2',3'-cyclic-r
CR06740WA	11.695137	10.830123	24.608088	20.442083	hypothetical protein CAA
CR06770CA	12.258819	11.480869	31.143955	32.850292	hypothetical protein CAA
CR06780WA	40.511341	35.139355	49.007732	49.344612	hypothetical protein CAA
CR06790CA	7.6478	7.959367	9.469393	8.088494	hypothetical protein CAA
CR06820WA	28.011473	35.429184	25.156221	20.861694	hypothetical protein CAA
CR06840WA	18.923473	21.221762	17.966343	17.019207	rRNA-binding ribosome b
CR06850CA	37.132885	39.886295	44.374043	56.212994	conserved hypothetical p
CR06870CA	12.108204	13.966343	0.866924	0.223023	hypothetical protein CAA
CR06920WA	1.455932	1.508119	8.441684	6.977047	hypothetical protein CAA
CR06930WA	15.221016	23.307154	23.551039	28.320969	hypothetical protein CAA
CR06960WA	14.743782	11.64397	22.861017	29.658638	origin recognition comple
CR06970CA	10.337161	14.371269	31.16028	27.600336	U5 snRNP complex subu
CR06980WA	20.466465	17.527403	24.042576	26.573729	ribosome biosynthesis pr
CR06990WA	32.580238	35.19754	31.163305	28.716402	hypothetical protein CAA
CR07020WA	266.344269	278.89447	365.173462	349.158875	thiosulfate sulfurtransfera
CR07030CA	19.292267	29.494392	17.492897	21.0063	rRNA-processing protein
CR07080WA	219.1465	205.832596	107.56768	128.566132	translation initiation facto
CR07110CA	5.060242	6.760236	8.336306	12.307861	hypothetical protein CAA
CR07120CA	19.174116	13.509402	62.410969	90.241722	hypothetical protein CAA
CR07140CA	5.740345	5.010536	3.799008	4.882226	hypothetical protein CAA
CR07160CA	11.331507	18.182627	21.637314	15.929945	hypothetical protein CAA
CR07170WA	18.628201	20.668003	74.765854	81.428955	hypothetical protein MEU

CR07190WA	46.3283	49.241745	49.722031	48.201248	hypothetical protein CAA
CR07200WA	11.240776	10.491955	12.159818	13.895853	hypothetical protein CAA
CR07220CA	3.046186	4.511758	10.237364	11.133442	hypothetical protein CAA
CR07230WA	47.862335	32.315662	94.430809	93.545929	hypothetical protein CAA
CR07250CA	26.590168	23.701784	21.935244	27.914984	hypothetical protein CAA
CR07260CA	1.038703	0	0	0.728843	hypothetical protein CAA
CR07300WA	0	0.073919	0.348493	0.688289	hypothetical protein CAA
CR07310WA	6.712056	7.703781	13.35001	18.002216	hypothetical protein CAA
CR07320CA	103.072746	111.658875	180.433197	194.29306	mitochondrial 54S ribos
CR07340CA	16.972166	19.196636	42.752045	49.171143	hypothetical protein CAA
CR07350WA	15.689716	13.234601	24.044128	31.359118	hypothetical protein CAA
CR07370WA	128.840439	126.256157	179.323212	201.191055	hypothetical protein CAA
CR07460CA	26.221821	28.269539	37.556492	45.691483	hypothetical protein CAA
CR07470WA	14.924846	20.641022	9.734358	14.429672	guanine nucleotide exch
CR07480WA	152.486069	149.108643	91.393929	83.956718	hypothetical protein CAA
CR07500WA	1.061805	0.720187	0.484248	0.94996	hypothetical protein CAA
CR07510WA	46.154873	36.936314	85.439232	122.415794	mRNA splicing protein
CR07540CA	3.762874	3.958956	1.008663	0.872648	hypothetical protein ME
CR07570WA	23.034662	30.44906	67.228622	54.351852	hypothetical protein CAA
CR07600WA	10.085727	12.272568	16.168495	14.172943	DNA-dependent ATPase
CR07640CA	12.235661	16.48521	31.815384	27.4732	hypothetical protein CAA
CR07660CA	105.962646	98.470566	85.825661	95.398003	signal recognition particl
CR07670WA	69.736572	64.175514	44.649532	45.528309	hypothetical protein CAA
CR07680CA	24.244198	23.24103	42.19054	47.64661	hypothetical protein CAA
CR07690WA	19.37154	17.744307	37.471714	45.310669	hypothetical protein CAA
CR07700WA	11.866033	14.399881	19.865803	28.917372	hypothetical protein CAA
CR07740WA	35.796398	31.829418	0.676156	3.669975	hypothetical protein CAA
CR07750CA	43.699932	49.304432	32.02737	33.275917	putative ATP-dependent
CR07760WA	114.832291	89.783356	302.661499	292.180542	mitochondrial 37S ribos
CR07780WA	19.398937	18.459814	26.500601	23.023233	hypothetical protein CAA
CR07820WA	6.074495	8.009739	8.523532	5.995348	hypothetical protein CAA
CR07830CA	1328.667725	1460.265503	1081.425781	1220.362793	hypothetical protein CAA
CR07840CA	302.504211	380.045868	285.227661	305.692749	hypothetical protein MG
CR07850WA	23.042572	20.749094	82.465965	92.701904	hypothetical protein CAA
CR07870WA	18.396379	16.506062	43.109207	42.831215	hypothetical protein MG
CR07910CA	18.426821	18.154514	28.95558	25.850365	DNA-dependent ATPase
CR07920WA	45.630623	49.575569	49.853725	55.383217	hypothetical protein CAA
CR07940WA	8.14707	6.959702	12.913364	15.09872	hypothetical protein CAA
CR08000CA	47.657177	51.964481	56.54805	39.851204	hypothetical protein W5
CR08040WA	55.269226	55.430534	47.220097	42.812992	S-adenosylmethionine-d
CR08050CA	83.125992	87.754463	153.027878	134.006058	hypothetical protein CAA
CR08080WA	6.028901	7.652093	6.93738	9.301148	hypothetical protein CAA
CR08110WA	10.000997	11.394355	23.138458	25.436167	hypothetical protein CAA
CR08130WA	28.700397	24.704473	80.441414	76.716156	hypothetical protein CAA
CR08170CA	12.007561	15.64011	26.459215	23.87314	leucine carboxy methyltr
CR08190WA	20.667423	20.620375	27.158976	14.250126	hypothetical protein CAA
CR08200CA	12.42082	12.483068	19.066406	22.165787	hypothetical protein ME
CR08260CA	1.800048	0.820552	3.984844	8.000087	hypothetical protein CAA
CR08270WA	29.545124	31.862114	75.355225	88.900421	hypothetical protein CAA
CR08280WA	44.463058	38.827091	39.100903	37.216038	hypothetical protein CAA
CR08290WA	23.671045	25.847744	50.090351	44.393353	hypothetical protein CAA
CR08300CA	15.534228	13.747708	15.340417	15.13876	lysophospholipase
CR08310CA	0.396247	1.224673	3.315659	3.571271	hypothetical protein CAA
CR08330WA	26.437021	19.657251	20.096155	26.619551	hypothetical protein CAA
CR08350WA	34.923191	44.943066	43.13625	37.173058	hypothetical protein CAA
CR08380CA	0.476878	0	0.94455	0.118453	hypothetical protein CAA
CR08400CA	161.2733	155.159729	406.059082	258.634155	putative mitochondrial 3
CR08410WA	17.904142	24.368803	24.87332	24.966822	hypothetical protein CAA
CR08420WA	76.992371	69.068718	100.536697	98.267281	hypothetical protein ME
CR08430WA	32.785042	35.903561	56.524357	64.517715	hypothetical protein CAA
CR08440WA	3.843412	5.876407	10.03141	9.920832	hypothetical protein CAA
CR08450CA	20.283474	14.053984	43.780632	60.343056	hypothetical protein CAA
CR08470WA	102.667313	96.000099	50.542488	51.209259	hypothetical protein CAA
CR08480CA	1025.101562	1072.517944	1161.987183	848.848022	40S ribosomal protein S

CR08500WA	70.267563	66.708542	44.700237	43.600288	hypothetical protein CAA
CR08520CA	30.291975	24.620842	62.317696	59.295322	hypothetical protein CAA
CR08550WA	84.231964	107.417717	101.019836	89.384392	fructose-2,6-bisphospha
CR08560CA	134.689407	124.423744	245.410507	184.929413	E2 SUMO-conjugating p
CR08580CA	11.599803	14.438418	13.728495	15.150742	hypothetical protein CAA
CR08590WA	10.731162	8.022639	12.107565	18.445395	AAA family ATPase
CR08610WA	189.041901	153.256729	196.450775	135.496155	mitochondrial pyruvate c
CR08620CA	23.844255	24.379969	47.404026	56.615433	hypothetical protein CAA
CR08640CA	41.977684	47.23077	74.192856	72.49234	serine C-palmitoyltransfe
CR08650CA	66.783951	78.05304	57.941677	50.225281	putative ubiquitin-protein
CR08670CA	44.331734	45.733852	56.647457	45.781494	hypothetical protein CAA
CR08680CA	13.2307	19.870754	23.169197	25.181589	hypothetical protein CAA
CR08710WA	93.317871	90.931183	237.909103	220.163406	hypothetical protein CAA
CR08720WA	5.106061	6.024271	10.266849	8.116826	hypothetical protein CAA
CR08740WA	0.272727	0	0.1721	1.128886	hypothetical protein CAA
CR08830WA	467.535004	331.213257	370.029297	443.561157	hypothetical protein CAA
CR08880CA	768.997559	930.462524	117.398895	76.263985	hypothetical protein CAA
CR08900CA	39.67524	35.222679	41.738628	43.213299	cleavage polyadenylation
CR08920WA	61.668781	57.216274	58.35104	56.232674	hypothetical protein CAW
CR08930CA	125.897095	123.4692	151.672073	127.593262	hypothetical protein CAA
CR08940WA	28.354065	27.004696	19.06226	18.838366	tRNA 1-methyladenosine
CR08980CA	8.96741	7.278438	15.70295	20.827917	hypothetical protein CAA
CR08990CA	92.509384	97.672592	20.907274	23.786873	hypothetical protein CAA
CR09010CA	43.212353	57.527912	22.635298	21.786993	putative cystathionine be
CR09040WA	174.41449	176.270569	41.691963	29.681385	hypothetical protein CAA
CR09050CA	16.154524	17.922073	37.828625	33.349644	hypothetical protein CAA
CR09060WA	11.365791	14.491816	5.250593	5.559946	hypothetical protein CAA
CR09070CA	39.664921	50.235867	63.85582	53.168037	hypothetical protein CAA
CR09090CA	7.812899	9.099301	17.813385	17.224489	hypothetical protein CAA
CR09100CA	56.5784	75.079819	36.737896	41.512074	pyridoxine 4-dehydrogen
CR09110CA	49.904408	65.961044	94.05143	86.824982	cytochrome-b5 reductas
CR09140CA	47.588848	48.986866	9.235967	7.732841	hypothetical protein CAA
CR09150WA	9.018772	15.534756	9.889826	13.335486	hypothetical protein CAA
CR09190CA	22.742531	16.91655	18.931063	17.970976	hypothetical protein CAA
CR09230CA	12.997234	13.361714	29.035278	30.592447	hypothetical protein CAA
CR09240CA	102.336678	102.638359	171.200439	139.448807	hypothetical protein CAA
CR09310WA	13.35982	16.228802	25.392014	26.272285	protein-lysine N-methyltr
CR09330CA	22.648352	24.93552	37.624889	47.229702	hypothetical protein CAA
CR09340WA	252.424469	275.060974	356.26651	270.687958	E2 ubiquitin-conjugating
CR09350CA	2.01035	2.922243	3.481268	2.033787	hypothetical protein CAA
CR09390CA	45.908566	75.381126	0.587213	0.549832	hypothetical protein CAA
CR09410WA	17.138836	17.919989	26.569805	32.218201	hypothetical protein CAA
CR09440CA	76.812355	73.413284	94.165009	97.492531	hypothetical protein CAA
CR09460CA	3322.787842	3944.510742	3481.574707	3136.878906	hypothetical protein CAA
CR09480WA	25.983194	29.348518	33.280891	35.647629	U4/U6-U5 snRNP compl
CR09490WA	4.578596	6.455195	7.81959	10.471784	hypothetical protein CAA
CR09500CA	55.730965	54.455605	68.45192	79.936935	putative ATP-dependent
CR09510CA	45.048588	53.61042	98.211105	92.95282	hypothetical protein CAA
CR09520CA	9.765509	8.004461	27.638437	34.704422	hypothetical protein MEV
CR09530CA	42.624424	53.07584	6.995752	5.40971	hypothetical protein W5C
CR09560CA	5.872279	7.498533	12.276345	12.21417	hypothetical protein CAA
CR09570WA	7.368994	11.964047	26.434521	15.925648	hypothetical protein MG9
CR09580CA	37.270756	56.42519	29.533192	36.186707	hypothetical protein CAA
CR09590WA	22.79105	25.306278	69.764534	80.882294	ubiquinone biosynthesis
CR09610CA	22.341642	24.919508	18.665987	29.629311	hypothetical protein CAA
CR09620CA	129.41188	150.280396	141.51384	123.672729	hypothetical protein CAA
CR09640CA	189.89415	240.329727	238.733185	247.410736	--
CR09660WA	10.32196	10.635167	19.318504	15.906234	hypothetical protein L150
CR09670CA	60.705433	65.539513	70.088379	73.901001	S-formylglutathione hydr
CR09700WA	8.774739	9.522012	4.82679	3.231023	hypothetical protein CAA
CR09740WA	68.111565	76.685081	28.788942	32.635906	RNA-dependent ATPase
CR09750CA	22.363384	27.81249	25.803501	23.256887	hypothetical protein W5C
CR09800CA	65.531654	58.235985	44.761703	40.830975	hypothetical protein CAA
CR09810WA	4.459729	7.358537	22.159735	24.303316	hypothetical protein CAA

CR09830WA	13.999047	11.498615	26.185255	23.193361	hypothetical protein ME
CR09840CA	12.127707	18.409998	29.010502	27.814085	hypothetical protein CAA
CR09920WA	458.928101	515.438416	90.707642	81.15332	hypothetical protein CAA
CR09930WA	19.005241	26.74461	6.600091	8.65738	hypothetical protein CAA
CR09940WA	1.301316	1.572877	2.87171	1.078635	hypothetical protein CAA
CR09990WA	11.007581	10.103255	21.592993	22.50256	hypothetical protein CAA
CR10000CA	41.360981	39.967659	64.337814	59.811359	hypothetical protein CAA
CR10020CA	17.898083	14.230324	30.569643	41.764359	hypothetical protein CAA
CR10040WA	30.374176	40.225563	41.458084	38.390625	hypothetical protein CAA
CR10060WA	39.627815	44.677097	27.598166	27.293018	U2 snRNP complex sub
CR10120CA	1.931267	2.949654	5.807146	14.830858	hypothetical protein CAA
CR10130WA	24.97051	27.667675	62.525143	58.237171	hypothetical protein CAA
CR10140WA	128.315811	121.841034	192.836411	187.577484	hypothetical protein CAA
CR10170CA	67.547318	66.083313	65.889137	69.482903	asparaginase
CR10180WA	6.246654	6.334192	29.902906	24.027149	hypothetical protein ME
CR10190CA	15.546307	18.490852	15.354624	24.830612	hypothetical protein CAA
CR10200WA	77.750801	69.377182	7.925517	5.337632	hypothetical protein CAA
CR10230WA	47.18293	46.157318	94.010025	95.404343	hypothetical protein CAA
CR10260WA	14.055972	14.285112	29.879093	18.181168	21S rRNA (uridine2791-
CR10280WA	90.312599	82.988358	162.92392	147.67868	hypothetical protein CAA
CR10290CA	6.074333	6.625126	18.781105	17.571297	hypothetical protein CAA
CR10310WA	5.852	5.419271	7.851075	10.925101	hypothetical protein CAA
CR10320WA	11.007864	6.414087	0	0	hypothetical protein CAA
CR10380CA	6.79276	9.555438	8.993263	6.178088	hypothetical protein CAA
CR10390WA	13.629654	11.999355	19.025122	18.056061	TRAPP subunit
CR10400WA	76.755821	72.929161	45.348419	46.767693	peptide alpha-N-acetyltra
CR10410CA	208.047134	204.432251	113.120636	84.438789	hypothetical protein CAA
CR10420WA	82.469215	88.074036	69.145164	67.719795	hypothetical protein CAA
CR10430CA	20.260855	16.389664	32.671627	40.892406	hypothetical protein CAA
CR10440WA	4.498937	4.488585	13.097943	13.293414	telomere length regulati
CR10470CA	59.128651	63.900387	27.788584	26.503193	rRNA-processing protein
CR10500CA	38.647667	38.63744	68.791649	70.911308	hypothetical protein CAA
CR10510WA	9.56303	5.787153	17.18066	17.462992	hypothetical protein CAA
CR10530WA	14.291185	9.93307	39.454048	31.184366	hypothetical protein CAA
CR10590WA	11.574495	12.62648	13.011997	18.582754	CORVET complex subu
CR10600CA	131.430908	141.453125	169.56839	116.433632	4-hydroxybenzoate octa
CR10610CA	16.805754	10.86292	53.926388	39.965359	anaphase promoting co
CR10620CA	25.067495	28.617798	13.573413	17.101433	biotin--
CR10630WA	16.516115	22.649912	0	20.311962	hypothetical protein CAA
CR10640WA	14.592638	15.308226	11.041284	14.440335	hypothetical protein CAA
CR10730CA	43.827328	46.33707	77.441765	71.38649	hypothetical protein CAA
CR10740WA	33.145912	47.495922	93.055534	63.274567	hypothetical protein CAA
CR10750CA	70.364685	62.845665	73.919441	71.010216	hypothetical protein CAA
CR10760CA	42.466949	54.577271	84.458595	65.287674	hypothetical protein CAA
CR10770WA	31.236717	33.629242	24.244337	27.663252	hypothetical protein CAA
CR10800CA	39.157974	33.669472	62.097103	62.490097	hypothetical protein CAA
CR10810CA	53.371658	45.563736	34.80122	40.358391	hypothetical protein CAA
CR10820WA	52.425152	65.855835	104.18856	82.822243	mRNA splicing protein
CR10830CA	74.498917	73.297684	241.155045	201.475342	mitochondrial 54S ribos
CRC1	73.918144	79.570107	63.32362	60.913006	carnitine:acyl carnitine a
CRD2	109.305557	123.401039	141.247177	126.69455	Crd2p
CRG1	34.02943	34.474163	78.730621	81.680603	Crg1p
CRH11	236.347031	201.016602	1492.799805	1714.872192	hypothetical protein MG
CRH12	80.268829	76.707245	19.9347	24.403873	Crh12p
CRK1	17.718082	11.522185	21.992529	23.805401	cyclin-dependent serine/
CRL1	49.303814	59.290371	74.933144	65.655853	Rho family GTPase
CRM1	29.42436	27.965376	47.551991	53.189499	exportin
CRN1	45.063492	50.921841	85.34436	84.240448	Crn1p
CRP1	68.841072	73.705536	10.240902	12.039789	Crp1p
CRZ1	37.341579	38.987873	45.871456	49.438332	DNA-binding transcriptio
CRZ2	13.194265	13.066222	0	0.198418	conserved hypothetical
CSA1	29.320831	29.180628	459.866913	477.192078	Csa1p
CSA2	4.493449	2.089815	227.218719	192.37587	hypothetical protein MG1
CSC25	17.497669	15.02078	22.001614	21.024971	Ras family guanine nucle

CSE4	78.36261	57.789474	244.413162	267.014801	histone H3-like centrome
CSH1	793.713135	969.57959	4.581149	3.344932	Csh1p
CSH3	187.390915	178.456497	207.319122	191.039093	hypothetical protein MG3
CSI2	69.201851	93.723793	49.164047	62.08815	Csi2p
CSM3	8.347364	7.720786	24.290939	28.480684	Csm3p
CSO99	12.667664	14.517042	16.597485	13.167539	Cso99p
CSP1	2.268665	1.142053	8.017405	9.599251	hypothetical protein MGE
CSP2	8.007665	9.10489	7.669817	13.567299	O-glycosylated covalentl
CSP37	146.746735	182.503922	39.588753	27.366621	Csp37p
CSR1	91.698235	86.521301	5.497384	4.418653	Csr1p
CST20	22.776064	23.048248	26.685907	25.852251	mitogen-activated protei
CST5	14.096287	22.348658	8.170661	10.207223	Cst5p
CTA1	50.062817	57.572594	82.74192	81.601082	Cta1p
CTA2	57.53231	56.335636	46.613384	34.712891	Cta2p
CTA24	78.127769	70.545929	107.995766	77.580238	Cta24p
CTA26	32.915298	34.117016	24.395025	19.242701	hypothetical protein MGE
CTA3	47.076435	47.142483	99.127213	95.289589	Cta3p
CTA4	109.666359	112.947784	26.423864	27.16774	oleate-activated transcrip
CTA6	24.587362	24.624191	67.518768	58.302513	hypothetical protein MEQ
CTA7	21.847178	20.448395	33.319843	36.959618	hypothetical protein W5C
CTA8	82.637833	82.718147	36.62405	43.34832	stress-responsive transc
CTA9	19.83103	20.98695	65.90715	61.536312	hypothetical protein MEK
CTF1	13.730321	11.298328	7.739789	6.055179	Ctf1p
CTF18	9.56512	9.005323	18.110041	20.164253	Ctf18p
CTF5	2.631091	2.725192	15.878648	19.118572	Ctf5p
CTF8	3.459528	4.193619	30.575857	24.476656	Ctf8p
CTM1	260.751953	285.058136	67.917297	78.546188	cytochrome c lysine N-m
CTN1	203.431564	195.748962	64.475349	60.042767	carnitine O-acetyltransfe
CTN3	43.296982	41.288685	4.38435	2.457453	carnitine O-acetyltransfe
CTP1	11.970604	15.546946	12.87604	10.825397	Ctp1p
CTR1	10598.25195	10628.15918	11746.52734	11071.90625	hypothetical protein MEC
CTR2	369.229492	366.002045	267.330933	188.265732	solute carrier family 31 (
CUE5	173.730927	170.216476	170.562714	152.024963	hypothetical protein MG3
CUP1	4349.375488	3673.144287	1971.771851	2048.372314	Cup1p
CUP2	82.781944	78.290222	81.557571	88.033844	Cup2p
CUP5	512.171204	467.864441	443.757935	382.876038	vacuolar ATP synthase 1
CUP9	1744.164673	1881.335327	367.407166	395.569702	Cup9p
CWC22	10.191319	13.781139	19.461916	17.540295	U2-type spliceosomal co
CWH41	8.1157	6.19285	14.949258	12.174845	Cwh41p
CWH43	42.279202	37.045418	70.04599	87.242783	Cwh43p
CWH8	79.992371	94.237358	176.57074	186.796417	Cwh8p
CWT1	33.928234	31.172194	49.306511	41.637844	hypothetical protein MEU
CYB2	63.360474	67.846497	88.310135	87.962952	L-lactate dehydrogenase
CYB5	153.306503	155.743912	197.452026	173.2332	Cyb5p
CYC1	328.045715	342.526581	619.965393	509.936646	cytochrome c isoform 1
CYC3	224.412201	234.137665	70.165131	52.788422	holocytochrome c syntha
CYK3	5.536968	5.96706	10.366571	12.40248	hypothetical protein MEU
CYM1	29.164989	23.778877	17.788837	21.441486	Cym1p
CYP1	1061.368896	1001.390259	988.473816	934.299011	peptidylprolyl isomerase
CYP5	245.08905	245.190872	365.245209	277.39093	peptidylprolyl isomerase
CYR1	18.615524	17.397749	18.82419	18.301033	adenylate cyclase
CYS3	954.067871	1071.769287	425.958282	415.305847	cystathionine gamma-lya
CYS4	106.678513	109.284714	186.172363	197.015335	cystathionine beta-synth
CYT1	400.417297	391.425171	396.496124	394.486725	ubiquinol--cytochrome-c
CYT2	16.220905	26.197971	40.058319	32.103798	cytochrome c heme-lyas
CZF1	9.284229	11.679911	14.864065	23.230356	Czf1p
DAC1	180.715439	134.451035	87.253502	72.369339	Dac1p
DAD1	6.908024	7.047761	71.858482	62.887173	predicted protein
DAD2	27.094868	16.643572	72.103683	71.21286	Dad2p
DAD3	16.044035	16.181656	61.928951	62.659122	Dad3p
DAD4	71.379471	60.172104	192.036667	177.208481	DASH complex subunit,
DAG7	187.83432	222.078293	203.448685	276.050751	Dag7p
DAK2	59.867138	60.515488	117.102058	125.850006	dihydroxyacetone kinase
DAL1	33.263977	29.601496	26.185261	13.599424	allantoinase

DAL4	6.371379	7.712242	6.489395	5.374797	allantoin permease
DAL5	11.203099	13.186711	14.000173	14.299551	allantoate permease
DAL52	0.266815	0.676946	0.376444	0.068558	Dal52p
DAL7	3.489001	4.832148	3.09598	2.035052	Dal7p
DAL8	4.823352	4.31143	6.43623	7.588368	Dal8p
DAL81	10.036266	10.829109	18.337097	18.026827	Dal81p
DAL9	10.515554	9.089558	7.085189	11.754725	Dal9p
DAM1	33.372841	32.354965	102.784546	87.757248	Dam1p
DAO1	66.079903	54.158672	46.9865	38.841057	D-amino-acid oxidase
DAO2	42.221363	45.375595	27.639629	21.498693	Dao2p
DAP1	17.858335	13.833889	35.57906	13.86702	Dap1p
DAP2	14.297018	15.01801	29.50672	34.089569	Dap2p
DBF2	16.484766	14.465387	58.209274	78.815292	serine/threonine-protein
DBF4	15.372933	16.494743	54.220104	48.564617	protein serine/threonine
DBP2	412.777863	428.422424	171.989166	141.984558	ATP-dependent RNA he
DBP3	119.761093	132.898209	40.870323	51.300594	ATP-dependent RNA he
DBP5	76.128761	70.191696	82.595695	95.420105	ATP-dependent RNA he
DBP7	44.029392	44.244308	23.212679	23.49407	putative ATP-dependent
DBP8	38.523376	45.575317	33.435993	30.80522	ATP-dependent RNA he
DBR1	11.752266	11.488084	18.067169	22.0686	RNA lariat debranching
DCC1	2.501402	4.261768	10.95163	16.19939	Dcc1p
DCG1	11.22086	2.791457	17.123161	19.431576	Dcg1p
DCK1	35.968201	40.315823	28.21101	27.362965	Dck1p
DCK2	6.930425	7.064638	13.47913	12.365303	Dck2p
DCP2	85.233475	79.361824	101.251518	110.064491	mRNA-decapping enzym
DCR1	6.094217	7.204782	11.015463	14.611541	ribonuclease III
DCW1	77.403267	81.624466	138.283401	124.804207	mannan endo-1,6-alpha-
DDC1	4.45975	2.637112	8.374428	8.303032	Ddc1p
DDI1	39.362633	42.785362	73.332092	55.075356	Ddi1p
DDR48	290.165466	349.675293	124.834923	112.711807	DNA damage-responsive
DED1	598.616638	666.58374	202.132919	190.792847	ATP-dependent RNA he
DED81	76.14743	93.514511	139.500717	137.829102	asparagine--tRNA ligase
DEF1	1.440717	1.697461	0.117775	0.443815	hypothetical protein MG1
DEM1	4.407939	7.547658	14.567595	16.668835	Dem1p
DES1	220.480942	226.553146	262.777863	194.186218	Des1p
DFG10	24.660412	30.06255	28.162661	33.206661	putative polyprenol reduc
DFG16	11.216004	12.391386	21.805037	17.497576	putative pH sensor Dfg1
DFG5	123.2817	123.181358	105.180168	97.181908	putative mannan endo-1
DFI1	740.854614	653.926636	528.316772	567.825928	hypothetical protein MEU
DFR1	22.993942	23.443983	40.224373	30.506031	dihydrofolate reductase
DHH1	18.48048	15.017101	30.899021	31.110714	ATP-dependent RNA he
DIE2	1.008071	2.137842	1.895535	3.180347	RecName: Full=Dol-P-G
DIM1	64.12252	55.218113	21.46981	17.779974	putative dimethyladenosi
DIP2	42.701107	47.117359	16.99185	19.037643	snoRNA-binding rRNA-p
DIP5	275.786102	298.679993	266.242371	225.6978	Dip5p
DIT1	2.228938	2.883233	5.800376	2.919068	Dit1p
DIT2	6.835045	9.602491	7.940686	5.422367	putative cytochrome
DJP1	30.961323	35.717041	42.239212	31.061226	hypothetical protein MEN
DLD1	23.947586	24.44738	34.38657	36.542454	Dld1p
DLD2	18.396635	20.618423	20.473791	22.821722	D-lactate dehydrogenase
DLH1	0.527507	0	0.304271	3.138976	recombinase
DNA2	2.636605	4.552538	6.19972	9.942951	bifunctional ATP-depend
DNM1	22.882835	30.537308	47.858135	47.929619	dynamin-related GTPase
DOA1	16.353458	19.171072	40.046776	35.806812	Doa1p
DOA4	7.459343	8.669709	11.560868	15.433433	ubiquitin carboxyl-termin
DOG1	5.389902	8.059245	6.652972	4.166783	2-deoxyglucose-6-phosp
DOS2	72.967827	75.012756	145.90477	135.800491	Dos2p
DOT1	14.175157	12.416329	41.942665	45.061871	histone methyltransferas
DOT4	95.5634	98.001129	25.695087	31.187654	ubiquitin-specific proteas
DOT5	101.978203	102.398117	78.09967	92.792473	thioredoxin peroxidase
DOT6	29.025459	33.386414	19.289637	23.33618	Dot6p
DPB2	8.218617	7.637669	21.713915	18.060469	DNA polymerase epsilon
DPB4	30.014616	22.434679	58.69183	64.40358	DNA polymerase epsilon
DPM1	89.995499	98.419197	209.875488	208.598129	dolichyl-phosphate beta-

DPM2	113.573471	71.916954	205.072281	182.260437	Dpm2p
DPM3	48.577076	70.089783	94.087608	108.414772	Dpm3p
DPP1	12.953372	13.436007	15.625475	21.126808	Dpp1p
DPP2	23.149611	16.493744	29.193003	18.620161	phosphatidate phosphat
DPP3	168.579361	157.646576	55.303532	52.091591	bifunctional diacylglycer
DPS1-1	97.356308	96.37529	115.531837	126.322258	aspartyl-tRNA synthetas
DQD1	88.450798	90.128311	186.306412	142.154861	Dqd1p
DRE2	87.247055	75.265007	53.890537	59.987274	electron carrier
DRG1	76.724693	81.269524	78.190933	60.531273	GTP-binding protein
DRS1	83.214798	79.731415	56.489902	55.327503	putative ATP-dependent
DSE1	77.599312	72.323502	251.853424	319.549164	Dse1p
DSL1	3.258731	4.751061	8.977904	8.944918	Dsl1p
DTD2	110.694458	99.277138	171.019135	115.590668	D-tyrosyl-tRNA(Tyr) dea
DUG3	222.673889	240.798264	141.979248	124.020195	glutamine amidotransfer
DUN1	8.516292	9.145371	25.22604	26.693699	serine/threonine-protein
DUO1	9.789918	12.02278	65.911018	52.660145	hypothetical protein ME
DUR1,2	3.401102	3.328375	3.680458	5.023378	urea amidolyase
DUR3	4.741	5.555649	2.012307	2.043694	Dur3p
DUR32	7.733609	7.320205	7.529708	8.424507	Dur32p
DUR35	1.242374	1.134742	1.330329	0.956056	Dur35p
DUR4	8.049714	5.782668	9.772882	9.372095	Dur4p
DUR7	5.781483	8.606809	6.872259	6.076302	solute:sodium symporter
DUS4	47.941902	49.795696	32.743576	29.871136	tRNA dihydrouridine syn
DUT1	28.790438	27.243357	172.934143	143.456696	bifunctional dITP/dUTP
DYN1	4.020098	4.448453	15.621947	17.726683	dynein heavy chain
EAF3	41.510834	37.859474	48.139481	39.524376	mortality factor 4-like pr
EAF6	21.155155	20.295197	39.926754	38.06284	Eaf6p
EAF7	29.990948	37.337978	52.038876	47.803562	hypothetical protein MG
EAP1	17.227009	14.046017	12.723579	16.886951	putative regulatory prote
EBP1	0.938575	3.214282	3.68246	5.870603	Ebp1p
EBP7	10.730503	15.805876	7.020591	7.788421	Ebp7p
ECE1	1.541749	0.146252	0	0.085532	Ece1p
ECI1	104.878746	99.85508	44.726795	41.898186	dodecenoyl-CoA isomer
ECM1	70.26329	84.548416	34.50201	45.683792	Ecm1p
ECM14	59.232758	53.414696	57.798996	65.566971	putative metallocarboxy
ECM15	95.755127	95.376152	165.879013	161.957581	Ecm15p
ECM17	23.549877	27.522614	21.958092	20.899837	sulfite reductase (NADP
ECM18	4.828802	6.452872	3.646459	3.803457	hypothetical protein CA
ECM21	484.042084	468.079102	171.20079	199.19252	Ecm21p
ECM22	142.364639	150.319641	56.793278	62.160564	hypothetical protein ME
ECM25	3.784238	2.68076	7.278646	6.303123	Ecm25p
ECM29	7.490937	6.360587	8.93968	10.768297	Ecm29p
ECM3	13.843169	12.481373	18.00456	14.564061	putative ATPase
ECM33	2081.165771	1759.920044	2022.984131	2634.568115	Ecm33p
ECM331	326.947754	244.846451	338.086426	373.567902	Ecm331p
ECM38	15.748406	14.372675	6.665036	9.572244	Ecm38p
ECM39	15.537918	16.980904	23.371208	25.56399	dolichyl-P-Man:Man(7)G
ECM4	150.053085	136.700104	90.36261	75.916298	omega-class glutathione
ECM42	32.590027	26.698826	26.605928	33.100761	glutamate N-acetyltransf
ECM7	17.37409	13.713295	18.081825	15.598467	Ecm7p
EDC3	24.214653	24.013636	21.379328	21.578465	Edc3p
EFB1	868.211487	952.311462	644.91394	627.412354	translation elongation fa
EFG1	7.337798	9.184628	8.175105	13.202375	Efg1p
EFH1	143.989929	101.317719	0.184565	0.311112	Efh1p
EFT2	879.078491	871.800659	724.649231	792.333801	elongation factor 2
EGD1	441.063995	411.336884	632.826416	670.999329	Egd1p
EGD2	246.134766	271.217896	383.101959	370.938721	Egd2p
EHD3	53.205345	52.434204	18.149944	18.194126	Ehd3p
EHT1	10.054458	12.40725	36.213398	36.981831	medium-chain fatty acid
EIF4E	230.647644	250.515488	443.241486	400.695709	translation initiation fact
ELA1	10.130325	13.955194	6.726514	10.047638	hypothetical protein ME
ELC1	30.867081	19.601366	54.389713	34.994789	elongin C
ELF1	153.32988	156.989273	42.382244	41.833897	Elf1p
ELP3	82.042015	84.00827	34.165623	30.912512	Elongator subunit

EMC9	51.65213	54.338383	53.62899	62.321358	Emc9p
EMP24	111.246742	111.993706	189.849304	187.767838	Emp24p
EMP46	8.09674	8.670306	21.736666	17.502424	Emp46p
EMP70	46.554531	51.505951	58.896854	69.062286	Emp70p
ENA2	128.903656	134.638474	191.099899	170.964905	Na(+)-exporting P-type A
ENA21	308.879578	303.059509	68.732384	59.291012	Ena21p
END3	26.018909	27.955946	37.820263	40.977749	End3p
ENG1	89.414505	66.18988	399.550079	512.746094	hypothetical protein MG3
ENO1	1529.098999	1649.045044	1632.50769	1479.584351	phosphopyruvate hydrata
ENP1	93.410057	98.317207	42.088104	53.18269	essential nuclear protein
ENP2	45.129398	43.205345	17.415762	20.156561	ribosome biosynthesis pr
ENT3	111.267548	109.825668	146.942459	175.569809	Ent3p
EPL1	134.574203	118.202919	114.078125	105.714622	Epl1p
ERB1	23.378393	26.386885	19.427589	25.159607	Erb1p
ERD1	11.634404	12.329374	15.773496	13.789856	Erd1p
ERF1	130.719757	151.730667	108.192635	105.545792	eukaryotic peptide chain
ERG1	103.896942	128.530579	154.365921	150.664429	squalene monooxygenas
ERG10	136.50293	107.216232	99.444221	106.161636	acetyl-CoA C-acetyltrans
ERG11	85.83226	95.130798	177.237579	180.837601	sterol 14-demethylase
ERG12	46.749409	42.406334	32.512329	39.846474	mevalonate kinase
ERG13	155.612	155.185364	134.930435	147.386887	hydroxymethylglutaryl-Co
ERG2	26.958084	23.942753	35.075737	35.721882	C-8 sterol isomerase
ERG20	42.692879	53.404999	65.206123	67.615524	bifunctional (2E,6E)-farn
ERG24	17.571495	16.399446	34.342056	27.858982	delta(14)-sterol reductas
ERG25	297.352875	312.250397	82.463806	89.241974	methylsterol monooxyge
ERG251	932.141174	1047.40332	1352.898804	1338.614746	C-4 methylsterol oxidase
ERG26	33.474426	37.49482	81.656975	94.638008	sterol-4-alpha-carboxylat
ERG27	22.575953	15.152662	54.691402	61.863316	3-keto-steroid reductase
ERG28	68.436539	91.389992	104.327423	108.616158	Erg28p
ERG3	89.330574	113.576294	76.001068	92.15464	RecName: Full=Delta(7)-
ERG4	132.897583	137.109787	208.417709	228.521454	delta(24(24(1)))-sterol re
ERG5	121.119766	111.341614	174.35585	209.674484	C-22 sterol desaturase
ERG6	110.352936	124.412239	210.99437	177.63446	sterol 24-C-methyltransfe
ERG7	22.626032	19.065762	43.002277	39.732574	lanosterol synthase
ERG8	23.00889	24.5879	37.06778	45.877914	phosphomevalonate kina
ERG9	59.762676	54.032089	119.920303	132.507263	bifunctional farnesyl-diph
ERO1	677.79248	719.237854	373.11673	446.959198	ER oxidoreductin
ERP5	87.279266	85.038925	216.967133	176.920212	Erp5p
ERV1	22.153288	15.031775	64.390823	65.220779	flavin-linked sulfhydryl ox
ERV25	138.450333	138.21196	230.516663	238.390976	Erv25p
ERV29	59.30159	69.922531	91.515388	98.609367	Erv29p
ERV46	31.583223	40.68784	64.647507	61.271793	Erv46p
ESA1	43.479698	38.342457	37.984856	33.259949	histone acetyltransferase
ESC4	1.609822	2.669629	11.048308	8.519857	hypothetical protein MG3
ESP1	3.403264	2.928175	15.250922	15.005023	separase
ESS1	106.449677	106.604393	111.141914	106.52607	peptidylprolyl isomerase
EST1	83.523521	87.681824	47.67572	35.238209	Est1p
EST3	3.474418	5.68269	15.855456	8.318755	telomerase subunit
ETR1	128.705872	123.828758	133.390137	105.854362	Etr1p
EXG2	2.599379	1.926863	12.37539	12.01784	glucan 1,3-beta-glucosid
EXM2	21.83741	31.186071	50.898621	56.715508	Exm2p
EXO1	9.187087	8.168716	24.593477	29.555887	Rad2 family nuclease
EXO70	28.84214	32.61834	60.664162	56.568653	GTP-Rho binding exocys
EXO84	9.650362	12.477417	15.159758	15.180875	exocyst complex compon
FAA2	14.00394	15.017759	11.239249	9.617174	Faa2p
FAA21	13.437314	15.95965	6.806578	7.688362	medium-chain fatty acid-
FAA2-1	16.761805	19.094223	33.395058	32.025135	Faa2-1p
FAA2-3	14.534173	11.54315	4.360367	6.129317	Faa2-3p
FAA4	789.812683	838.718628	225.721786	240.344772	long-chain fatty acid-CoA
FAB1	8.265511	7.319088	22.518133	21.842409	hypothetical protein L150
FAD1	10.175453	8.050629	12.401815	18.502329	FMN adenylyltransferase
FAD2	166.993805	182.565033	151.743271	155.029907	Fad2p
FAD3	74.690346	66.800209	45.78421	41.11578	Fad3p
FAL1	25.984926	20.893826	18.504841	28.177	ATP-dependent RNA he

FAR1	12.676917	13.989527	9.797921	9.801062	cyclin-dependent protein
FAS1	75.696465	71.53347	120.777031	125.98777	tetrafunctional fatty acid
FAS2	94.683441	87.513016	129.24295	137.03392	trifunctional fatty acid syı
FAT1	33.719391	35.049217	18.952044	18.701986	long-chain fatty acid tran
FAV1	1.750075	2.209241	3.108893	2.514875	hypothetical protein MEV
FAV2	11.144073	13.339506	14.266028	11.92326	Fav2p
FAV3	18.538652	17.30921	32.998943	27.602612	putative alpha-1,6-mann
FBA1	749.338806	723.512451	536.354553	568.077148	fructose-bisphosphate al
FBP1	333.237579	320.045532	417.706543	360.612915	fructose 1,6-bisphosphat
FCA1	23.503153	28.127289	39.543808	39.906376	cytosine deaminase
FCR1	57.275375	49.120728	78.773857	97.396545	Fcr1p
FCR3	22.590441	28.271433	22.446112	21.894711	Fcr3p
FCY2	6.175102	4.288785	38.115452	32.14959	Fcy2p
FCY21	301.020874	343.016479	237.593109	223.393509	purine-cytosine permeas
FCY23	20.804155	17.414459	12.099492	13.687789	Fcy23p
FCY24	10.976995	9.253894	8.213534	12.522667	Fcy24p
FDH1	910.270142	982.857666	3364.976562	3117.451904	formate dehydrogenase
FDH3	113.760933	136.380646	187.835312	172.53064	bifunctional alcohol dehy
FEN1	200.263641	243.829514	81.815361	75.890724	fatty acid elongase
FEN12	152.571823	139.264206	77.52803	105.091576	fatty acid elongase
FESUR1	303.312805	253.369186	284.95105	263.900909	Fesur1p
FET3	8.527628	8.449887	5.340431	5.401262	iron transport multicoppe
FET31	241.562592	295.063629	179.755157	177.106201	iron transport multicoppe
FET33	10.465882	12.338758	10.156606	8.9956	putative oxidoreductase
FET34	1.135738	1.032108	0.439449	1.170383	iron transport multicoppe
FET99	0.211327	0.030137	0	0.413688	Fet99p
FGR10	7.163723	5.272582	5.202724	8.989571	Fgr10p
FGR13	12.890614	11.513889	16.559818	18.176367	hypothetical protein MEY
FGR14	30.621456	23.694418	47.146439	55.33004	Fgr14p
FGR15	15.393695	15.47335	22.742699	19.331249	Fgr15p
FGR16	10.229559	11.700368	22.143761	29.081415	U4/U6-U5 snRNP compl
FGR17	3.519383	3.313515	2.736788	4.177385	Fgr17p
FGR18	7.307971	6.261729	0	0.30459	Fgr18p
FGR2	20.749256	17.068882	5.330595	3.643912	Fgr2p
FGR22	7.044436	10.987207	5.765981	7.21034	Fgr22p
FGR23	11.532342	11.087671	7.518459	9.063531	Fgr23p
FGR24	27.226597	32.562229	37.689312	32.372478	hypothetical protein I503
FGR27	14.505298	18.447233	18.93434	26.587036	Fgr27p
FGR28	2.953766	5.977022	5.859612	9.536415	Fgr28p
FGR29	9.082075	8.456535	19.129595	22.166983	hypothetical protein MEN
FGR3	28.278864	33.562756	21.347832	26.196873	Fgr3p
FGR32	24.726063	24.96126	55.134846	59.657497	Fgr32p
FGR34	16.878143	22.384729	42.310665	40.762501	Fgr34p
FGR37	2.934574	0.727377	0	2.996983	Fgr37p
FGR38	9.01061	6.883815	20.490177	13.973646	Fgr38p
FGR39	25.339911	23.966986	39.46508	40.674156	Fgr39p
FGR41	475.574921	340.064301	1266.541626	1705.246338	hypothetical protein MEQ
FGR42	0	1.262869	0.453454	0	Fgr42p
FGR43	3.68864	5.086038	9.359753	7.791759	Fgr43p
FGR44	30.921389	22.048601	30.591234	39.341969	Fgr44p
FGR46	0.469972	1.169851	1.042588	1.793553	Fgr46p
FGR47	6.131558	5.383954	9.269599	10.057261	Fgr47p
FGR50	8.405066	19.434214	30.112324	29.901628	Fgr50p
FGR51	20.825508	20.278072	28.962345	30.181061	Fgr51p
FGR6-10	6.160672	6.858844	37.05402	39.234993	Fgr6-10p
FGR6-4	11.598589	8.340913	40.357712	42.17115	Fgr6-4p
FHL1	30.065578	23.494186	31.984598	37.529354	Fhl1p
FIG1	1.58495	0.292869	1.947526	3.038932	Fig1p
FKH2	27.316687	30.706099	59.276123	64.896126	forkhead family transcrip
FLC1	170.950027	191.697021	98.315376	107.458626	putative flavin adenine di
FLC2	75.347237	71.752106	73.734863	84.90419	hypothetical protein MGK
FLC3	40.000641	40.058422	16.667797	15.489246	Flc3p
FLO8	173.756302	171.938614	97.903557	106.632599	Flo8p
FLO9	7.964712	8.196535	5.758049	11.242455	LOW QUALITY PROTEI

FLU1	88.591919	92.154129	36.579826	42.909084	Flu1p
FMA1	9.404231	6.718816	32.345779	42.807953	Fma1p
FMO1	17.376211	10.68364	4.250487	6.464918	Fmo1p
FMO2	7.518445	6.61568	2.686725	3.793179	Fmo2p
FMP27	5.63849	5.382897	14.664781	18.83135	Fmp27p
FMP45	132.481262	142.789825	48.075092	32.60463	hypothetical protein MG
FMT1	12.475155	18.385544	34.683083	28.298437	methionyl-tRNA formyltr
FOL1	18.637747	20.025492	29.627611	34.707348	trifunctional dihydroptero
FOX2	155.8685	140.811081	36.635441	38.32568	peroxisomal hydratase-d
FOX3	62.443932	56.200703	30.274389	32.295948	Fox3p
FPG1	32.438839	29.387371	55.240978	39.715698	Fpg1p
FRE10	8.478808	10.93914	4.369919	4.601437	Fre10p
FRE3	6.095922	7.620933	4.480317	4.376648	Fre3p
FRE30	229.123505	273.780182	647.93988	640.815857	Fre30p
FRE7	571.032654	675.09668	1303.224731	1243.146973	Fre7p
FRE9	1.792836	3.898479	13.516568	13.604548	Fre9p
FRP1	42.487503	54.293076	150.699707	115.296638	Frp1p
FRP2	32.970394	27.748455	58.91312	56.805504	Frp2p
FRP3	1088.350098	902.563049	86.655266	66.674599	hypothetical protein ME
FRP5	2.572753	1.139319	2.644413	3.235399	Frp5p
FRP6	321.976288	311.359497	115.882439	98.475761	Frp6p
FRS1	81.115082	82.888687	112.55722	120.129364	phenylalanine--tRNA lig
FRS2	129.045013	143.068039	168.263474	158.033844	phenylalanine--tRNA lig
FTH1	44.522987	40.012844	31.346313	33.522179	Fth1p
FTH2	19.422579	21.865623	13.762238	18.300209	Fth2p
FTR1	95.54071	105.525665	89.439651	83.280212	high-affinity iron permea
FTR2	147.270493	122.125656	45.200729	44.814674	Ftr2p
FUM11	102.389908	124.322655	82.983582	83.992012	fumarase
FUM12	187.892166	171.223587	206.364502	207.874359	Fum12p
FUN12	83.72084	84.79908	74.36554	69.351906	translation initiation facto
FUN31	43.798141	48.679409	34.544899	31.952417	protein-serine/threonine
FUR1	33.546616	28.65309	28.776083	28.785368	uracil phosphoribosyltra
FUR4	7.266718	10.121012	8.448579	7.675892	allantoin permease
FUS1	2.151549	2.409212	1.595017	0.083876	Fus1p
FYV5	24.022678	31.395451	18.742271	18.478567	rRNA-processing protei
FZO1	116.759125	122.361092	86.778969	82.899925	mitofusin
GAC1	1664.414551	1513.330566	164.268021	200.668015	protein phosphatase reg
GAD1	121.75692	149.614044	42.21508	44.205246	glutamate decarboxylas
GAL1	267.397247	298.412109	201.181076	209.156097	galactokinase
GAL10	250.837158	285.48764	172.046555	159.577728	bifunctional UDP-glucos
GAL102	186.87088	181.394882	58.288406	61.457722	Gal102p
GAL4	196.968262	207.895615	81.779015	72.811363	galactose-responsive tra
GAL7	544.262146	608.856812	180.785904	140.862198	UDP-glucose:hexose-1-
GAP1	95.862366	106.309639	139.134277	132.821869	Gap1p
GAP2	82.560562	89.144569	60.695034	42.058689	amino acid permease
GAP4	326.723663	383.950104	49.571083	44.475956	Gap4p
GAP5	141.647949	146.584457	104.351021	95.262154	Gap5p
GAP6	411.310181	416.68338	111.101913	103.259087	hypothetical protein L15
GAR1	309.962402	299.655945	238.396225	212.338821	H/ACA ribonucleoprotei
GAT1	6.295014	7.057796	4.619927	6.487039	GATA type zinc finger pr
GBP2	100.897064	110.251785	137.816803	116.371162	single-stranded telomeri
GCA1	8.116248	7.812207	1.512617	1.435311	Gca1p
GCA2	14.810396	15.557904	4.706735	4.129566	Gca2p
GCD1	49.227299	53.542267	63.010605	52.037865	translation initiation facto
GCD11	236.619354	246.807632	136.488098	134.706512	translation initiation facto
GCD2	56.949291	78.295654	60.69178	65.735641	translation initiation facto
GCD6	54.413387	50.425594	44.651333	43.385521	translation initiation facto
GCD7	86.648415	86.115685	68.479187	65.305222	translation initiation facto
GCF1	117.603661	119.29538	446.563416	484.319336	Gcf1p
GCN1	23.99408	24.639917	25.314182	20.599216	Gcn1p
GCN2	3.86866	3.838489	10.206154	8.473554	serine/threonine-protein
GCN20	22.065882	28.990232	33.361977	26.784418	protein GCN20
GCN3	43.336761	40.894974	53.201637	50.777107	translation initiation facto
GCN4	670.54126	738.694824	430.657898	430.638336	amino acid starvation-re

GCN5	24.555637	18.344658	66.171188	54.885792	histone acetyltransferase
GCR3	28.247095	27.385464	34.660126	43.306122	Gcr3p
GCS1	99.951942	100.35759	28.959482	36.62915	glutamate--cysteine ligas
GCV1	149.63945	165.561996	164.028	206.589813	glycine decarboxylase su
GCV2	306.591034	327.642487	442.059509	434.479156	glycine decarboxylase su
GCV3	519.470947	537.724487	628.847839	626.888245	glycine decarboxylase su
GCY1	18.839739	20.983313	32.979103	29.712965	glycerol 2-dehydrogenas
GDA1	69.239441	77.791672	67.704247	67.599113	guanosine diphosphatas
GDB1	6.182126	7.852376	2.224886	3.338244	glycogen debranching en
GDE1	64.060333	53.549332	23.096537	24.020208	hypothetical protein MGE
GDH2	425.338898	442.391357	349.893311	337.122467	glutamate dehydrogenas
GDH3	241.153931	277.349335	75.509369	68.913757	glutamate dehydrogenas
GDI1	151.645966	139.257935	160.148514	147.607529	Gdi1p
GDS1	377.025635	390.125946	69.123901	78.039696	Gds1p
GDT1	38.506405	39.161785	29.713999	30.380322	putative ribosome biosyn
GEA2	9.223454	8.927667	15.602835	21.335369	Arf family guanine nucle
GEF2	25.681149	30.981298	41.036224	40.363285	Gef2p
GFA1	136.06427	123.254234	170.233276	177.595505	glutamine--fructose-6-ph
GGA2	47.15007	45.068584	57.558826	73.280777	phosphatidylinositol 4-ph
GIG1	57.470741	55.240154	153.554199	180.905106	Gig1p
GIM5	41.748291	34.812019	56.918659	55.620438	Gim5p
GIN1	3.965608	3.954687	19.969339	17.771246	chromatin-modulating pr
GIN4	15.282479	18.124393	47.924042	45.733273	protein kinase
GIR2	49.377354	68.357262	33.784325	25.625717	hypothetical protein MG3
GIS2	329.118591	333.505554	497.345551	378.966156	mRNA-binding translatio
GIT1	5.064979	4.250893	0.417902	0.761907	hypothetical protein CAW
GIT2	609.841431	421.052002	46.985119	40.994789	Git2p
GIT3	36.771339	40.083454	16.324903	13.621727	Git3p
GIT4	1.210396	1.602784	0.592476	1.616941	Git4p
GLC3	40.066875	50.86713	31.741768	28.753847	1,4-alpha-glucan branch
GLC7	194.730637	204.44342	256.487701	236.067352	type 1 serine/threonine-p
GLE1	21.173634	19.196756	20.472378	23.849497	hypothetical protein MEC
GLE2	71.587265	77.801414	69.394852	61.964619	RNA export factor
GLG2	52.413853	49.201691	80.561775	71.820419	Glg2p
GLK1	101.340996	109.625633	96.136848	76.348076	glucokinase
GLK4	44.832806	62.951778	53.689316	35.116016	Glk4p
GLN1	2375.398438	2753.878906	1051.378174	989.897888	glutamate--ammonia liga
GLN3	114.948753	112.742683	71.616493	74.897369	nitrogen-responsive tran
GLN4	38.82262	40.604603	62.477367	65.157227	glutamine--tRNA ligase
GLO1	62.197193	74.384315	108.10994	93.653404	lactoylglutathione lyase
GLO2	37.573963	44.998192	56.989048	55.568726	hydroxyacylglutathione h
GLO3	87.369179	95.003578	141.990753	132.51738	ADP-ribosylation factor G
GLR1	56.479668	64.219307	76.78051	66.474426	glutathione-disulfide redu
GLT1	47.410843	43.534168	29.530832	28.865799	glutamate synthase (NAI
GLX3	657.966858	773.40564	108.214951	90.139648	glutathione-independent
GLY1	864.281189	1073.871338	547.088501	526.690491	threonine aldolase
GNA1	32.792103	27.974461	52.479729	60.254002	glucosamine 6-phosphat
GND1	653.590149	655.333252	482.859192	470.868896	phosphogluconate dehyd
GNP1	1593.573975	1664.942993	1399.263184	1241.877441	amino acid transporter
GNP3	36.337807	34.540188	14.46383	17.587358	Gnp3p
GOA1	10.861843	11.517068	15.37934	22.60741	Goa1p
GOR1	11.785909	7.418716	4.341151	2.150206	glyoxylate reductase
GPA2	56.729256	48.384361	53.706341	57.927792	guanine nucleotide-bindi
GPD1	147.361252	143.05928	45.218327	36.708599	glycerol-3-phosphate deh
GPD2	1062.760376	1268.943115	47.736267	48.064552	Gpd2p
GPH1	324.55368	349.653259	140.830338	126.146156	glycogen phosphorylase
GPI1	3.224727	6.894741	6.954061	7.511243	phosphatidylinositol N-ac
GPI13	6.787168	7.222527	10.929801	13.641596	mannose-ethanolamine
GPI19	4.721936	4.804026	17.810343	9.650494	phosphatidylinositol glyca
GPI2	13.265339	8.992978	17.790869	24.603374	phosphatidylinositol N-ac
GPI7	7.345053	8.069823	11.718293	12.174671	mannose-ethanolamine
GPI8	18.515621	24.324921	39.153694	34.919415	GPI-anchor transamidas
GPM1	664.970764	671.2677	706.979126	707.996033	phosphoglycerate mutas
GPM2	48.894573	54.076797	68.798683	63.479828	Gpm2p

GPR1	75.853554	72.902977	24.749613	30.311577	G protein-coupled recept
GPT1	4.509326	3.525676	3.962069	3.522355	Gpt1p
GPX1	8.933734	3.485109	4.805499	4.723863	Gpx1p
GPX2	27.902048	31.323023	2.233238	6.430142	Gpx2p
GPX3	46.806263	51.841724	64.342384	81.658043	Gpx3p
GRE2	52.819214	56.201313	55.459892	49.826778	Gre2p
GRE3	74.297897	74.737953	108.538567	103.377106	NAD(P)H-dependent D-
GRF10	245.245468	266.414124	57.353848	58.433159	Grf10p
GRP1	7.798077	8.347411	8.579574	11.343596	Grp1p
GRP2	165.067444	180.908722	31.916685	33.079426	Grp2p
GRR1	61.911404	52.072338	49.04921	45.895523	SCF ubiquitin ligase com
GRS1	104.451859	98.621986	146.863174	129.183578	glycine--tRNA ligase
GRX1	2.326892	0.165752	0.525092	2.416622	hypothetical protein
GRX3	136.710419	146.110748	116.231087	123.66925	Grx4 family monothiol gl
GSC1	54.757439	61.270393	53.845703	56.979332	1,3-beta-glucan synthas
GSG1	5.07995	3.420591	4.951353	9.95048	Gsg1p
GSH2	34.055481	40.169201	51.13282	43.722641	glutathione synthase
GSL1	5.980933	4.763357	6.404994	6.315777	Gsl1p
GSL2	6.847925	5.787874	15.44187	15.907496	Gsl2p
GSP1	436.47757	412.758636	536.27124	552.520325	Ran GTPase
GST1	16.091574	34.264778	1.199332	1.812381	Gst1p
GST2	23.45458	25.589043	21.7642	13.270574	Gst2p
GST3	17.205994	11.73	5.211166	6.04923	Gst3p
GSY1	263.498505	256.10733	107.599037	96.51683	glycogen (starch) syntha
GTR1	9.19432	10.936792	29.891495	23.014688	Rag GTPase
GTT1	1.009725	4.695473	2.977689	7.455122	Gtt1p
GTT11	136.861237	161.310181	155.44838	152.697311	Gtt11p
GTT12	9.181565	8.115202	14.933283	14.9775	bifunctional glutathione t
GTT13	36.273746	38.224594	24.501528	21.006214	Gtt13p
GUA1	181.793243	215.464691	115.698288	94.853165	GMP synthase (glutamin
GUK1	83.418823	98.343674	154.042816	104.007774	guanylate kinase
GUP1	7.233598	8.004813	14.147105	12.894472	O-acyltransferase
GUS1	48.459919	54.508556	81.969307	79.088539	glutamate--tRNA ligase
GUT1	56.136517	57.56881	24.567417	25.231455	glycerol kinase
GUT2	150.37468	165.337158	49.731144	60.844528	glycerol-3-phosphate de
GVP36	130.908051	155.754059	217.008255	213.34491	Gvp36p
GWT1	24.122944	17.105844	31.581001	34.831791	glucosaminyl-phosphoti
GYP1	8.530849	11.107416	15.793818	11.225734	Gyp1p
GYP2	11.66241	13.805022	21.113712	24.549259	Gyp2p
GYP5	106.640007	114.791939	111.523148	104.045609	Gyp5p
GYP7	87.784027	84.369514	110.211601	110.888542	hypothetical protein MG
GYP8	6.019681	6.524212	9.838889	10.804799	Gyp8p
GZF3	117.608147	113.964615	71.264023	91.913704	Gzf3p
HAC1	588.344543	603.237854	460.053284	517.945496	hypothetical protein MG
HAK1	0.251044	0.326176	0.277165	0.199155	Hak1p
HAL21	63.886887	56.921547	21.007334	15.733418	RecName: Full=3'
HAL22	12.012848	7.628271	10.784629	7.652644	Hal22p
HAL9	6.624219	6.489071	10.282324	7.83281	Hal9p
HAM1	36.795105	30.308876	44.882313	36.160011	nucleoside triphosphate
HAP2	27.85804	24.086214	37.207108	35.086594	predicted protein
HAP3	30.975666	26.186752	36.818726	48.380978	Hap3p
HAP31	75.6353	52.78096	93.574486	97.460793	Hap31p
HAP41	408.437286	460.2005	293.959503	299.061554	Hap43p-repressed prote
HAP42	10.51642	11.885916	15.991657	20.486269	hypothetical protein MG
HAP43	93.156044	86.729103	113.587852	148.630569	Hap43p
HAP5	29.84556	25.133461	39.488899	38.907883	Hap5p
HAS1	117.531677	106.795029	59.088383	55.491467	ATP-dependent RNA he
HAT1	11.175457	13.519571	54.80793	61.22353	histone acetyltransferas
HAT2	33.064934	32.867298	108.26564	90.183289	Hat2p
HBR1	57.885807	66.211464	60.728081	64.226753	nucleoside-triphosphata
HBR3	110.642036	113.24707	50.561485	41.725082	RNA-binding protein NO
HCA4	48.482834	42.610222	26.133114	20.354708	RNA-dependent ATPase
HCH1	45.443424	42.976265	78.883644	55.872566	Hch1p
HCM1	13.647197	11.771799	77.307068	80.309952	Hcm1p

HCR1	150.174561	164.971588	142.34137	149.198029	eukaryotic translation init
HDA1	22.716789	19.829782	38.282181	37.668839	histone deacetylase 6/10
HEM1	166.836945	175.578232	90.769798	95.908531	5-aminolevulinate syntha
HEM13	735.625	768.50647	1726.733643	1492.242065	coproporphyrinogen oxid
HEM14	12.386833	13.882637	21.633911	27.257704	oxygen-dependent proto
HEM15	36.867233	43.170815	48.567451	57.631523	ferrochelatase
HEM2	33.637802	38.2644	53.087383	50.387207	porphobilinogen synthas
HEM3	303.925415	349.666992	169.377731	137.455978	hydroxymethylbilane syn
HEM4	15.781042	13.813451	27.558609	22.826668	uroporphyrinogen-III syn
HET1	218.69014	187.913818	320.691772	252.055283	Het1p
HEX1	22.348759	21.991684	38.049068	31.305147	Hex1p
HEX3	33.777355	32.385071	35.181576	35.316887	hypothetical protein MG3
HFL1	18.882929	20.778851	33.357582	36.557098	DNA polymerase epsilo
HFL2	101.451149	103.29599	167.276855	135.58815	negative cofactor 2 trans
HGC1	14.722545	13.671772	19.37652	21.212954	cyclin
HGH1	22.416632	29.243528	25.970539	24.988262	Hgh1p
HGT1	1320.081177	1555.322266	48.829021	41.908855	Hgt1p
HGT10	22.44989	24.742149	110.750252	88.825348	glucose-inactivated glyce
HGT12	3.005957	2.01544	4.07409	1.137742	Hgt12p
HGT13	5.394923	4.526549	8.355267	8.446128	Hgt13p
HGT14	15.833764	18.526173	9.936201	7.416593	Hgt14p
HGT16	9.016151	9.842018	12.206215	11.723679	Hgt16p
HGT17	3.83546	7.06486	1.339005	2.543346	Hgt17p
HGT18	51.809528	59.095634	50.109192	34.216667	Hgt18p
HGT19	8.372846	5.960032	7.477113	3.597576	Hgt19p
HGT2	348.033203	369.14505	318.435089	312.075653	Hgt2p
HGT20	2.655684	3.609704	12.343213	6.934993	Hgt20p
HGT3	3.303641	4.620584	8.419005	8.689908	Hgt3p
HGT4	27.468521	33.118027	16.763556	13.391376	glucose sensor
HGT5	13.1496	15.489883	19.047792	20.300716	sugar porter (SP) family
HGT6	34.726044	33.818752	3.621152	4.520317	sugar porter (SP) family
HGT7	352.541199	430.576141	101.693298	110.127739	Hgt7p
HGT8	55.959042	63.651051	19.870918	25.160135	Hgt8p
HGT9	5.420578	7.249758	13.12152	15.610918	Hgt9p
HHF1	2099.579834	2173.998779	10347.16016	8887.544922	hypothetical protein SPA
HHF22	1909.310425	2120.020264	6450.105469	5761.387207	hypothetical protein SPA
HHO1	930.566406	899.842041	5293.644043	5409.647461	histone H1/5
HHT1	1055.984497	1172.662842	1275.317505	1097.197144	Hht1p
HHT2	1950.62793	2318.782227	6520.382324	5624.350586	Hht21p
HHT21	3172.58667	3504.927734	14903.72656	13890.33887	Hht21p
HIP1	127.796577	134.659958	51.511875	49.456242	Hip1p
HIR1	16.023602	15.608039	32.366531	29.780491	Hir1p
HIS1	65.085892	79.625107	98.615608	88.429169	ATP phosphoribosyltrans
HIS3	30.830711	45.25095	10.330583	16.237375	imidazoleglycerol-phosp
HIS4	44.078686	39.357231	47.291073	44.121635	trifunctional histidinol de
HIS5	18.946177	18.405235	31.280565	25.940897	histidinol-phosphate tran
HIS7	16.537081	15.52523	39.304611	38.339825	imidazoleglycerol-phosp
HIT1	18.383343	21.153915	12.869318	10.913337	Hit1p
HLJ1	30.751942	30.14883	35.633495	32.58646	type I HSP40 co-chaper
HMG1	29.243143	27.782078	36.143906	35.354614	hydroxymethylglutaryl-C
HMI1	12.005555	17.663406	19.458269	13.727447	ATP-dependent 3'
HMO1	1122.00354	1184.029175	2285.623779	2421.093262	Hmo1p
HMS1	85.21936	88.684395	207.206573	237.491455	Hms1p
HMT1	97.173233	100.573235	75.095863	70.074463	protein-arginine omega-
HMX1	162.910416	177.987778	573.760071	461.116882	Hmx1p
HNM1	95.783401	115.64669	81.088661	102.882439	Hnm1p
HNM3	10.34575	0	11.980026	8.505443	Hnm3p
HNM4	5.315259	6.582051	1.308848	2.769588	hypothetical protein W5
HNT1	158.109085	107.788429	91.764946	92.985535	adenosine 5'-mon
HNT2	6.496402	8.088864	16.178904	10.860109	bis(5'-adenosyl)-tr
HOC1	26.750362	27.46706	26.546017	24.693802	alpha-1,6-mannosyltrans
HOF1	16.801394	13.564921	64.395149	92.668098	formin-binding protein
HOG1	66.960136	67.410065	91.919144	80.300606	mitogen-activated protei
HOL1	0.339784	0.355787	0.115774	0.512271	Hol1p

HOL4	246.325912	325.05307	282.457489	238.831116	Hol4p
HOM2	69.750259	64.238281	67.395111	68.402794	aspartate-semialdehyde
HOM3	9.188288	8.474321	14.821787	12.512455	aspartate kinase
HOM6	86.060829	100.217148	110.230309	91.691414	homoserine dehydrogen
HOS1	11.955877	10.572453	11.099282	13.357702	histone deacetylase
HOS2	16.025324	18.423571	21.271189	18.473499	histone deacetylase
HOS3	39.768753	38.147957	75.482742	71.496216	histone deacetylase
HPA2	38.855782	46.694302	36.066566	29.433014	D-amino-acid N-acetyltr
HPC2	13.205657	9.973874	20.829296	22.546843	hypothetical protein MG
HPD1	155.572769	130.038025	53.186092	52.004589	Hpd1p
HPT1	221.000885	241.077271	74.286621	62.428726	hypoxanthine phosphori
HRK1	50.47377	51.164711	67.35157	75.315453	hypothetical protein MG
HRQ2	11.437677	10.848701	8.84602	8.212897	Hrq2p
HRR25	790.301086	737.940918	793.478577	946.020569	discs overgrown protein
HRT1	148.896255	200.436539	146.536575	154.465012	SCF ubiquitin ligase co
HRT2	14.369532	19.629681	30.300842	27.867472	putative methyltransfera
HSE1	59.55164	56.09116	86.845818	92.567581	ESCRT-0 subunit protei
HSK3	49.515068	45.719578	98.020683	108.281189	Hsk3p
HSL1	12.161655	10.920577	27.469812	35.289967	protein kinase
HSM3	32.538399	38.953396	45.141727	52.049553	DNA mismatch repair pr
HSP104	2046.60791	1879.726318	2199.341064	2225.426025	heat shock protein 104
HSP12	38.427155	51.232803	11.000253	8.277955	Hsp12p
HSP21	1672.324463	1859.170166	1049.050537	1055.175659	Hsp21p
HSP30	171.695648	187.452087	30.593306	25.874346	Hsp30p
HSP31	15590.47461	14047.07227	28759.34961	28741.31445	Hsp31p
HSP60	200.609665	215.412277	403.213623	346.985748	chaperone ATPase
HSP70	691.024109	793.633118	796.83075	765.168091	Hsp70 family chaperone
HSP78	72.065269	68.880524	86.236458	83.490273	hsp78-like protein
HSP90	407.088928	424.468933	448.481812	516.219177	Hsp90 family chaperone
HST1	14.007818	12.605717	24.077419	21.279072	histone deacetylase
HST2	6.993143	9.049442	6.858016	7.146493	histone deacetylase
HST3	23.170485	20.301863	86.408424	79.521088	NAD-dependent histone
HST6	2.41179	2.951231	0.235746	0.334906	alpha-factor-transporting
HST7	51.026527	51.198158	52.568439	56.009686	mitogen-activated protei
HSX11	6.666598	6.043094	14.344651	14.300222	Hsx11p
HTA1	1613.34436	1539.72583	4737.781738	4269.83252	Hta1p
HTA2	2314.293457	2624.165283	11202.46094	10288.46582	histone H2A.1
HTA3	407.523346	370.959686	2430.595947	2095.085693	histone H2AZ
HTB1	2529.672363	2766.347412	10608.40918	11040.9043	histone H2B
HTS1	157.975906	161.048798	131.70166	109.689117	histidine--tRNA ligase
HUT1	6.164386	6.779287	14.126831	16.467779	Hut1p
HWP1	1.595642	0.663529	2.60958	1.867944	Hwp1p
HWP2	0.092452	0.054704	0.197877	0	hypothetical protein ME
HXK1	166.211655	134.199814	113.336044	91.923676	hexokinase 1
HXK2	153.299652	167.827499	113.067154	102.001709	hexokinase 2
HXT5	1.399659	2.255165	1.874264	0.860062	sugar porter (SP) family
HYM1	23.075148	29.308622	28.383865	31.204643	Hym1p
HYR1	16.370596	16.34672	5.352221	5.23188	Hyr1p
HYR3	76.626282	81.165276	59.88126	61.821449	hypothetical protein W5
HYR4	123.693947	88.345642	15.323864	17.328743	Hyr4p
HYS2	18.550552	15.241476	36.45977	26.909378	DNA-directed DNA poly
HYU1	13.422643	16.1374	26.00708	27.907967	5-oxoprolinase
IAH1	57.527809	55.92178	74.607224	75.363525	isoamyl acetate-hydrolyz
ICL1	1066.824707	1036.947388	1636.986206	1674.948486	isocitrate lyase 1
IDH1	421.001923	407.651001	421.279236	470.862701	NAD+-specific isocitric d
IDH2	362.798828	338.727356	413.455841	400.993744	isocitrate dehydrogenas
IDI1	107.428665	96.771049	61.907158	60.774117	isopentenyl-diphosphate
IDP1	44.875782	54.006016	59.190922	43.704018	isocitrate dehydrogenas
IDP2	361.513123	380.519257	319.161743	317.417053	isocitrate dehydrogenas
IFA14	6.61752	7.025038	2.820451	3.351632	Ifa14p
IFA21	11.805035	11.666031	16.832417	14.523305	Ifa21p
IFA4	3.899106	3.733569	6.760222	5.63714	Ifa4p
IFD3	20.44154	24.682793	18.995066	19.791227	Ifd3p
IFD6	77.563728	83.110291	2.05832	3.032492	Ifd6p

IFE1	7.184821	9.611918	2.329378	2.970371	putative dehydrogenase
IFE2	7508.530762	7938.328125	6601.472656	5481.906738	Ife2p
IFF11	8.238688	7.616159	12.928476	13.070027	hypothetical protein MG3
IFF3	17.006268	13.172496	23.190626	20.186169	Iff3p
IFF4	9.852457	11.392252	6.003183	7.511306	Iff4p
IFF5	10.296997	9.235243	10.584632	11.544866	Iff5p
IFF6	278.14212	338.606812	326.650787	374.397522	hypothetical protein MG
IFF8	24.056374	21.170776	30.46174	41.732903	hypothetical protein MG7
IFF9	19.129236	16.787575	26.576914	22.538767	Iff9p
IFG3	71.059021	73.025986	29.80176	31.069275	Ifg3p
IFH1	56.021729	65.940727	53.77058	50.75935	Ifh1p
IFI3	23.598755	25.827993	23.946583	22.974491	Ifi3p
IFK2	10.330897	13.965702	15.486015	17.55813	Ifk2p
IFM1	18.561943	20.889891	49.14135	47.031391	translation initiation facto
IFM3	95.157295	101.61731	28.793488	27.246553	hypothetical protein MG1
IFR1	3.946747	6.479952	0	0.341616	Ifr1p
IFR2	120.594322	138.860184	246.210144	217.037369	Ifr2p
IFU5	293.489502	276.652832	492.796753	340.366394	hypothetical protein MG3
IHD1	5.821445	6.71948	2.591821	2.434158	Ihd1p
IHD2	45.705189	57.543121	6.148314	11.21322	Ihd2p
ILS1	79.215515	89.755211	81.833839	85.504501	isoleucine--tRNA ligase
ILV1	18.426704	19.541832	23.667822	26.05336	threonine ammonia-lyase
ILV2	72.730782	72.190666	42.270004	34.319614	acetolactate synthase ca
ILV3	76.068314	80.569916	55.867447	56.75359	dihydroxy-acid dehydrata
ILV5	144.804535	164.588501	132.511078	104.160912	ketol-acid reductoisomer
ILV6	59.329479	57.062336	68.870537	67.800758	acetolactate synthase, s
IME2	2.213624	0.730453	2.89158	2.511933	protein kinase
IMG2	32.980877	37.796726	61.895138	50.788269	mitochondrial 54S riboso
IMH3	449.541656	482.990204	211.253204	200.805817	IMP dehydrogenase
IML1	17.748529	16.57835	15.836555	16.051498	Iml1p
IML2	21.11869	19.502872	22.9049	27.670019	Iml2p
IMP1	14.519602	19.135309	37.81057	45.572304	endopeptidase catalytic
IMP2	45.367428	34.799717	60.480133	50.093006	endopeptidase catalytic
IMP4	203.68364	210.776596	99.995461	109.842659	snoRNA-binding rRNA-p
INN1	90.39946	88.899658	171.961716	229.42717	Inn1p
INO1	470.522797	457.746948	1026.556152	983.346802	inositol-3-phosphate syn
INO2	34.121395	28.669804	20.056	23.77442	Ino2p
INO4	76.447884	82.554451	101.724022	112.24604	Ino4p
INP51	7.176682	8.994925	12.174977	16.046196	phosphoinositide 5-phos
INT1	34.473282	31.897987	84.095703	104.652657	Int1p
IPK1	38.242485	51.126606	31.666451	36.843033	inositol pentakisphospha
IPK2	37.729862	36.657089	73.948196	69.715462	inositol polyphosphate m
IPL1	24.363958	21.257574	12.051441	16.196499	spindle assembly checkp
IPP1	424.453308	406.639893	455.982025	497.274567	inorganic diphosphatase
IPT1	15.973434	18.103945	0	0.474662	inositolphosphotransfera
IQG1	17.000944	11.805582	24.978025	36.372753	Iqg1p
IRA2	14.477271	14.020811	17.974722	21.539017	Ras GTPase activating p
IRE1	24.183247	22.662477	27.601162	29.653721	serine/threonine-protein
IRO1	12.409275	11.80585	11.585344	8.207353	Iro1p
IRR1	9.448887	9.809457	50.282448	47.946358	Irr1p
IRS4	32.092724	30.546553	39.07061	36.593029	Irs4p
ISA1	179.020142	181.424393	233.25528	241.041977	Fe-binding Fe/S cluster a
ISA2	107.435532	112.275772	63.535938	67.439003	Isa2p
ISC1	13.755758	19.468081	22.052011	19.367472	inositol phosphosphingol
ISN1	20.707798	22.88883	25.689667	31.178564	IMP 5'-nucleotidas
IST1	21.631828	24.566484	42.990456	44.482594	Ist1p
IST2	151.373077	182.263596	126.289261	139.261108	Ist2p
ISU1	643.168274	684.861206	606.656555	502.970978	iron-binding protein
ISW2	17.283031	10.026642	21.749462	24.979345	DNA translocase
ISY1	21.620426	14.458262	26.800503	28.470417	pre-mRNA-splicing facto
ITR1	58.961716	64.317627	35.287697	30.652758	sugar porter (SP) family
JAB1	19.33499	22.097141	38.943375	41.565369	COP9 signalosome cata
JEM1	13.952006	10.169919	15.237147	16.946226	hypothetical protein MEK
JEN1	3.624643	4.485081	4.965189	1.866852	Jen1p

JEN2	87.805176	82.11866	385	381.012726	Jen2p
JIP5	36.21941	36.944611	18.727749	14.829296	Jip5p
KAP120	45.423439	44.532288	35.514626	32.763332	hypothetical protein MG5
KAR2	305.958954	313.425323	241.650681	263.56369	Hsp70 family ATPase
KAR3	6.015482	5.652421	20.184628	23.642052	Kar3p
KAR4	15.340564	10.258684	17.619652	10.490159	Kar4p
KAR5	2.834656	0.734043	2.719431	3.577039	Kar5p
KAR9	5.94475	5.206654	11.43362	11.032276	Kar9p
KCH1	14.852023	12.093343	10.384517	8.964897	Kch1p
KCS1	67.46627	61.061413	16.48995	19.984034	inositol polyphosphate ki
KEL1	50.448273	46.633316	55.468025	64.421921	hypothetical protein MGE
KEM1	20.610548	21.338463	39.423176	41.947227	chromatin-binding exonu
KEX2	20.955093	21.414337	17.996384	21.860788	kexin
KGD1	157.153061	174.14299	160.936234	147.153549	alpha-ketoglutarate dehy
KGD2	250.455872	239.181152	240.891663	256.225739	alpha-ketoglutarate dehy
KIC1	30.956327	29.244392	33.277851	38.997417	hypothetical protein MEV
KIN2	37.202652	38.527081	42.539085	45.125263	serine/threonine protein
KIN3	94.722054	78.384697	85.315376	70.781891	serine/threonine protein
KIP1	6.106359	8.082575	35.244091	34.179119	kinesin family member 1
KIP2	9.458829	8.545419	32.622875	47.227715	Kip2p
KIP3	6.172953	4.942909	19.413782	16.052963	tubulin-dependent ATPa
KIP4	18.500391	23.986191	62.548241	62.311058	Kip4p
KIS1	81.667259	84.084663	65.485756	84.654808	Kis1p
KIS2	15.103026	14.23598	13.678505	15.768333	conserved hypothetical p
KNS1	36.487549	40.39072	25.61928	28.717173	conserved hypothetical p
KOG1	22.524817	21.575012	21.466743	21.895966	ubiquitin-binding TORC1
KRE1	108.990089	103.790909	12.062369	13.703733	Kre1p
KRE30	171.117615	190.286179	97.911819	95.193344	ATP-binding cassette fa
KRE5	6.121282	6.865187	11.086181	12.763653	Kre5p
KRE6	68.740524	71.060715	6.877439	5.975106	beta-glucan synthesis-as
KRE62	0.844888	0.63853	0	0	Kre62p
KRE9	157.293411	132.352692	216.489151	236.452179	Kre9p
KRR1	83.880035	79.84613	27.078331	36.16048	ribosomal RNA assembl
KRS1	147.853958	160.485519	137.006668	127.737579	lysine--tRNA ligase
KSP1	19.635073	19.741703	46.469696	52.139919	protein-serine/threonine
KSR1	21.545746	27.520105	43.365242	42.121128	3-dehydrosphinganine re
KTI11	155.13324	164.308929	41.239082	30.575972	Kti11p
KTI12	39.341404	35.816124	26.464149	19.438982	Kti12p
KTR2	1.785833	2.698298	6.719692	7.175404	mannosyltransferase
KTR4	13.737471	18.831594	15.573078	24.090385	mannosyltransferase
LAB5	185.280792	188.224503	144.321686	160.335007	putative lipoate synthase
LAC1	21.613264	22.521315	40.296185	43.718773	Lac1p
LAG1	60.057858	57.500175	53.541451	46.111221	sphingosine N-acyltransf
LAP3	416.094116	471.038269	19.637924	21.409231	bleomycin hydrolase
LAP4	16.723177	19.124708	23.347021	22.555681	Lap4p
LAP41	44.917717	55.148586	64.89135	71.013626	aminopeptidase I
LAS1	41.712204	40.964535	26.569513	25.911388	rRNA-processing protein
LAT1	176.15358	149.444885	232.572067	247.148514	pyruvate dehydrogenase
LCB2	49.780704	51.490608	69.405678	65.425804	serine C-palmitoyltransfe
LCB4	11.77868	12.798152	19.535694	22.630234	sphinganine kinase
LDG3	0.274638	0	1.715556	3.164177	Ldg3p
LEA1	22.551722	32.963333	26.630602	35.859859	U2 snRNP complex subu
LEM3	83.618385	94.559822	132.136215	117.401474	Lem3p
LEU1	36.483692	41.385868	20.239399	22.949036	3-isopropylmalate dehyd
LEU2	30.739481	26.262333	17.408358	19.178528	3-isopropylmalate dehyd
LEU3	21.539919	23.527649	22.385323	26.952951	leucine-responsive trans
LEU4	6.727967	8.883718	1.198385	2.25102	2-isopropylmalate syntha
LEU42	257.058624	247.732681	147.031937	129.274078	Leu42p
LEU5	44.378464	47.592209	24.315258	25.586494	coenzyme A transporter
LHP1	53.723042	61.079231	55.158058	67.21875	lupus La protein
LHS1	27.465122	28.199812	30.799208	38.679703	Hsp70 family chaperone
LIG1	22.383219	21.681431	19.114239	18.157	tRNA ligase
LIG4	4.03521	5.668028	9.024647	7.944846	DNA ligase (ATP)
LIP1	2.490117	1.953678	0.586557	0.031096	Lip1p

LIP10	0	0.382722	0	0	Lip10p
LIP2	14.809136	8.909418	0.975101	1.728724	Lip2p
LIP3	1.404808	0.559763	2.683083	3.133916	Lip3p
LIP4	9.816147	12.352102	6.70222	5.305099	Lip4p
LIP5	6.174045	6.483717	8.305546	10.450831	Lip5p
LIP6	6.423084	9.443558	7.534636	8.45779	Lip6p
LIP7	1.67816	1.619475	0	0.243957	Lip7p
LIP8	17.685911	12.239758	39.052746	57.606232	Lip8p
LIP9	7.172025	6.492793	773.308105	880.356079	Lip9p
LKH1	45.136963	61.692024	86.198151	85.229294	bifunctional aminopeptid
LMO1	24.622353	24.947376	38.32172	38.628624	Lmo1p
LPD1	684.73114	699.551636	422.453522	427.52298	dihydrolipoyl dehydroge
LPG20	36.042957	43.476326	34.613712	27.219402	aldo-keto reductase sup
LPI9	149.78273	138.543854	116.751099	122.005104	protein phosphatase reg
LPT1	31.988792	31.569782	40.067623	52.531639	lysophospholipid acyltra
LRG1	31.712746	30.776102	75.049217	91.881966	hypothetical protein MG
LRO1	49.951435	44.801327	36.173927	32.049156	phospholipid:diacylglyce
LSC1	480.481262	468.67514	596.10022	563.891785	succinate--CoA ligase (
LSC2	388.983063	424.334656	854.08136	788.214783	succinate--CoA ligase (
LSM6	82.852982	89.784203	135.186386	106.14151	U4/U6-U5 snRNP compl
LSP1	532.620178	519.021606	590.819946	617.011414	lipid-binding protein
LTE1	6.776382	5.38713	23.375242	24.276598	mitotic regulator
LTP1	71.831154	67.344215	96.16201	91.919891	tyrosine protein phospha
LTV1	78.329361	95.696548	38.363117	39.163052	Ltv1p
LYP1	3.723096	5.801308	4.440316	5.65857	Lyp1p
LYS1	68.225357	84.4468	162.665665	177.61412	saccharopine dehydroge
LYS12	121.969818	122.622818	120.186089	94.437874	homoisocitrate dehydrog
LYS14	7.567781	7.951049	4.248569	3.880449	hypothetical protein ME
LYS142	6.111316	8.140089	15.141922	16.452755	Lys142p
LYS143	4.2569	3.697188	7.301358	10.723409	Lys143p
LYS144	7.724256	9.247827	15.914842	16.154955	Lys144p
LYS2	18.927269	19.177408	24.680317	22.728987	L-aminoadipate-semiald
LYS21	50.355621	46.910427	63.548046	60.636082	homocitrate synthase
LYS22	8.458876	14.460842	41.535728	38.626644	Lys22p
LYS4	17.385691	14.961205	20.825523	19.450563	homoaconitate hydratas
LYS5	4.667996	4.949446	13.864519	11.636477	Phosphopantetheinyl tra
LYS9	90.980797	102.944817	93.571915	86.489616	saccharopine dehydroge
MAC1	23.027134	16.229082	82.029724	98.071312	Mac1p
MAD2	11.481451	10.578811	34.715313	27.491077	spindle checkpoint prote
MAE1	39.867798	62.726105	27.776791	28.386076	malate dehydrogenase (
MAF1	55.062233	61.626556	154.086121	151.812347	hypothetical protein MG
MAK16	169.181229	174.723236	38.733253	55.230751	protein MAK16
MAK21	72.87468	72.440468	26.989239	24.589031	RNA-binding ribosome b
MAK32	11.262444	11.417961	21.302584	22.112316	Mak32p
MAK5	21.248077	20.794954	18.207575	16.854275	putative ATP-dependent
MAL2	20.581022	20.399937	14.384927	9.609385	oligo-1,6-glucosidase IM
MAL31	52.892868	58.471226	18.371286	15.768103	maltose permease
MAM33	246.956924	297.034515	898.339722	705.959167	Mam33p
MAS1	33.000359	36.765701	77.746643	58.366123	Mas1p
MAS2	19.970161	20.986126	43.848988	44.225925	mitochondrial-processin
MBF1	364.684143	413.899353	400.659515	306.635498	Mbf1p
MBP1	35.584152	35.923225	38.625977	38.831356	transcription factor
MCA1	106.995598	109.776337	80.431152	75.399605	metacaspase-1
MCD1	11.608816	14.272832	51.072773	50.489368	kleisin alpha
MCD4	10.80953	10.754419	10.087817	10.210834	GPI ethanolamine phos
MCI4	205.221771	218.624069	352.045898	332.749878	Mci4p
MCM1	57.510948	70.711044	107.760162	117.929466	transcription factor
MCM2	13.366636	17.304548	59.426685	51.029266	hypothetical protein L15
MCM3	32.684788	31.432474	90.248436	77.658279	minichromosome mainte
MCM6	15.699086	18.766628	110.035637	84.138123	minichromosome mainte
MCR1	255.683289	248.957916	295.964142	235.706055	cytochrome-b5 reductas
MCT1	74.671227	101.600922	76.885384	83.4179	
MCU1	12.599705	13.960922	28.782438	27.182386	Mcu1p
MDG1	193.536209	187.101059	266.561188	265.706696	Mdg1p

MDH1	571.554565	645.247742	398.369812	422.408661	malate dehydrogenase
MDH1-1	963.562317	871.32312	932.756348	938.768127	malate dehydrogenase
MDH1-3	79.126717	79.833351	56.181053	52.252838	malate dehydrogenase,
MDJ1	72.820808	74.029648	62.069633	44.883099	Mdj1p
MDJ2	11.646824	10.106247	25.374763	37.262321	Mdj2p
MDL1	14.051047	14.520426	19.733906	18.561216	ATP-dependent permea
MDL2	9.796715	10.522271	15.786278	17.911234	Mdl2p
MDM10	12.971708	10.29129	24.820257	30.741013	Mdm10p
MDM34	1150.118408	1246.056763	669.250366	704.896362	ERMES complex subuni
MDN1	4.933661	5.284767	9.994493	12.127467	AAA family ATPase mid
MDR1	7.987444	5.206656	5.046127	5.25027	Mdr1p
MDS3	12.28524	10.322628	14.502736	14.819076	Mds3p
MEA1	5.53147	7.40147	6.501443	6.556069	Mea1p
MEC1	8.485336	5.825538	8.077681	8.968764	protein kinase
MEC3	7.083806	8.917439	19.521952	19.119457	Mec3p
MED1	16.293289	17.889935	30.950886	33.700569	Med1p
MED10	12.150465	9.888881	28.383873	27.855715	mediator complex subun
MED11	10.47921	15.345268	40.557323	36.481953	Med11p
MED14	8.880277	10.040978	12.501813	11.421783	Med14p
MED15	44.278255	41.242367	34.852455	39.050865	Med15p
MED16	7.895222	7.911104	18.454256	21.878262	hypothetical protein L15
MED17	7.209159	13.758559	20.041719	24.293964	Med17p
MED18	23.047915	21.878281	47.65659	45.568275	Med18p
MED19	48.482506	51.498753	106.759453	101.728683	Med19p
MED20	17.158594	15.593193	49.512306	34.622524	Med20p
MED21	9.52601	13.813873	39.066795	36.523369	Med21p
MED22	13.610489	24.108294	20.049095	20.253202	Med22p
MED3	40.780247	51.521976	47.72364	34.409283	Med3p
MED4	26.229401	23.681	43.072193	52.742817	Med4p
MED5	6.492712	6.987783	8.05886	9.710439	Med5p
MED7	18.984598	19.4174	27.082575	23.64934	mediator complex subun
MED8	14.69519	16.198082	28.486204	23.629131	Med8p
MED9	37.537518	42.273487	37.886837	28.779024	Med9p
MEF2	9.593372	11.887012	34.518639	28.879185	RecName: Full=Riboson
MEP1	41.453598	47.014099	8.450958	10.356709	ammonium permease
MEP2	12.397387	12.035431	12.73038	15.053695	ammonium permease
MES1	36.13163	35.739513	54.31612	55.46439	methionine--tRNA ligase
MET1	18.899603	19.95656	18.95665	9.225433	uroporphyrinogen-III C-m
MET10	21.106508	29.038179	16.725657	16.595783	sulfite reductase subunit
MET13	19.361816	25.016914	26.984806	22.338587	methylenetetrahydrofola
MET14	30.224852	28.763275	19.258051	22.594261	adenylyl-sulfate kinase
MET15	122.826042	139.606155	123.199532	158.163727	bifunctional cysteine syn
MET16	25.128723	26.648676	28.645443	21.466619	phosphoadenylyl-sulfate
MET18	3.170077	4.409545	7.970356	9.793606	Met18p, partial
MET2	44.917255	54.348763	46.947643	42.494408	homoserine O-acetyltran
MET28	166.74057	219.064636	453.601868	400.569946	Met28p
MET3	29.739485	30.195684	26.143953	29.143148	sulfate adenylyltransfera
MET4	34.666538	33.565144	49.971043	53.999958	Met4p
MET6	445.33786	492.571228	670.101868	679.59021	5-methyltetrahydropteroy
MET8	22.61223	24.053696	29.325708	35.165123	bifunctional precorrin-2
MEU1	50.011051	58.79332	38.50061	27.268272	S-methyl-5-thioadenosin
MEX67	42.976044	49.100578	39.889904	45.108124	Mex67p
MFA1	71.622261	83.793243	5.57421	0	Mfa1p
MFG1	46.717983	47.538628	17.579628	19.810974	Mfg1p
MGE1	246.679886	295.073456	364.934906	323.598694	Mge1p
MGM101	33.099064	40.207989	100.607018	111.750809	Mgm101p
MHP1	180.144211	169.065613	137.253052	157.410858	Mhp1p
MIA40	39.556011	48.432243	76.324051	78.11483	Mia40p
MID1	20.379011	21.293171	34.923214	36.082977	calcium channel MID1
MIF2	159.081467	188.066116	263.366547	269.773865	Mif2p
MIG1	396.228485	433.349762	103.6493	101.132668	transcription factor
MIH1	28.48695	22.678532	87.54882	129.685883	putative tyrosine protein
MIM1	102.467506	96.449615	162.2211	125.075607	Mim1p
MIR1	791.432983	833.599609	690.838013	672.59613	Mir1p

MIS11	97.034088	109.44651	148.221085	151.117752	trifunctional formate-tetra
MIS12	77.11158	78.260307	26.644238	28.158953	Mis12p
MIT1	546.039001	530.926025	346.443756	381.490662	mannosylinositol phosph
MKC1	55.042946	54.87875	62.05444	69.243492	mitogen-activated serine
MKK2	27.70537	28.620531	16.256891	17.688633	mitogen-activated protei
MLC1	115.588943	122.018555	434.903534	310.885895	Mlc1p
MLH1	4.517205	3.711175	8.168954	9.93238	mismatch repair ATPase
MLH3	20.999607	28.124884	21.688255	25.363737	mismatch repair protein
MLP1	29.735884	30.383284	50.689503	54.988808	Mlp1p
MLS1	1508.27356	1611.331421	2116.83374	2227.12793	malate synthase
MLT1	16.82144	20.530722	18.574909	18.183977	Mlt1p
MMD1	461.405609	478.257965	494.5065	363.500977	isoleucine biosynthesis p
MMS21	9.554202	15.266155	30.113987	35.900982	SUMO ligase
MMS22	1.370259	2.04871	7.137662	6.775401	Mms22p
MNL1	42.403011	40.886505	45.259918	49.567165	Mnl1p
MNN1	12.374713	15.480502	12.856134	10.001666	Mnn1p
MNN10	44.319016	52.417976	63.868683	72.429893	alpha-1,6-mannosyltrans
MNN11	26.853519	23.895803	24.645367	30.50959	alpha-1,6-mannosyltrans
MNN12	9.299732	10.198226	2.478492	1.337408	alpha 1,3-mannosyltrans
MNN13	3.542463	4.580379	9.727866	8.300885	hypothetical protein MG
MNN14	18.465353	17.406342	4.134711	2.36887	Mnn14p
MNN15	16.842678	22.405548	7.975391	7.361863	putative alpha-1,3-mann
MNN2	31.706301	26.433784	141.274826	152.111389	Mnn2p
MNN21	14.641387	16.886106	20.936468	21.747961	alpha-1,2-mannosyltrans
MNN22	2.813177	2.204778	4.043247	2.177556	Mnn22p
MNN23	47.496696	51.43108	268.767914	284.258789	conserved hypothetical p
MNN24	15.045782	16.60038	13.976582	19.992245	Mnn24p
MNN26	7.055446	6.952374	13.629188	15.404473	Mnn26p
MNN4	61.295807	59.377998	3.193524	4.483715	Mnn4p
MNN4-4	45.090782	31.940897	3.841979	3.086904	Mnn4-4p
MNN9	36.998512	30.930428	38.546253	44.265015	mannosyltransferase co
MNR2	18.312056	22.765306	22.524803	22.536135	putative Mg(2+) transpor
MNS1	28.405527	31.720995	80.927376	64.314003	mannosyl-oligosaccharid
MNT1	215.817368	235.24765	292.785248	278.824005	alpha-1,2-mannosyltrans
MNT2	23.885086	22.232967	8.994206	7.08293	alpha-1,2-mannosyltrans
MNT3	24.980419	28.634365	16.788929	14.300642	Mnt3p
MNT4	2.296294	2.142341	2.810187	2.077604	Mnt4p
MOB1	36.339294	33.841167	129.03894	134.044189	Mob1p
MOB2	48.760586	49.054047	49.467236	53.601994	Mob2p
MODF	19.164328	18.300682	27.962244	27.783007	Modfp
MOH1	114.798424	140.487091	63.145962	67.473473	hypothetical protein MGM
MON2	5.754588	8.822653	16.213615	15.852039	Mon2p
MP65	1822.911133	1873.781982	3592.001709	3779.664795	putative family 17 glucos
MPH1	4.015443	3.688672	15.561564	17.299341	3'-5' DNA h
MPP10	91.159866	104.266548	74.908829	60.287529	U3 small nucleolar RNA-
MPS1	5.802476	5.319406	22.719473	29.55592	serine/threonine/tyrosine
MPT5	16.55158	15.426379	10.368234	11.724901	Mpt5p
MRE11	9.489582	9.309759	18.162413	22.052025	MRX complex nuclease
MRF1	151.535934	165.100632	58.185333	47.561127	Mrf1p
MRP17	130.655304	133.294724	212.822433	182.305435	mitochondrial 37S riboso
MRP2	113.428802	107.649994	229.58757	233.61824	mitochondrial 37S riboso
MRP20	85.831482	88.865448	174.563126	162.141953	mitochondrial 54S riboso
MRP7	38.676716	44.483498	94.061867	94.804153	mitochondrial 54S riboso
MRP8	41.85099	50.68943	41.508469	48.590553	Mrp8p
MRPL10	60.127502	54.47393	122.03215	90.733902	mitochondrial 54S riboso
MRPL19	82.368156	67.419487	199.621033	142.058853	mitochondrial 54S riboso
MRPL27	96.124619	114.845306	213.718765	191.569321	mitochondrial 54S riboso
MRPL3	63.454102	69.927559	99.935837	93.190186	mitochondrial 54S riboso
MRPL33	72.094681	89.037697	231.929733	217.900558	mitochondrial 54S riboso
MRPL36	109.193893	129.653946	150.00676	154.091965	mitochondrial 54S riboso
MRPL37	77.165604	73.988258	156.536224	140.232895	mitochondrial 54S riboso
MRPL40	111.71431	118.982323	147.678116	141.909286	mitochondrial 54S riboso
MRPL6	33.867085	29.645466	90.686295	84.171097	mitochondrial 54S riboso
MRPL8	63.601711	74.084526	146.2668	116.691628	mitochondrial 54S riboso

MRPS9	98.145508	104.17173	165.567749	159.022934	mitochondrial 37S riboso
MRR1	10.085464	8.229892	19.823652	21.624189	multidrug resistance regu
MRR2	15.248505	15.305564	17.397646	26.633696	hypothetical protein MG5
MRS2	9.668989	8.16106	16.89389	21.448418	Mrs2p
MRS4	35.234604	33.998409	54.638084	44.338108	Fe(2+) transporter
MRS7	80.161964	78.578667	91.825829	96.234406	Mrs7p
MRT4	123.782616	164.302231	93.918152	89.507721	Mrt4p
MRV1	3.799793	4.683715	1.20875	0.849171	Mrv1p
MRV2	2069.327881	2107.650391	286.342743	276.444	Mrv2p
MRV3	6.378691	8.740864	2.223669	3.482949	Mrv3p
MRV4	30.127676	29.864967	1.314261	1.609156	Mrv4p
MRV5	4.661427	3.373898	0	1.778347	Mrv5p
MRV6	7.791046	6.68728	1.865341	0.817846	Mrv6p
MRV8	5.9743	8.43959	0.609426	1.759873	Mrv8p
MSB1	15.110312	13.015882	19.301172	29.124077	hypothetical protein MEY
MSB2	63.182392	78.27758	45.282963	52.78664	Msb2p
MSC7	16.432512	20.938074	36.459694	33.84071	meiotic recombination di
MSF1	34.447933	37.221077	87.41687	70.585175	phenylalanine--tRNA liga
MSH2	26.304724	26.821424	42.845711	45.090488	mismatch repair ATPase
MSH3	2.342846	5.12736	7.003888	7.113638	mismatch repair protein
MSH6	8.623877	7.843123	29.386169	31.037104	mismatch repair ATPase
MSI3	196.187698	225.94928	198.236481	208.815964	adenyl-nucleotide excha
MSK1	10.672145	13.336205	30.618874	29.221256	lysine--tRNA ligase
MSM1	9.052876	9.340593	35.128292	27.260109	methionine--tRNA ligase
MSN4	32.113777	33.218994	45.299294	53.620304	stress-responsive transc
MSN5	136.643539	134.639023	133.35672	123.097061	exportin-5
MSO1	113.874802	86.612068	218.671112	178.646744	hypothetical protein MEC
MSS11	148.514435	155.225006	43.980713	56.550446	Mss11p
MSS116	77.522934	80.924965	79.278397	75.352966	ATP-dependent RNA he
MSS4	103.178894	105.204582	37.648994	39.838947	1-phosphatidylinositol-4-
MSS51	50.691452	61.115986	106.620728	99.990044	Mss51p
MST1	20.197058	21.394321	37.912888	36.073288	threonine--tRNA ligase
MSTRG.3310	89.972366	75.547348	109.612083	86.063553	hypothetical protein I503
MSTRG.4391	2.044416	3.985213	1.552459	2.271198	hypothetical protein Can
MSTRG.5096	51.909168	48.786163	125.185547	101.153259	hypothetical protein MG1
MSTRG.5652	10.311909	9.620947	9.087302	7.307375	OPT family small oligope
MSU1	5.538138	3.900294	8.571052	9.950147	Msu1p
MSW1	15.239813	14.307684	39.208206	39.245892	tryptophan--tRNA ligase
MTG1	29.867041	25.377546	20.962143	15.854071	putative GTPase
MTG2	10.818455	11.499966	16.219271	18.267309	putative GTPase
MTLA1	36.143505	41.670441	39.126583	46.761116	mating-type-like protein
MTLA2	10.403666	15.869492	16.686792	14.697192	Mtla2p
MTM1	19.313015	26.122463	28.44202	20.017424	Mtm1p
MTO1	7.904436	7.376426	9.90527	12.220967	tRNA modification protei
MTR10	11.488277	12.290832	17.473658	16.54524	Mtr10p
MTR2	60.248116	61.867264	51.731304	53.410755	RecName: Full=mRNA t
MTS1	96.536102	109.236153	127.804718	134.455765	Mts1p
MTW1	15.169747	13.190676	41.945129	41.82877	MIND complex subunit
MUB1	14.146603	14.048696	30.523151	28.416721	Mub1p
MUC1	39.792759	40.575558	45.780941	50.530064	Muc1p
MUM2	58.56583	69.456528	48.663185	39.865894	Mum2p
MUP1	811.038147	794.399292	318.781036	303.659943	Mup1p
MUQ1	66.816811	77.860619	91.854103	81.916023	ethanolamine-phosphate
MVB12	24.496067	25.592463	48.701977	54.996029	Mvb12p
MVD	151.584335	144.932755	247.141876	237.550659	diphosphomevalonate de
MXR1	70.214912	77.037094	177.467728	187.20842	peptide-methionine-S-su
MYO1	3.929591	2.814972	13.646567	14.796996	myosin 1
MYO2	20.944166	23.015076	59.135056	59.402889	myosin 2
MYO5	37.958248	36.347565	42.392506	49.193562	myosin-5
NAB3	113.999817	105.277855	74.528442	89.032417	nuclear polyadenylated
NAG1	261.206726	210.125198	182.084534	132.015076	Nag1p
NAG3	30.868214	26.675991	32.591145	28.511938	Nag3p
NAG4	10.992002	7.796593	9.666709	7.781695	Nag4p
NAG6	118.123795	114.755051	69.802261	57.801605	dynamin-like GTPase

NAM2	11.452862	10.553113	40.187546	38.323204	leucine--tRNA ligase
NAM7	57.226864	57.033527	52.269394	54.981789	ATP-dependent RNA he
NAN1	83.997528	86.319916	33.115211	34.360664	Nan1p
NAP1	278.024567	289.308899	230.333176	219.87825	conserved hypothetical p
NAR1	33.490826	36.256542	25.315639	22.871618	Nar1p
NAT2	183.832825	199.957214	414.400696	269.91333	Nat2p
NAT4	14.362192	8.220958	6.118151	7.943781	Nat4p
NAT5	49.221836	63.846409	92.691147	66.948677	peptide alpha-N-acetyltra
NBN1	22.15937	28.971619	31.055817	55.251686	histone acetyltransferase
NBP2	37.41011	30.105915	40.370682	43.948715	Nbp2p
NCB2	39.655308	47.690071	109.986588	109.521584	negative cofactor 2 trans
NCE102	2904.4021	2983.762695	1004.568237	980.201233	Nce102p
NCE103	69.72673	63.310081	77.599655	49.579052	carbonic anhydrase, part
NCE4	10.52065	7.210688	28.616232	21.803699	Nce4p
NCP1	43.926636	53.024956	73.461182	78.226097	Ncp1p
NCR1	22.220139	22.060137	28.386169	29.238474	sphingolipid transporter
NCS2	77.442238	82.473343	38.3634	32.123169	Ncs2p
NDE1	106.668419	129.514023	48.585785	53.458618	NADH-ubiquinone reduc
NDH51	218.353622	235.491592	263.28479	237.469162	Ndh51p
NDT80	390.277008	340.304932	271.310333	289.099121	predicted protein
NEP1	68.273499	68.106621	36.652451	38.132023	18S rRNA pseudouridine
NGG1	11.582156	18.446472	32.064476	34.519718	transcriptional adapter 3
NGS1	8.624771	9.632167	30.775063	23.317848	Ngs1p
NGT1	80.892418	69.694351	34.220947	38.27449	Ngt1p
NHP2	236.883804	256.243805	181.729248	179.123917	snoRNA-binding protein
NHP6A	1419.9104	1623.207886	6887.814941	4930.950684	high-mobility group nucle
NHX1	28.63493	28.848778	32.746265	39.795185	bifunctional K:H/Na:H an
NIF3	39.279114	31.422031	63.104111	67.218414	Nif3p
NIK1	37.75629	42.694073	57.35265	52.220539	Nik1p
NIP1	75.776161	79.750992	69.09893	73.277046	translation initiation facto
NIP100	9.837428	10.063719	22.319492	25.078737	Nip100p
NIP7	129.840591	123.865677	45.110607	54.437191	ribosome biosynthesis pr
NIT2	12.153938	23.762159	27.278931	19.692678	putative hydrolase
NIT3	46.095417	50.273247	67.189171	62.727104	putative hydrolase
NMA111	23.194996	27.654089	22.846802	19.798965	Nma111p
NMD3	101.670235	117.123756	46.351204	45.785297	ribosome-binding protein
NMD5	17.385717	18.191328	13.578717	16.438601	Nmd5p
NMT1	28.095499	28.125711	42.922871	44.841312	glycylpeptide N-tetradeca
NOC2	59.62788	61.872429	33.321175	32.031296	nucleolar complex protei
NOC4	58.060204	64.813316	30.767414	31.343386	ribosome biosynthesis pr
NOG1	137.402588	136.730896	55.131313	61.244995	putative GTPase
NOG2	172.181244	167.209305	54.033104	68.078918	putative GTPase
NOP1	411.503204	425.043732	281.567932	255.935135	rRNA methyltransferase
NOP10	246.206894	226.637787	218.529861	169.084579	snoRNP complex protein
NOP13	80.885101	86.167572	27.573906	29.382643	Nop13p
NOP14	116.449333	107.493988	23.544445	24.174017	snoRNA-binding rRNA-p
NOP15	90.456078	95.157539	42.389175	46.653458	rRNA-binding ribosome b
NOP4	76.511925	74.290703	39.873558	36.584297	nucleolar protein 4
NOP5	296.431427	320.033447	175.815521	145.969055	RNA-processing protein
NOP6	102.439804	78.449471	48.345154	40.578182	nucleolar protein 6
NOP8	20.70528	16.719027	13.063016	11.02222	Nop8p
NOT3	19.074932	20.410568	19.522589	26.003197	CCR4-NOT core subunit
NOT4	40.527199	36.357357	55.765675	57.189758	CCR4-NOT transcription
NOT5	62.923782	64.141647	70.711578	63.051659	CCR4-NOT transcription
NPL3	410.942017	406.508575	622.564636	527.934082	mRNA-binding protein
NPL4	11.924497	12.588271	24.874643	28.169844	Npl4p
NPL6	34.879387	50.22644	88.598427	81.75383	Npl6p
NPR1	12.730496	13.482726	13.76394	12.23139	serine/threonine protein
NPR2	7.790686	5.877288	14.690064	13.637127	nitrogen permease regul
NPT1	27.012701	25.159689	44.198944	40.329922	nicotinate phosphoribosy
NRG1	791.871887	603.631348	658.348022	654.429443	Nrg1p
NRG2	0	0.149031	0	0	Nrg2p, partial
NRM1	11.149397	12.911394	38.84745	34.831516	Nrm1p
NRP1	11.102563	13.442807	17.216896	21.671545	hypothetical protein MG5

NSA1	68.133148	69.516266	25.622589	20.697222	ribosome biosynthesis p
NSA2	129.991974	134.192886	46.655632	0	rRNA-processing protein
NSP1	88.463646	97.166443	116.009552	112.562057	FG-nucleoporin
NTF2	405.199036	402.193085	635.187012	687.013611	nuclear transport factor
NTG1	41.282192	44.621796	34.188515	25.867155	bifunctional N-glycosylas
NTH1	23.098753	26.342833	8.138916	12.020802	alpha,alpha-trehalase N
NUC2	148.769302	149.629807	153.028595	149.761353	Nuc2p
NUF2	11.292845	14.921882	77.932709	80.301445	RecName: Full=Probabl
NUO1	163.676971	159.71022	167.550491	164.528656	Nuo1p
NUO2	220.975754	225.060181	352.308594	312.352051	Nuo2p
NUP	2.138492	0.505808	5.525263	5.695627	Nupp
NUP159	25.475344	25.818172	38.565166	34.446548	FG-nucleoporin
NUP188	15.030046	16.389742	26.45643	28.684992	Nup188p
NUP49	37.022076	40.869205	52.704903	50.888767	nucleoporin p58/p45
NUP60	39.597759	39.670982	29.747602	38.474659	FG-nucleoporin
NUP82	23.117971	22.400331	39.933651	40.689148	linker nucleoporin
NUP84	25.212429	23.015354	38.578461	39.599644	Nup84p
NUP85	18.695288	19.422926	47.817177	43.980469	Nup85p
OAC1	9.939453	9.151759	5.287976	1.969626	Oac1p
OBPA	124.210228	129.795776	213.088623	173.948792	oxysterol-binding protein
OCA1	17.252939	19.099503	43.478382	40.479527	putative tyrosine protein
OCA6	23.410927	16.903404	51.652046	33.611366	protein-tyrosine-phospha
OCH1	51.275532	60.10688	28.414513	28.75728	Och1p
OFD1	54.741531	69.753555	102.421265	96.625427	oxidative DNA demethyl
OFI1	35.022816	34.268452	16.115429	18.456793	hypothetical protein MGI
OFR1	200.244034	210.975052	298.958527	268.78302	Ofr1p
OGG1	4.114123	12.332111	16.4928	15.361888	8-oxoguanine glycosylas
OLE1	3283.608887	3734.84668	3085.688232	2575.04126	stearoyl-CoA 9-desatura
OLE2	80.475121	86.934387	29.992752	33.350735	Ole2p
OP4	180.635208	233.898117	44.675606	50.943634	Op4p
OPI1	26.169903	27.049294	47.035599	54.142517	transcriptional regulator
OPI3	74.952324	76.456993	260.533539	256.522949	bifunctional phosphatidyl
OPT1	15.445958	17.9923	12.828914	9.673776	oligopeptide transporter
OPT2	7.803751	7.439576	4.158724	3.384951	Opt2p
OPT3	23.173435	22.517712	4.935452	7.614191	Opt3p
OPT4	24.24543	33.172916	15.869777	8.536985	OPT family small oligope
OPT5	0.178651	0.394784	0.188907	0.563404	Opt5p
OPT6	12.005348	10.745474	5.952335	7.286732	Opt6p
OPT7	3.533467	4.231987	5.112936	5.152308	Opt7p
OPT8	5.654822	5.857328	11.971789	12.453506	Opt8p
OPY2	132.367599	139.599945	69.206978	68.763756	hypothetical protein MG
ORC1	20.38316	18.197311	35.84758	29.687037	origin recognition compl
ORC3	11.843008	15.340887	19.887314	21.498894	origin recognition compl
ORC4	21.665754	18.566532	28.970217	32.124176	origin recognition compl
ORM1	87.534088	95.665207	124.345375	128.941788	uncharacterized endopla
OSH3	24.789415	24.184052	38.377636	43.245785	oxysterol-binding protein
OSM1	427.685699	456.612976	358.648407	313.173553	Osm1p
OSM2	81.308266	83.814674	155.154816	141.550247	fumarate reductase
OST1	39.189014	49.231346	68.060028	56.590942	dolichyl-diphosphooligos
OXR1	17.045876	12.090291	35.801819	31.082275	Oxr1p
OYE2	57.849766	76.043083	43.331669	39.867214	NADPH dehydrogenase
OYE22	17.848534	16.612282	23.487913	17.596619	Oye22p
OYE23	3.709839	3.420104	0	0.183427	Oye23p
OYE32	17.392689	21.546951	26.09716	18.635046	Oye32p
PAD1	6.350442	9.780789	6.730528	6.073539	phenylacrylic acid decar
PAM16	247.334763	254.79837	290.202362	290.25174	mitochondrial import inne
PAM17	76.424484	82.977425	138.365936	128.567291	Pam17p
PAM18	76.764687	103.479401	116.458603	73.428558	Pam18p
PAN1	48.382004	50.303314	53.23037	50.274303	Pan1p
PAN3	10.410589	10.077131	21.964577	24.393291	Pan3p
PAN6	51.847164	72.974655	53.728394	38.785912	pantoate--beta-alanine l
PAP1	21.947941	22.107576	38.850876	35.801109	Poly(A) polymerase PAP
PBP2	72.864113	97.306862	128.508865	140.940781	Pbp2p
PBR1	4.069854	3.930952	2.899489	5.506388	Pbr1p

PBS2	72.4692	78.939079	45.238064	52.07016	hypothetical protein L15
PCD1	141.300644	181.033722	40.899605	34.694916	8-oxo-dGTP diphosphat
PCK1	3322.90332	3410.298584	2430.62915	2588.452881	phosphoenolpyruvate ca
PCL1	47.676899	42.11998	34.121422	38.739571	Pcl1p
PCL2	7.327341	10.90061	49.736752	45.372997	cyclin
PCL5	127.934326	163.869171	96.949165	117.381462	Pcl5p
PCL7	20.350578	22.203949	29.651199	30.756132	Pcl7p
PCT1	40.942513	41.750599	57.151005	65.021072	choline-phosphate cytidy
PDA1	418.058868	441.363708	683.400635	590.154358	pyruvate dehydrogenase
PDB1	216.819717	210.947784	423.072571	330.771301	pyruvate dehydrogenase
PDC11	1069.389771	1372.883667	395.748291	431.345184	indolepyruvate decarbox
PDC12	6.101714	5.970376	11.842121	14.24461	Pdc12p
PDC2	10.062283	11.177643	12.242892	11.772282	Pdc2p
PDE1	31.747274	34.480228	16.572319	15.752294	3'\5'-cyclic-
PDE2	120.188812	142.024246	41.511314	38.677509	3',5'-cyclic-
PDI1	147.495819	134.729477	155.913269	190.328339	protein disulfide isomera
PDK2	68.734894	56.518723	82.006737	89.419006	protein kinase
PDR16	34.01696	42.870552	42.225571	47.873898	phosphatidylinositol trans
PDR17	3.389198	2.769188	2.218691	4.900251	Pdr17p
PDR6	20.865139	18.725155	27.064121	25.430504	Pdr6p
PDS5	6.076087	7.259771	27.771864	29.354942	Pds5p
PDX1	137.296249	149.008377	145.239716	162.458862	Pdx1p
PDX3	1356.279907	1509.668701	187.651718	170.713364	pyridoxamine-phosphate
PEA2	28.173653	29.610296	27.45442	34.255116	hypothetical protein MG
PEL1	39.906914	43.825138	11.162636	11.854304	CDP-diacylglycerol--glyc
PEP1	44.145466	44.743801	35.783894	41.683895	hypothetical protein ME
PEP12	39.849354	32.828407	60.158928	63.723949	syntaxin 7
PEP3	22.203442	20.562056	35.550289	34.567699	tethering complex subun
PEP7	15.258959	20.000206	25.140308	26.124144	Pep7p
PEP8	60.810097	76.06192	100.011604	74.902313	retromer subunit
PES1	118.952179	128.287277	61.15744	55.582497	mRNA-binding ribosome
PET100	110.366325	127.690178	356.932861	357.372375	Pet100p
PET127	32.250748	29.638088	25.543053	22.430395	Pet127p
PET9	3173.06958	3338.608398	1936.80835	1681.511963	ADP/ATP carrier protein
PEX1	7.65083	7.144794	11.607466	11.726318	AAA family ATPase perc
PEX11	111.145851	137.04158	83.961517	84.941963	hypothetical protein ME
PEX12	48.72295	63.407997	30.459932	39.449116	ubiquitin-protein ligase p
PEX13	139.937347	155.545456	110.931	106.386444	peroxin-13
PEX14	32.686245	39.403522	63.947983	63.65765	Pex14p
PEX17	21.250578	27.387381	40.304447	50.215187	Pex17p
PEX19	67.329803	74.305519	100.566933	91.509689	Pex19p
PEX2	24.346754	29.506947	37.83049	32.357727	ubiquitin-protein ligase p
PEX22	15.493384	18.846285	11.214486	17.498486	Pex22p
PEX3	16.373159	20.193842	27.938931	27.738892	Pex3p
PEX4	51.332756	65.639557	31.811531	34.675575	E2 ubiquitin-protein ligas
PEX5	83.697212	88.454369	58.830086	52.848351	Pex5p
PEX6	5.074285	3.766485	8.452735	10.158182	peroxin-6
PEX7	7.15473	7.146029	20.004427	29.001612	Pex7p
PEX8	6.766781	6.296161	10.732949	11.894371	Pex8p
PFK1	111.876785	119.923004	49.668804	53.468094	6-phosphofructokinase s
PFK2	89.672897	86.019691	70.091362	61.620647	6-phosphofructokinase s
PFK26	66.357307	72.342514	23.133875	26.292231	Pfk26p
PFY1	227.975693	209.468323	300.367645	215.95639	profilin
PGA1	135.126221	123.932396	317.732819	251.839752	Pga1p
PGA10	7.377148	9.869819	16.457794	16.510809	Pga10p
PGA11	23.470474	24.533899	8.477494	10.647521	Pga11p
PGA12	1.647985	0.602161	0	0.843906	Pga12p
PGA13	31.729557	43.926731	2.256457	3.435848	hypothetical protein MG
PGA14	1413.792236	1313.47644	2161.298096	2031.130615	Pga14p
PGA15	11.19679	14.374464	11.394481	12.973087	Pga15p
PGA16	2.054291	0	0	0.829498	Pga16p
PGA17	22.642893	21.501377	9.904535	10.423802	Pga17p
PGA18	19.531687	16.362591	24.633173	29.89971	hypothetical protein MG
PGA19	4.41145	1.893893	2.461137	1.334578	hypothetical protein MEY

PGA22	5.291175	4.485044	1.081998	1.14178	hypothetical protein MG1
PGA23	181.585098	142.466782	87.302086	87.43251	hypothetical protein MG
PGA25	23.700729	24.333979	18.531881	20.282442	Pga25p
PGA26	2261.253418	1425.916382	4015.447998	4502.098633	Pga26p
PGA27	2.443938	2.510148	8.637969	11.26289	Pga27p
PGA28	75.318138	75.344711	83.558342	92.807297	hypothetical protein ME
PGA30	5390.413574	4113.984863	83.666878	102.876823	Pga30p
PGA31	107.263878	96.216736	44.646446	84.992149	Cell wall protein
PGA32	15.325945	10.363517	20.311409	21.268156	Pga32p
PGA33	45.395924	40.094456	44.98151	54.885139	Pga33p
PGA34	1074.800781	841.676086	1101.228027	1222.696533	putative GPI-anchored p
PGA37	24.835129	27.015142	70.979904	49.582726	Pga37p
PGA38	390.765533	302.609222	1986.710083	2794.188232	Pga38p
PGA39	31.744179	32.643673	24.291201	25.189091	hypothetical protein MG
PGA4	378.388428	399.879547	766.299561	714.877502	1\3-beta-glucanosyltrans
PGA41	10.516693	11.09699	4.776474	6.319154	hypothetical protein MG
PGA42	4.643044	3.332481	2.013311	3.368759	Pga42p
PGA43	9.873131	13.113264	11.748197	9.429471	Pga43p
PGA44	4.941397	4.191149	1.84579	3.227679	Pga44p
PGA45	15.900438	23.736782	16.847029	19.38138	Pga45p
PGA46	0.643233	1.186024	1.227997	1.684227	putative GPI-anchored p
PGA48	1613.39917	1304.523682	2038.7677	2320.970459	Pga48p
PGA49	8.66309	8.647501	13.225461	11.410938	Pga49p
PGA5	1.257097	1.065768	9.093526	7.423841	hypothetical protein I503
PGA50	0.866598	0.772082	0.307179	0.311389	Pga50p
PGA52	403.96817	387.543762	517.479675	532.21814	protein precursor, partial
PGA53	1168.211182	1013.3797	375.695251	394.939087	hypothetical protein ME
PGA54	75.392731	90.697571	226.082687	258.989471	hypothetical protein MG1
PGA55	9.452868	10.893128	12.185492	10.590449	hypothetical protein MGI
PGA56	28454.5293	26630.88867	13296.65137	12071.53027	--
PGA57	9.352458	8.22745	13.96865	12.899262	hypothetical protein ME
PGA58	13.120811	12.081301	22.253685	26.571165	hypothetical protein MGI
PGA59	19695.18164	16532.20117	23240.70898	21162.83203	hypothetical protein ME
PGA6	61.446678	53.846687	234.86322	237.195694	Pga6p
PGA60	165.610886	118.660316	0.274222	1.185371	Pga60p
PGA61	3.470369	4.796439	0.64312	0.367384	Pga61p
PGA62	3871.120117	3863.942627	791.6026	1041.768799	Pga62p
PGA63	36.469433	31.938486	39.709999	49.197498	Pga63p
PGA7	115.24324	106.591881	441.784027	362.585907	Pga7p
PGI1	335.27478	362.663452	273.825745	268.87915	glucose-6-phosphate iso
PGK1	1068.127075	1094.148926	491.720001	474.753235	phosphoglycerate kinase
PGM2	105.56884	122.659187	70.544518	71.561958	phosphoglucomutase
PHA2	6.818021	5.965991	5.051378	8.782727	prephenate dehydratase
PHB1	65.852417	74.243904	130.246292	119.726547	Phb1p
PHB2	125.570435	128.627655	250.961044	219.37291	prohibitin subunit
PHHB	110.06459	113.944901	103.112984	75.361404	4a-hydroxytetrahydrobio
PHM5	25.09008	25.847261	30.221401	25.880661	endopolyphosphatase
PHM7	107.354065	117.336456	29.407095	30.721418	Phm7p
PHO100	53.645901	66.393776	2.562252	4.447569	Pho100p
PHO112	26.241032	29.561558	2.296336	3.05068	Pho112p
PHO113	38.058758	47.508083	4.711078	4.914494	acid phosphatase
PHO114	72.780052	72.861816	16.014252	18.280964	Pho114p
PHO13	7.731434	16.796513	17.668016	14.033777	Pho13p
PHO15	26.810959	30.868431	47.629776	41.467808	4-nitrophenylphosphatas
PHO23	19.078529	17.934879	36.206352	36.262684	Pho23p
PHO4	92.903236	81.352928	84.388847	85.202293	phosphate-sensing trans
PHO8	194.876862	218.852173	5.750637	8.645592	Pho8p
PHO81	10.162789	8.422825	7.730747	7.689974	Pho81p
PHO84	820.600403	882.030212	170.282211	163.153839	phosphate transporter
PHO85	87.659889	101.5336	91.604347	102.532478	hypothetical protein ME
PHO86	78.936836	72.809387	33.782555	40.50729	Pho86p
PHO87	17.753666	17.660206	23.249659	22.041813	SPX domain-containing
PHO88	131.311279	119.080482	128.505844	159.556686	Pho88p
PHO89	3090.89917	2842.262207	245.422852	239.837311	Pho89p

PHO91	55.693634	58.805458	48.406696	47.978901	Pho91p
PHR1	736.242737	726.923401	1533.747437	1663.195312	pH-responsive protein 1
PHR2	162.143784	140.475906	85.090492	104.569046	protein EPD1 precursor
PHR3	76.306129	67.414665	28.213488	30.592802	hypothetical protein MG1
PIF1	19.478813	20.657373	26.389111	28.767036	DNA helicase
PIKA	18.671869	18.784149	24.123762	24.694468	1-phosphatidylinositol 4-
PIL1	989.083496	1082.532104	1028.751099	1056.032349	lipid-binding protein
PIM1	19.732471	17.529737	57.506451	58.966675	ATP-dependent protease
PIN3	526.406799	569.02887	520.69281	500.848053	Pin3p
PIN4	17.574791	15.982921	28.152433	36.929848	Pin4p
PIR1	722.738708	673.51001	834.246155	1167.741821	beta-1,3-glucan linked p
PIR32	1.454295	0.490594	3.205539	1.435718	Pir32p
PKC1	29.017004	29.613995	73.528572	84.094009	protein kinase C
PKH2	17.14855	13.995176	23.222525	25.127064	serine/threonine protein
PKH3	12.783646	12.595973	25.695652	27.062336	protein-serine/threonine
PLB1	6.7481	10.080764	0.99386	0	Plb1p
PLB2	4.093123	6.240957	4.771939	5.290449	Plb2p
PLB3	616.609741	713.470581	665.059326	644.286377	lysophospholipase
PLB4.5	14.098585	13.690663	69.284973	71.348999	Plb4.5p
PLB5	7.369109	7.065632	13.144079	14.975584	lysophospholipase 3
PLC1	6.08909	6.736954	4.516321	6.196875	phosphatidylinositol phos
PLC2	105.207542	129.149094	76.376572	93.557304	phosphatidylinositol phos
PLD1	19.55365	17.115335	23.946297	20.256346	phospholipase D
PMA1	180.091858	209.661804	235.166046	231.786606	H(+)-exporting P2-type A
PMC1	419.011078	468.953857	180.505615	199.929092	calcium-transporting ATP
PMI1	35.06958	39.131645	84.261711	103.909538	mannose-6-phosphate is
PMM1	47.771702	62.069736	83.226044	87.306175	phosphomannomutase
PMR1	22.863916	22.272835	38.46524	33.646801	calcium-transporting P-ty
PMS1	2.033177	2.372924	14.623693	14.173618	ATP-binding mismatch r
PMT1	73.025421	63.11174	116.014297	126.394005	dolichyl-phosphate-mann
PMT2	63.09745	58.278717	103.849915	105.060204	dolichyl-phosphate-mann
PMT4	39.285004	36.139565	47.702007	46.099628	dolichyl-phosphate-mann
PMT5	9.951201	9.176616	16.115278	24.384674	putative dolichyl-phospha
PMT6	11.751702	13.357237	21.267679	20.740126	dolichyl-phosphate-mann
PNC1	31.053349	32.445385	47.124321	37.158245	nicotinamidase
PNG2	471.057526	498.678711	168.169525	186.415543	Png2p
PNP1	67.477852	60.458462	96.493713	72.339233	purine-nucleoside phosp
POB3	69.361717	78.689911	120.282303	112.871635	FACT complex subunit
POL1	9.389807	12.96942	40.735519	33.579758	DNA polymerase (pol2)
POL2	3.132348	4.236109	12.038751	13.671551	DNA polymerase epsilon
POL3	19.28669	21.459974	40.114902	43.292782	DNA-directed DNA polym
POL30	42.383781	44.193222	249.95079	251.60289	proliferating cell nuclear
POL32	9.934934	9.825299	28.664494	29.352272	DNA polymerase delta s
POL5	7.423464	7.808222	15.172603	18.019562	DNA-directed DNA polym
POL93	350.587036	302.321442	194.631454	204.494644	Pol93p
POM152	7.806148	8.607791	20.08029	18.440435	Pom152p
POP2	55.579525	60.082798	52.603306	51.807987	CCR4-NOT core DEDD
POP3	49.355881	42.854462	25.97752	23.399807	Pop3p
POP4	17.742279	11.937674	21.498363	24.388083	RNase P/RNase MRP co
POR1	1738.757568	1614.498657	909.761047	858.78418	porin
POS5	13.200424	14.702142	24.363058	20.683205	NADH kinase
POT1	115.822075	110.632957	61.495575	60.96085	acetyl-CoA C-acyltransfe
POT1-2	16.905251	16.665194	22.075258	15.657163	Pot1-2p
POX1	13.582964	14.85075	21.998976	27.985115	Pox1p
POX1-3	315.391693	272.942596	95.897629	106.37278	acyl-CoA oxidase
POX18	7.030649	8.743712	7.790104	6.036092	Pox18p
PPE1	12.025446	9.416164	17.987904	17.422194	carboxylesterase-mitoch
PPG1	21.014507	18.204063	36.581207	35.035454	putative serine/threonine
PPH21	49.613403	43.093597	52.945786	50.772812	phosphoprotein phospha
PPH3	7.904796	9.951579	27.364782	28.99217	phosphoprotein phospha
PPR1	2.937956	4.260646	4.299163	5.014901	Ppr1p
PPS1	4.930191	5.158634	6.360575	6.962698	hypothetical protein MEK
PPT1	34.942833	37.710854	10.621717	12.699207	protein serine/threonine
PPT2	23.796694	29.221045	26.628017	23.088369	holo-

PPZ1	23.049597	25.078262	54.726204	60.332085	hypothetical protein L150
PR26	67.200783	76.116219	117.129265	108.216682	proteasome regulatory p
PRA1	2993.272461	2686.117432	33.794132	38.420055	Pra1p
PRB1	293.168243	318.256683	478.794434	391.282684	cerevisin
PRC2	46.040245	45.629871	16.357754	16.117407	Prc2p
PRC3	66.769234	59.389637	29.176756	30.675512	carboxypeptidase C
PRD1	46.874279	54.567432	115.517609	105.932404	metalloendopeptidase
PRE1	110.944565	151.167206	205.571671	187.750244	proteasome core particle
PRE10	57.446735	62.033337	132.071426	102.698746	proteasome core particle
PRE2	101.120331	116.661354	158.26207	177.210922	proteasome core particle
PRE3	108.662056	107.607521	189.780579	200.700043	proteasome core particle
PRE5	160.611572	191.610092	200.693054	181.531372	proteasome core particle
PRE6	109.509911	130.770798	201.000412	192.60997	proteasome core particle
PRE8	79.353699	79.547646	143.464539	140.098434	proteasome core particle
PRE9	75.698654	75.221001	73.487633	70.675468	proteasome core particle
PRI2	4.778701	5.656275	22.635611	23.276667	DNA primase large subu
PRK1	36.355782	34.105022	41.716949	46.921032	serine/threonine protein
PRM1	2.020174	0.691164	0.942367	0.840257	pheromone-regulated pr
PRM9	1.4067	2.615363	4.90272	6.002059	Prm9p
PRN1	26.0473	27.402679	34.62685	22.591148	hypothetical protein MEC
PRN2	9.927028	8.626035	7.85381	6.175323	Prn2p
PRN3	11.986512	17.982281	4.343244	4.3919	Prn3p
PRN4	56.341187	61.575989	4.957564	6.759941	Prn4p
PRO1	42.73579	41.74831	55.326389	47.787792	glutamate 5-kinase
PRO2	27.937244	28.374311	45.477783	38.815403	glutamate-5-semialdehy
PRO3	95.253075	78.930496	68.595901	54.976879	pyrroline-5-carboxylate r
PRP13	17.452662	19.497208	28.547621	24.317236	Prp13p
PRP22	8.220165	6.04553	10.4912	11.766879	DEAH-box ATP-depende
PRP3	7.769085	12.113591	18.10499	16.176191	U4/U6-U5 snRNP compl
PRP39	6.578317	10.101645	6.874746	5.018251	Prp39p
PRP42	11.737051	11.099471	20.084942	21.234907	mRNA splicing protein
PRP45	12.826474	10.589625	13.8475	20.180588	mRNA splicing protein
PRP5	25.410231	32.9548	23.601475	21.306702	DEAD-box RNA helicase
PRP8	12.946861	12.417591	19.706142	20.822134	U4/U6-U5 snRNP compl
PRR2	76.250008	80.187439	30.430359	38.519886	Prr2p
PRS	11.975589	11.702184	32.290726	35.897511	putative proline--tRNA li
PRS1	163.623398	201.362991	120.268318	86.737671	ribose phosphate diphos
PRS5	213.422653	200.28067	131.131226	127.214279	ribose-phosphate pyroph
PRT1	121.889038	133.136215	89.145317	90.890305	translation initiation facto
PRX1	45.64064	51.544693	51.53368	50.418362	thioredoxin peroxidase
PRY1	3.345211	3.513452	1.130735	1.388083	hypothetical protein MG
PSA2	97.311554	92.82093	129.529327	129.067398	mannose-1-phosphate g
PSD1	75.939606	83.749741	141.776184	119.820869	phosphatidylserine deca
PSD2	9.497242	9.145902	13.291662	14.220946	phosphatidylserine deca
PSF1	4.48682	4.229815	20.656361	20.12187	DNA replication complex
PSF2	8.887284	10.38223	15.120828	22.306246	DNA replication protein
PSF3	9.89428	20.355795	91.699966	66.543686	DNA replication protein
PSO2	18.498955	15.864589	21.008951	19.375023	Pso2p
PSP1	156.103912	164.84375	51.185276	50.93322	Psp1p
PST1	116.344345	115.989517	20.07122	18.225313	Pst1p
PST2	10.456365	5.24005	16.297977	18.693796	Pst2p
PST3	300.195099	307.595337	406.76062	426.29837	flavodoxin-like fold family
PSY2	3.566313	3.925999	9.459726	12.434867	Psy2p
PTC1	38.167068	40.180672	52.363964	41.960579	protein phosphatase
PTC2	314.046204	343.828552	143.594727	153.3237	type 2C protein phospha
PTC4	31.960001	37.93222	48.999325	30.696909	type 2C protein phospha
PTC5	82.711372	82.743462	64.350662	60.733311	type 2C protein phospha
PTC6	17.570135	12.246527	12.698771	13.758865	type 2C protein phospha
PTC7	75.305687	88.14399	124.647148	116.167381	hypothetical protein MG
PTC8	189.744095	227.342941	139.51683	136.92128	Ptc8p
PTH1	26.347784	20.757046	41.039185	35.605309	putative phosphatidate c
PTH2	25.547501	18.046942	7.528497	8.057874	hypothetical protein MG
PTK2	98.509193	96.245651	17.91913	17.788269	serine /threonine protein
PTP1	60.27993	57.852222	45.99469	43.821972	protein-tyrosine phospha

PTP2	138.656937	141.570786	145.526703	154.380417	tyrosine protein phospha
PTP3	29.935141	31.047102	47.0439	52.921833	tyrosine protein phospha
PTR2	0.322779	0.27944	0	0.773481	RecName: Full=Peptide
PTR22	1470.296997	1464.022095	1179.771118	1042.227661	Ptr22p
PTR3	4.2673	5.494582	7.838427	9.088437	Ptr3p
PUF3	16.536749	18.410553	34.657337	37.448776	mRNA-binding protein
PUP1	195.820618	234.779648	277.501251	220.502441	proteasome core particle
PUP2	84.680458	116.000275	163.244064	162.208847	proteasome core particle
PUP3	95.712685	98.227478	178.031891	156.593262	proteasome core particle
PUS4	37.027206	39.24588	43.057388	40.652153	pseudouridine synthase
PUS7	20.225142	22.981611	22.881718	23.143305	pseudouridine synthase
PUT1	330.485657	354.969727	38.029499	45.188339	proline dehydrogenase
PUT2	151.103745	157.513031	67.395958	65.007523	1-pyrroline-5-carboxylate
PUT3	13.348128	12.442719	16.455324	17.083172	hypothetical protein MEN
PUT4	4.245592	4.032606	11.52845	10.533726	Put4p
PWP1	61.125072	78.287163	51.275826	50.031933	rRNA-processing protein
PWP2	38.997963	39.499897	16.886705	17.715599	snoRNA-binding rRNA-p
PXA1	64.108246	71.873466	39.8419	36.014202	ATP-binding cassette, su
PXA2	19.524439	20.641045	14.07618	16.358366	ATP-binding cassette lor
PXP2	114.624481	104.735855	9.799253	7.428847	Pxp2p
PYC2	49.466618	57.003941	41.862213	35.211025	pyruvate carboxylase 2
PZF1	24.439201	29.186741	21.310953	22.544014	Pzf1p
QCR2	303.963501	296.143829	345.812714	369.56308	ubiquinol--cytochrome-c
QCR7	375.073151	417.082977	625.418396	624.830322	ubiquinol--cytochrome-c
QCR8	626.985107	553.66925	728.401123	545.863098	ubiquinol--cytochrome-c
QCR9	417.365082	365.994751	527.642212	403.236206	hypothetical protein L15C
QDR1	75.226631	75.833664	9.310281	7.266679	multidrug transporter
QDR2	55.140266	64.289986	26.970432	23.651651	Qdr2p
QDR3	17.660275	16.152	3.669509	3.123098	Qdr3p
RAC1	70.582306	90.559166	200.607101	174.316269	Rho family GTPase
RAD1	13.171047	15.035776	23.556337	23.933969	ssDNA endodeoxyribonu
RAD10	6.1009	10.387105	19.157661	22.557785	Rad10p
RAD14	11.956008	10.38098	21.732136	24.640347	Rad14p
RAD16	6.488984	8.778425	10.698906	11.369911	DNA repair protein
RAD18	3.308352	10.270481	17.244192	14.378516	E3 ubiquitin-protein ligas
RAD2	5.942107	5.554269	10.648345	8.433777	ssDNA endodeoxyribonu
RAD23	89.38858	111.090187	168.886398	165.473923	UV excision repair protei
RAD3	30.814745	27.602198	44.676376	32.682411	TFIIH/NER complex ATP
RAD32	18.536699	20.369095	25.622982	30.433441	DNA polymerase eta sub
RAD50	5.783344	6.236392	13.689924	13.884588	MRX complex DNA-bind
RAD51	49.48177	49.288681	102.902199	97.334297	recombinase
RAD52	11.853745	12.032104	24.515423	31.910305	recombination protein ra
RAD53	6.262924	7.492923	17.0644	18.419661	serine/threonine/tyrosine
RAD54	7.226977	6.009621	18.786131	21.073584	DNA repair and recombi
RAD57	7.115977	7.37595	15.932881	15.459281	putative DNA-dependent
RAD59	18.945137	19.732121	38.917957	47.480751	Rad59p
RAD6	45.609951	43.207775	95.399399	113.26223	ubiquitin-conjugating enz
RAD7	9.951719	8.585073	17.328535	24.272202	DNA repair protein RAD7
RAD9	6.532172	4.588288	12.6974	14.709335	chromatin-binding protei
RAM1	4.583436	4.169815	7.858359	8.549846	protein farnesyltransfera
RAM2	29.619949	33.138454	43.266155	37.754402	bifunctional protein farne
RAP1	12.518139	16.289814	37.40313	29.071611	myb-like DNA-binding pr
RAS1	187.354004	196.524521	85.880936	97.871674	Ras family GTPase
RAS2	48.206921	48.694843	8.307526	10.797723	Ras2p
RAT1	34.569405	38.03017	34.460621	38.663864	ssRNA exonuclease
RAV2	15.703058	17.143192	27.083614	30.202356	Rav2p
RAX1	89.079536	76.654282	74.627647	95.848618	hypothetical protein MG3
RAX2	14.059991	14.800887	22.964119	23.492208	Rax2p
RBD1	48.536831	46.40057	39.904373	41.997955	Rbd1p
RBE1	536.524475	429.333374	2410.489502	2697.718994	hypothetical protein MGC
RBF1	43.940731	47.245113	72.081123	78.734673	transcription factor RBF1
RBK1	30.699028	28.421112	26.421291	26.353216	ribokinase
RBP1	409.869293	367.536407	641.730713	556.129395	peptidylprolyl isomerase
RBR1	1954.732178	1401.16687	225.35347	208.354645	--

RBR2	124.671432	91.35173	81.981514	80.613281	hypothetical protein MGE
RBR3	10.606075	11.509718	15.415771	12.666669	Rbr3p
RBT1	2.892485	3.795759	1.656528	3.081804	hypothetical protein MEU
RBT4	48.869156	39.618805	0.779886	0.751529	Rbt4p
RBT5	1616.297363	1771.634521	2989.664062	3053.63501	hypothetical protein MG1
RBT7	15.591939	18.501141	3.522702	5.860338	Rbt7p
RCA1	140.761749	141.079636	109.074387	78.744148	Rca1p
RCE1	29.180285	36.388958	28.451569	33.647018	CAAX prenyl protease
RCH1	72.495392	64.097618	21.2481	18.081343	Rch1p
RCK2	43.396793	46.475842	53.00309	64.147606	serine/threonine protein
RCL1	80.973595	77.545044	59.100121	42.983021	rRNA-processing endoril
RCN1	8.636258	8.413272	13.668364	21.077471	Rcn1p
RCT1	1180.471558	1156.085083	371.350739	290.222565	Rct1p
RCY1	6.535398	6.119972	10.732479	14.670141	Rcy1p
RDH54	7.302899	5.744039	16.857786	14.445188	DNA-dependent ATPase
RDI1	137.119858	121.23922	165.61496	158.051804	Rdi1p
REG1	227.242477	235.313004	217.643997	210.481888	protein phosphatase reg
REI1	96.635597	91.31488	33.240986	37.52462	pre-60S factor REI1
REP1	318.698761	239.576614	100.554314	107.627892	Rep1p
RER2	62.594318	57.884109	30.736158	24.170088	ditrans\polycis-polypreny
RET2	30.396137	31.416582	53.913227	54.759201	coatomer subunit delta
REV3	6.465679	6.234336	10.380734	11.947035	Rev3p
REX2	28.720463	37.292736	73.604179	84.813591	Rex2p
REX3	2.044609	1.61086	9.314537	9.033174	RNA exonuclease
RFA1	33.647064	41.355705	159.177002	137.243835	replication factor A subu
RFA2	44.659813	53.899044	187.660141	172.307159	replication factor A2
RFC1	29.213316	25.499281	51.771835	54.942711	replication factor C subu
RFC2	11.573093	15.944945	30.163177	28.863176	replication factor C subu
RFC3	16.665363	16.035046	42.538696	37.902161	replication factor C subu
RFC4	41.694752	44.614613	81.523109	66.196449	replication factor C subu
RFC5	30.937855	34.381371	57.889431	64.480873	replication factor C subu
RFG1	67.064041	70.895378	255.171249	287.059692	Rfg1p
RFX1	9.425807	10.224854	5.812829	11.842157	Rfx1p
RFX2	7.542873	8.207391	7.773689	9.747475	Rfx2p
RGA2	26.274216	24.901052	14.532148	10.918482	Rga2p
RGD1	13.370665	11.924341	30.29105	33.843334	hypothetical protein W5C
RGD3	39.82793	42.702263	38.665531	40.491615	Rgd3p
RGS2	100.535881	114.046333	52.224396	43.652584	GTPase-activating prote
RGT1	42.458336	39.246384	31.107599	41.774906	Rgt1p
RHB1	376.327606	491.255707	86.538658	97.577797	putative GTPase
RHD1	17.951889	28.351381	3.481094	3.699213	Rhd1p
RHD2	14.475252	12.377209	13.701838	16.459475	Rhd2p
RHD3	14921.40918	11483.40918	29393.62109	31298.90039	Rhd3p
RHO1	415.646423	435.976807	441.280548	507.960175	Rho family GTPase
RHO2	9.677921	9.768767	22.193697	9.32724	Rho family GTPase
RHO3	70.952736	79.362846	143.179337	108.087868	Rho family GTPase, puta
RHR2	195.570801	216.040085	59.115658	50.578758	glycerol-1-phosphatase
RIA1	57.618736	51.677086	28.91379	26.019133	GTPase
RIB1	88.128471	92.445938	88.208755	86.767487	GTP cyclohydrolase II
RIB3	573.02356	649.939392	404.63324	421.564636	3,4-dihydroxy-2-butanon
RIB4	99.381447	81.617088	162.035187	184.672043	lumazine synthase
RIB5	107.887985	104.841415	92.361298	71.467041	riboflavin synthase
RIC1	3.421518	3.845962	15.369226	12.119557	Ric1p
RIM1	270.291138	259.026123	733.234375	648.460449	Rim1p
RIM101	2051.008545	2115.622803	902.287903	944.991699	pH-response transcriptio
RIM11	30.57972	32.161324	15.374457	19.988659	hypothetical protein CAA
RIM13	12.967946	13.234739	30.384907	28.704666	Rim13p
RIM15	16.415022	14.945045	13.699944	18.177586	serine/threonine-protein
RIM2	43.731209	52.876442	61.907642	67.097359	Rim2p
RIM20	12.208139	13.33099	18.001915	15.879455	Rim20p
RIM21	18.888741	18.990137	19.31687	13.705833	Rim21p
RIM8	65.131516	73.299492	20.88357	25.773191	Rim8p
RIM9	85.217056	64.703331	10.038777	15.429306	Rim9p
RIO2	78.346222	87.01326	76.290161	63.4366	RIO kinase 2

RIP1	489.465637	576.546265	682.687683	612.889526	ubiquinol--cytochrome-c
RIT1	18.32234	15.337707	16.690351	9.13426	tRNA '-O-ribosylpl
RIX7	21.928686	25.624647	22.232609	19.679411	putative AAA family ATP
RKI1	42.064941	52.948372	36.370144	44.092693	ribose-5-phosphate isom
RLI1	166.494781	173.49437	126.062393	123.099571	Fe-S cluster-binding ribo
RLM1	15.160562	15.058621	10.164856	13.699512	Rlm1p
RLP24	192.982056	177.306931	92.667374	97.444847	ATPase-activating riboso
RME1	3.692983	2.93263	0.994935	0.900205	Rme1p
RMP1	8.973124	7.290429	6.241638	7.428547	Rmp1p
RMS1	69.691765	91.397209	23.413731	23.025307	SET domain-containing p
RMT2	29.502352	44.725082	21.569929	22.466366	guanidinoacetate N-meth
RNA1	50.817741	53.423958	102.333618	114.133873	GTPase-activating prote
RNH1	57.325039	54.999802	95.300095	81.967506	Rnh1p
RNH35	7.627726	6.437457	20.300188	23.276001	ribonuclease H2 catalytic
RNR1	56.828533	69.840202	413.447876	447.270477	ribonucleotide-diphospha
RNR21	200.67984	221.005432	1359.969482	1243.236084	ribonucleotide-diphospha
RNR22	69.039108	91.043404	215.976944	204.759583	Rnr22p
RNR3	34.44717	33.644547	39.045376	35.373455	Rnr3p
RNY11	20.908258	21.500479	5.55481	6.63213	ribonuclease T2-like 1-A
ROA1	98.546478	105.354622	33.140068	36.097412	Roa1p
ROB1	68.632027	73.800262	177.775818	210.617508	Rob1p
ROD1	46.559303	43.086464	5.455011	4.470047	Rod1p
ROM2	24.974405	21.979246	23.264814	32.588795	Rho family guanine nucle
ROT1	53.73251	53.711163	50.801174	37.490402	Rot1p
ROT2	20.258646	19.190399	30.22979	32.638626	glucan 1\3-alpha-glucosi
RPA12	35.262585	24.517878	30.048349	18.764526	DNA-directed RNA polyr
RPA135	35.475063	38.283379	31.733749	23.587078	DNA-directed RNA polyr
RPA190	28.326664	28.039492	21.560064	23.276001	DNA-directed RNA polyr
RPA34	55.678596	53.953888	29.555071	41.371029	DNA-directed RNA polyr
RPB11	50.188221	53.671715	129.167831	126.961876	DNA-directed RNA polyr
RPB4	57.254974	59.902279	61.439732	51.373543	DNA-directed RNA polyr
RPB7	43.059635	63.789623	95.049904	98.490143	DNA-directed RNA polyr
RPB8	52.454006	54.784828	76.937332	58.672874	DNA-directed RNA polyr
RPC10	63.741096	57.009617	72.007401	73.721092	DNA-directed RNA polyr
RPC11	71.131119	69.657745	122.059212	76.398476	DNA-directed RNA polyr
RPC19	273.783264	298.275177	78.266159	117.445938	DNA-directed RNA polyr
RPC31	20.998213	25.995577	47.470921	43.511753	DNA-directed RNA polyr
RPC40	82.901237	105.83712	48.825043	61.996868	DNA-directed RNA polyr
RPC53	20.355549	19.87483	16.191591	20.189274	DNA-directed RNA polyr
RPD3	46.524998	42.491699	54.529888	56.273228	Rpd3p
RPD31	25.534546	25.840631	59.90974	56.31105	histone deacetylase RPD
RPF1	131.395462	149.396378	116.352242	113.339066	rRNA-binding ribosome l
RPF2	77.584251	92.332771	32.190899	37.959435	rRNA-binding ribosome l
RPG1A	61.590847	67.483185	73.977142	79.838722	translation initiation facto
RPL10	1569.373413	1672.674194	1599.604248	1528.020142	ribosomal 60S subunit pr
RPL10A	1369.210938	1411.275146	1579.466553	1386.490723	ribosomal 60S subunit pr
RPL11	814.380066	906.390747	885.437256	747.536804	ribosomal 60S subunit pr
RPL12	1745.432007	1802.471436	2076.320557	2081.636475	ribosomal 60S subunit pr
RPL13	1872.380005	1920.749878	1703.360596	1693.501465	ribosomal 60S subunit pr
RPL14	1475.554688	1570.185547	1235.558228	1088.793091	ribosomal 60S subunit pr
RPL15A	1484.125732	1592.529175	1474.070801	1158.425171	60S ribosomal protein L1
RPL16A	1635.189941	1710.647827	1653.410522	1420.869629	ribosomal 60S subunit pr
RPL17B	818.596191	996.103333	776.909851	733.0495	ribosomal 60S subunit pr
RPL18	1295.507202	1522.110962	1391.264771	1289.62854	ribosomal 60S subunit pr
RPL19A	1994.291748	2107.288574	2230.925781	2186.135986	ribosomal 60S subunit pr
RPL2	1671.33728	1824.695557	1679.200195	1314.134521	60S ribosomal protein L2
RPL20B	1095.13147	1239.904907	1215.645874	1220.042603	ribosomal 60S subunit pr
RPL21A	1659.945068	1565.437134	1461.883179	1473.708374	ribosomal 60S subunit pr
RPL23A	1301.935913	1330.536499	1435.9552	1293.148193	ribosomal 60S subunit pr
RPL24A	1176.558105	1249.1875	1735.902832	1420.2854	ribosomal 60S subunit pr
RPL25	1596.302368	1494.785645	1598.744629	1217.885498	60S ribosomal protein L2
RPL27A	1366.903076	1340.147095	1398.838989	1330.369751	60S ribosomal protein L2
RPL28	2085.520996	2030.168457	2286.259277	1964.848877	60S ribosomal protein L2
RPL29	853.120605	788.195801	784.057373	584.483582	ribosomal 60S subunit pr

RPL3	1217.244141	1243.359375	1246.638794	1056.702393	ribosomal 60S subunit p
RPL30	1570.528076	1509.139526	1581.5625	1339.322266	60S ribosomal protein L
RPL32	1337.785645	1392.658081	1222.964478	1216.198242	ribosomal 60S subunit p
RPL35	926.538147	1109.577393	1189.438599	1217.15686	ribosomal 60S subunit p
RPL37B	1684.115112	1595.55835	1738.414307	1449.113281	ribosomal 60S subunit p
RPL38	1264.524414	1151.713867	1296.055298	1101.582275	60S ribosomal protein L
RPL39	878.072571	864.361816	861.691406	655.535645	60S ribosomal protein L
RPL40B	1010.843811	1066.946533	1213.750244	979.220215	hypothetical protein ATE
RPL42	1165.652832	1134.599487	1372.361816	1193.144043	60S ribosomal protein L
RPL43A	1595.3927	1514.784912	1957.269043	1712.910034	60S ribosomal protein L
RPL4B	1036.572144	1073.972412	897.275146	782.82959	60S ribosomal protein L
RPL5	1076.477783	1180.4646	1126.767578	1052.247559	ribosomal 60S subunit p
RPL6	1239.24292	1358.841553	1003.691528	1125.65332	60S ribosomal protein L
RPL7	168.758881	167.152725	74.882149	86.016151	Rpl7p
RPL82	480.204163	500.949799	495.335632	552.342163	Rpl82p
RPL8B	910.745483	930.311768	771.844604	806.934021	ribosomal 60S subunit p
RPL9B	928.824463	895.898193	1047.410645	971.905762	ribosomal 60S subunit p
RPM2	28.062237	32.029491	67.237587	63.857838	ribonuclease P
RPN1	53.037426	53.579144	79.03714	78.521576	proteasome regulatory p
RPN10	93.98687	88.585976	127.330421	121.785393	26S proteasome regulat
RPN2	44.817684	49.962738	73.818596	80.846741	proteasome regulatory p
RPN3	60.041542	55.523373	70.58989	94.514801	proteasome regulatory p
RPN4	460.532806	556.869446	323.747711	323.552277	stress-regulated transcri
RPN5	48.651199	61.513733	96.156227	95.360924	proteasome regulatory p
RPN6	23.575314	34.572906	46.312485	51.55518	26S proteasome regulat
RPN7	62.014374	67.168686	152.490997	151.519547	proteasome regulatory p
RPN8	77.071495	74.791557	124.12706	115.660751	26S proteasome regulat
RPO21	49.706841	41.059341	70.033508	79.662109	DNA-directed RNA polyr
RPO26	233.987167	257.72287	160.885239	145.980255	DNA-directed RNA polyr
RPO41	50.208645	55.97718	50.603909	56.30175	DNA-directed RNA polyr
RPP0	1419.507568	1466.706299	1406.812744	1313.455688	ribosomal protein P0
RPP1	24.131777	25.66646	21.403252	17.967857	ribonuclease P/MRP pro
RPP1A	1602.952637	1619.619995	1612.893555	1473.272583	60S acidic ribosomal pro
RPP1B	980.475586	1027.274048	925.850159	850.472961	ribosomal protein P1B
RPP2A	923.911133	948.786865	1087.252686	947.098938	ribosomal protein P2A
RPP2B	1503.789185	1608.442261	1255.409546	1019.671326	ribosomal protein P2B
RPR2	43.948921	38.698486	31.013723	47.132599	conserved hypothetical
RPS1	1433.036499	1571.102661	1265.504639	1232.389526	ribosomal 40S subunit p
RPS10	1899.971558	1888.830688	1928.970703	1769.350952	ribosomal 40S subunit p
RPS12	613.431824	666.172058	612.608826	489.524658	ribosomal 40S subunit p
RPS13	1088.606445	1103.044556	959.578125	913.327271	40S ribosomal protein S
RPS14B	1356.930054	1466.343994	1664.965088	1552.032715	ribosomal 40S subunit p
RPS15	1419.890625	1494.259399	1945.676025	1745.396606	40S ribosomal protein S
RPS16A	1412.850098	1470.514038	1595.281372	1602.720581	40S ribosomal protein S
RPS17B	1201.679688	1234.715454	1385.747681	1323.78894	40S ribosomal protein S
RPS18	1151.983887	1330.858643	1371.111816	1232.502319	40S ribosomal protein S
RPS19A	1191.607056	1209.374146	1056.958008	1081.061279	40S ribosomal protein S
RPS20	1449.298462	1490.422363	1560.579346	1587.171143	40S ribosomal protein S
RPS21	1106.148804	1224.061523	841.506897	748.516785	ribosomal 40S subunit p
RPS21B	943.352966	944.494385	1011.926147	808.667664	ribosomal 40S subunit p
RPS22A	799.433228	774.948486	755.943665	677.404419	ribosomal 40S subunit p
RPS23A	1729.085693	1934.371826	2031.821655	1692.884033	40S ribosomal protein S
RPS24	1493.370728	1542.024414	1608.895996	1420.538574	ribosomal 40S subunit p
RPS25B	1629.861328	1732.552124	2311.747559	2141.844482	ribosomal 40S subunit p
RPS26A	1672.555542	1710.620728	1936.793945	1674.514404	ribosomal 40S subunit p
RPS27	1320.610474	1362.187012	1463.572998	1602.55481	40S ribosomal protein S
RPS27A	293.259735	317.468353	76.888237	67.998886	40S ribosomal protein S
RPS28B	1111.793457	1187.571777	1335.099243	1292.019409	40S ribosomal protein S
RPS3	1102.206543	1243.534668	918.5896	807.924622	40S ribosomal protein S
RPS30	1103.356323	1172.641357	1119.526978	976.264221	40S ribosomal protein S
RPS42	317.42218	367.417236	297.943085	276.87854	ribosomal 40S subunit p
RPS4A	895.13916	919.081665	924.707642	790.113708	Rps4ap
RPS5	1122.315186	1121.820557	857.35376	920.774597	ribosomal 40S subunit p
RPS6A	1201.312866	1390.951538	1362.737671	1186.361206	ribosomal 40S subunit p

RPS7A	959.202148	1039.55188	900.103149	981.550354	ribosomal 40S subunit p
RPS8A	2245.530518	2310.871094	1890.056641	1803.289429	ribosomal 40S subunit p
RPS9B	1603.981323	1633.749512	1592.768555	1561.134644	40S ribosomal protein S
RPT1	109.365067	131.912766	149.092133	120.243561	26S proteasome subunit
RPT2	122.365784	125.126007	137.903976	149.038696	proteasome regulatory p
RPT4	86.25219	97.196159	107.697403	110.440796	proteasome regulatory p
RPT5	114.003456	103.044464	160.828552	171.792801	proteasome regulatory p
RPT6	108.036392	107.669312	122.288223	102.769417	proteasome regulatory p
RRD1	15.70248	17.731136	32.266491	27.118404	peptidylprolyl isomerase
RRN11	21.429594	23.049063	13.316889	12.894246	Rrn11p
RRN3	60.576637	53.469048	30.425957	39.891777	rDNA-binding RNA polyr
RRP15	91.243835	97.063148	44.083672	49.419514	Rrp15p
RRP42	29.657476	31.248495	31.696846	19.587036	exosome non-catalytic c
RRP6	37.01712	36.785912	30.035391	22.258141	exosome complex exonu
RRP8	103.323181	96.479828	102.527565	112.197189	ribosomal RNA-processi
RRP9	47.020195	54.446709	18.476076	20.691866	Rrp9p
RRS1	116.802277	125.737923	74.876045	74.031189	Rrs1p
RSM22	19.962824	18.619293	20.113213	21.566401	mitochondrial 37S riboso
RSN1	63.947567	61.636028	4.194004	3.980192	Rsn1p
RSP5	39.867008	43.628704	48.49934	47.951771	E3 ubiquitin-protein ligas
RSR1	120.521477	111.969582	102.118874	88.061638	Ras family GTPase
RTA2	220.73378	270.494354	92.961121	77.943626	phospholipid-translocatin
RTA3	27.467272	29.543007	24.700294	21.986874	Rta3p
RTA4	69.881279	94.875969	38.597515	25.702	Rta4p
RTF1	31.655758	35.24073	62.4744	67.544846	Rtf1p
RTG1	62.832809	70.26062	133.883682	102.804642	Rtg1p
RTG3	71.97747	62.858379	71.107719	86.280792	hypothetical protein MEK
RTS1	40.483002	44.576099	78.241661	84.44754	protein phosphatase 2 (f
RTT101	5.101676	4.0186	12.245237	11.042791	cullin
RTT109	5.713889	11.407397	21.778381	14.472819	H3 histone acetyltransfe
RUB1	78.059502	66.287918	179.197021	155.141449	ubiquitin-like protein with
RVB2	66.45723	71.295143	103.117126	103.674873	RuvB family ATP-depend
RVS161	500.856812	495.793854	442.389984	303.25531	amphiphysin-like protein
RVS162	12.02728	12.219251	24.558451	26.610781	hypothetical protein MG
RVS167	278.979736	282.483643	334.548157	328.896362	amphiphysin
RXT3	58.13903	50.273952	56.996758	62.573471	Rxt3p
SAC1	22.770693	16.813484	55.739735	45.395947	phosphatidylinositol-3-ph
SAC3	7.886458	7.618889	14.709893	15.015511	Sac3p
SAC6	178.390518	200.975449	268.77951	208.987015	fimbrin
SAC7	113.601196	99.598457	127.061546	118.198082	Sac7p
SAH1	414.861176	483.244385	479.771942	427.604218	adenosylhomocysteinase
SAL6	102.573395	109.856262	139.98793	133.184692	Sal6p
SAM2	213.608398	216.711273	212.916977	200.233185	S-adenosylmethionine sy
SAM35	36.287819	29.769087	42.726185	31.041765	SAM complex subunit
SAM37	10.045472	9.290451	14.589634	9.475444	SAM complex subunit
SAM4	21.497339	15.897285	38.452465	51.401451	S-adenosylmethionine-h
SAM50	7.462616	12.337406	10.951488	13.49078	hypothetical protein MEY
SAM51	17.451208	24.170435	32.841084	31.631533	hypothetical protein MG
SAP1	7.770769	12.640256	8.66836	11.629612	Sap1p
SAP10	17.536554	23.560833	55.606358	41.969173	candidapepsin
SAP2	11.493083	14.375114	15.910663	16.680187	Sap2p
SAP3	0.271706	0.324026	1.093348	0.704036	Sap3p
SAP30	2.988275	1.434741	7.101017	4.506051	Sap30p
SAP4	3.517718	1.310152	0	1.269307	Sap4p
SAP5	1.484893	1.345001	4.592951	1.093935	Sap5p
SAP6	3.99671	2.509614	4.397733	6.068686	Sap6p
SAP7	1.483409	0.882508	4.741713	3.71992	Sap7p
SAP8	7.806402	7.530677	9.650428	6.515303	candidapepsin-8
SAP9	1600.03894	1809.78186	738.903076	784.170715	aspartyl protease
SAP98	23.273874	16.725025	9.462326	14.99471	Sap98p
SAP99	5.8358	3.201192	7.907493	8.433729	Sap99p
SAR1	165.633514	169.578705	208.070755	197.27681	small COPII coat GTPas
SAS10	69.580994	67.187805	35.229259	41.494522	rRNA-processing protein
SAS2	8.786424	6.862964	19.683264	20.84572	Sas2p

SAS3	7.582645	6.897819	19.640938	18.276203	histone acetyltransferase
SBA1	217.347382	200.092133	197.90213	177.898483	predicted protein
SBP1	379.768188	361.855255	699.058044	557.831116	Sbp1p
SCH9	82.355232	91.622391	36.79451	34.576454	serine/threonine protein
SCL1	97.347687	109.714241	142.15535	142.514908	proteasome core particle
SCO1	144.226517	163.792297	502.782867	381.425049	Cu-binding protein
SCP1	12.818496	17.270475	14.683437	15.317379	hypothetical protein MG
SCS7	627.375366	648.690857	311.679657	252.26445	fatty acid alpha-hydroxyl
SCT1	57.589211	57.121334	36.436161	38.821968	glycerol-3-phosphate O-
SCT2	27.78437	22.782438	18.961184	20.33794	conserved hypothetical
SCW11	218.088669	162.08551	945.32135	1300.365967	hypothetical protein ME
SCW4	8.237489	7.440789	5.151834	4.831261	Scw4p
SDA1	67.39724	67.549477	36.220314	37.262554	Sda1p
SDC1	16.497313	22.328934	90.704742	97.679848	Sdc1p
SDH1	18.870903	14.041941	40.444935	26.109232	succinate dehydrogenas
SDH12	289.221893	314.158295	278.566406	266.309021	Sdh12p
SDH2	330.934113	364.246826	350.54834	353.362396	succinate dehydrogenas
SDH4	35.011246	32.226139	49.743568	39.573917	Sdh4p
SDS22	80.722473	92.805023	81.382637	64.272163	type 1 protein phosphat
SDS24	3013.287842	2929.474121	1639.205933	1709.807617	protein SDS23
SEC1	17.84325	20.56978	27.67753	33.447788	syntaxin-binding protein
SEC10	25.909168	26.323112	64.245941	52.717991	exocyst subunit
SEC12	23.737253	19.772089	30.797871	42.512402	hypothetical protein I503
SEC13	107.027733	105.632042	167.17305	140.515137	GTPase-activating prote
SEC14	663.173401	778.713379	224.185333	246.569153	phosphatidylinositol/pho
SEC15	9.927857	11.69171	17.29998	16.958759	Rab GTPase-binding ex
SEC18	22.99708	19.435995	28.785414	31.422964	AAA family ATPase
SEC2	51.420006	53.43684	36.142414	42.042767	guanine nucleotide exch
SEC20	7.599703	9.898312	15.658246	14.573315	Sec20p
SEC21	32.36721	34.025963	59.661636	67.970367	coatomer subunit gamm
SEC22	41.664604	43.503319	70.350983	64.1931	SNAP receptor
SEC23	53.839806	56.400757	110.928719	113.917099	GTPase-activating prote
SEC24	91.833733	91.884232	144.718063	150.032974	protein transporter SEC
SEC26	45.813572	44.291348	81.503166	77.442558	coatomer subunit beta
SEC27	38.654167	37.78574	59.307152	60.659199	coatomer subunit beta&
SEC3	17.168365	19.828594	34.942802	39.279354	hypothetical protein MG
SEC34	19.108583	18.171116	47.392715	49.518578	Golgi transport complex
SEC4	209.824554	220.347595	391.076782	355.052063	Ras-related protein Sec
SEC5	7.608176	11.150598	18.437611	16.783239	exocyst subunit
SEC6	64.125015	63.553146	101.069458	74.588905	SNARE-binding exocyst
SEC61	197.353851	193.028168	202.92691	209.640533	SEC61 protein
SEC62	42.967667	48.857273	109.433807	89.000031	Sec63 complex subunit
SEC65	78.848679	77.066116	96.903221	108.850922	RNA-binding signal reco
SEC7	17.955923	18.678051	31.474821	34.005894	Arf family guanine nucle
SEC72	61.535839	61.092022	108.563202	115.008293	Sec63 complex subunit
SEC8	7.801944	6.432002	10.519621	12.405706	exocyst subunit
SEC9	58.91925	58.985733	58.004715	68.428886	synaptosomal-associate
SEF1	86.751114	82.022156	36.967789	43.927486	hypothetical protein MG
SEF2	3.816886	7.154864	12.193004	13.66216	Sef2p
SEH1	36.339577	31.562435	84.459946	80.210785	Seh1p
SEN1	5.893567	7.230844	11.698834	11.440939	putative DNA/RNA helic
SEN15	13.057023	11.176673	25.003504	31.737402	Sen15p
SEN2	41.118877	45.166904	7.292676	8.886466	tRNA-intron endonuclea
SEO1	8.129762	7.016458	8.774017	5.283049	putative permease
SER1	83.71917	75.487442	138.172073	112.139122	O-phospho-L-serine:2-o
SER2	27.769115	26.974712	29.601936	23.848623	phosphoserine phospha
SER33	131.117462	150.596115	164.07634	162.958038	phosphoglycerate dehyd
SES1	160.44046	159.913879	166.560501	180.252701	serine--tRNA ligase
SET1	9.162239	8.186317	40.474098	59.115482	histone-lysine N-methylt
SET2	10.93869	8.71991	16.672737	17.436794	histone methyltransfera
SET3	19.76152	20.044489	27.525127	30.969519	histone-binding protein
SET6	24.993902	21.55102	31.879065	28.775826	Set6p
SFC1	213.175797	168.077637	201.968231	205.535049	Sfc1p
SFH5	13.187088	16.676373	50.278721	40.694286	Sfh5p

SFI1	9.51095	9.502701	16.44482	20.492262	Sfi1p
SFL1	36.325237	35.828682	32.083584	38.251514	Sfl1p
SFL2	92.468613	91.799995	26.391144	36.318027	Sfl2p
SFP1	81.48539	68.526794	80.27964	78.327263	hypothetical protein MG3
SFT1	94.511581	77.129776	66.545906	55.999035	conserved hypothetical p
SFT2	52.149288	52.252834	63.582478	42.476978	hypothetical protein MEY
SFU1	31.475229	27.473179	97.686623	106.90654	Sfu1p
SGA1	7.88035	8.151461	27.963295	23.887096	glucan 1,4-alpha-glucosi
SGD1	32.998955	33.332794	21.820658	16.152117	hypothetical protein MG7
SGE1	9.780042	10.098183	23.226366	24.631353	Sge1p
SGO1	29.17078	26.559872	65.685722	60.493641	Sgo1p
SGS1	36.455837	30.948204	50.699631	53.162376	ATP-dependent DNA he
SGT1	121.980019	137.715622	139.408417	131.257858	co-chaperone
SGT2	155.419785	145.535721	198.571838	199.049438	Sgt2p
SHA3	1244.052979	1429.682129	1223.83606	1310.763794	hypothetical protein MG
SHE3	17.939678	17.570314	28.49403	34.862083	She3p
SHE9	9.55806	6.664165	14.536102	12.25365	She9p
SHM1	271.712067	300.562775	207.795242	184.152435	glycine hydroxymethyltra
SHM2	349.904083	383.98291	320.943726	317.78653	glycine hydroxymethyltra
SHP1	48.101913	43.539223	70.111717	62.961922	protein phosphatase reg
SHY1	51.121525	47.746613	122.833191	109.844894	Shy1p
SIK1	295.447968	303.11972	201.191772	187.717468	nucleolar protein 56
SIM1	293.505676	335.48761	398.456635	445.043335	SUN family protein
SIN3	30.047592	29.410238	57.760788	61.87331	paired amphipathic helix
SIP5	86.401566	94.676712	69.612221	65.42186	protein SIP5
SIR2	11.439569	12.37655	7.710056	10.68072	Sir2p
SIS1	380.731873	385.509491	710.720093	607.392456	type II HSP40 co-chaper
SIT1	53.21558	54.415863	79.143883	62.778381	siderophore transporter
SIT4	52.960712	44.18782	71.582405	40.628338	type 2A-related serine/th
SIW14	12.076416	8.592049	12.914034	19.532412	putative tyrosine protein
SIZ1	17.995047	15.616681	27.813139	30.158419	E3 SUMO-protein ligase
SKI2	25.276047	25.371971	33.62484	30.604345	SKI complex RNA helica
SKI3	10.607977	11.796171	19.66527	19.86484	SKI complex subunit tetr
SKI8	19.56695	20.010748	23.204363	31.085825	SKI complex subunit WD
SKN1	262.952026	283.360809	341.939789	337.648682	Skn1p
SKN2	28.664501	24.007021	94.044098	94.083427	Skn2p
SKN7	12.853594	14.450412	31.478399	29.968622	kinase-regulated stress-
SKO1	21.897127	18.855614	30.028942	25.002499	hypothetical protein ME
SKP1	351.779694	339.091736	450.718323	459.200531	SCF ubiquitin ligase sub
SLA1	28.614086	25.816942	32.695404	38.811035	cytoskeletal protein-bind
SLA2	38.9566	38.617645	53.661385	59.241554	Sla2p
SLC1	149.060989	144.755325	102.172447	101.361015	1-acylglycerol-3-phospha
SLD1	39.100983	39.392231	69.664246	62.940979	Sld1p
SLD5	4.628658	5.708291	13.928879	23.937025	DNA replication protein
SLF1	8.206141	9.829324	27.257185	16.521435	hypothetical protein ME
SLK19	162.603256	171.270172	111.211014	109.677185	Slk19p
SLM2	41.644817	35.779125	46.000156	61.572609	phosphatidylinositol 4,5-
SLN1	36.560524	37.469528	24.345663	24.829357	Sln1p
SLP2	37.769897	34.552944	69.670975	68.254753	hypothetical protein MG
SLR1	315.98642	340.127411	305.978516	201.565506	Slr1p
SLU7	11.718403	9.220703	29.138941	21.182138	mRNA splicing protein
SLY41	97.668861	107.114799	50.563011	64.245193	Sly41p
SMC1	6.282061	7.477391	22.001307	25.05414	cohesin subunit
SMC2	5.82562	5.507142	20.510136	22.17218	condensin subunit
SMC3	3.746466	4.586957	18.780645	18.29138	cohesin subunit
SMC4	9.926532	10.514395	24.458956	26.418793	condensin subunit
SMC5	4.565036	3.807658	13.619801	14.441485	DNA repair ATPase
SMC6	17.826387	21.841343	22.461676	19.971022	DNA repair protein
SMD2	28.615482	17.572611	58.726234	59.963573	mRNA splicing protein
SMD3	79.007332	59.035477	114.541931	88.015182	mRNA splicing protein
SMF12	376.365936	438.5625	580.891785	559.760986	metal ion (Mn2+/Fe2+) t
SMF3	19.162029	27.749083	28.284706	23.357582	putative divalent metal ic
SMI1	198.40834	205.101807	154.161667	146.473145	hypothetical protein MEK
SMI1B	8.704389	7.502443	11.719448	10.185049	Smi1bp

SMM1	132.084854	132.943527	68.946365	70.677704	Smm1p
SMP2	23.94294	23.975916	46.19511	53.053665	phosphatidate phosphat
SMP3	5.051335	8.106883	7.217376	4.72973	glycosylphosphatidylinos
SMT3	301.233002	362.986511	586.811829	481.96463	SUMO family protein
SMX4	52.543282	54.578438	107.219727	78.929039	U4/U6-U5 snRNP compl
SNF1	118.068993	126.281357	111.931122	102.410431	carbon catabolite-derepr
SNF2	27.374456	24.51125	38.533504	44.223297	ATP-dependent helicase
SNF4	63.638718	87.376228	69.803879	73.677048	AMP-activated serine/thr
SNF5	23.458237	17.043171	50.593811	40.308796	Snf5p
SNF7	87.171257	88.118561	104.690834	117.33226	ESCRT-III subunit protei
SNG3	16.915764	22.583529	12.395168	14.28774	Sng3p
SNG4	21.731874	17.548136	20.934202	15.640481	Sng4p
SNL1	75.10025	106.4076	96.641479	58.473858	Snl1p
SNM1	37.250484	40.626305	55.017868	46.992626	Snm1p
SNO1	46.50058	47.817368	56.983799	43.527603	putative pyridoxal 5&apo
SNP3	59.841118	63.364983	140.073257	101.810547	RNA processing comple
SNQ2	19.164612	19.124151	23.237257	23.807669	ATP-binding cassette tra
SNT1	85.030579	77.635956	61.863064	62.061638	Snt1p
SNU114	15.388296	14.082572	16.142181	17.380264	U5 snRNP GTPase
SNX4	19.434679	18.814259	26.234137	35.538174	Snx4p
SNZ1	370.251587	404.894531	451.522308	461.275696	pyridoxine biosynthesis
SOD1	168.069397	182.234879	14.119705	6.519	superoxide dismutase
SOD2	171.789276	199.067032	132.101517	109.499214	superoxide dismutase
SOD3	6224.510254	6051.660156	3451.770996	2640.487549	Sod3p
SOD4	54.75174	53.828739	44.156235	44.949394	hypothetical protein ME
SOD5	6.898067	9.038894	0	1.003788	Sod5p
SOD6	115.886642	116.262505	76.137375	66.78463	Sod6p
SOF1	93.300194	109.758705	69.846603	64.46357	rRNA-processing protein
SOG2	27.652514	25.17893	57.978386	60.845001	Sog2p
SOH1	14.99938	14.245625	34.529488	35.63261	Soh1p
SOK1	534.999146	564.279663	204.921326	213.850281	Sok1p
SOL1	67.127052	64.149353	187.22229	208.66893	Sol1p
SOL3	47.031796	63.507114	84.978096	84.016777	6-phosphogluconolacton
SOU1	18.425053	19.348274	6.573184	3.69765	Sou1p
SOU2	3.3835	4.867554	1.56551	1.010803	hypothetical protein MG
SPA2	19.311071	19.766592	25.233688	33.325508	Spa2p
SPB1	62.713516	66.498161	23.128084	26.229965	27S pre-rRNA (guanosin
SPB4	24.995462	22.142534	19.261026	22.747538	putative ATP-dependent
SPC19	10.732509	9.457263	32.92561	47.580635	DASH complex subunit
SPC2	33.808483	49.834698	86.236595	84.318123	signal peptidase comple
SPC3	67.134132	67.010048	135.943085	157.380615	signal peptidase comple
SPC34	9.807964	10.690983	35.63401	32.826015	Spc34p
SPC98	6.833978	8.991501	26.625954	20.132383	Spc98p
SPE1	70.375458	72.357948	82.136078	80.407631	ornithine decarboxylase
SPE2	181.666229	180.220673	103.74987	105.404884	adenosylmethionine dec
SPE3	165.686035	135.020859	161.98764	160.294144	spermidine synthase
SPF1	21.398417	23.261839	31.368402	34.62447	ion-transporting P-type
SPL1	186.568771	205.353104	187.220856	180.181427	Spl1p
SPO1	3.699307	2.22428	24.466522	24.195621	putative carboxylic ester
SPO11	1.736811	4.403648	4.515786	2.458626	Spo11p
SPO22	0.446189	0	0.12299	0.265487	Spo22p
SPO7	43.185825	43.180401	41.879063	31.341221	Nem1-Spo7 phosphatas
SPO72	12.035515	12.155123	11.287978	12.654799	Spo72p
SPO75	8.218675	7.934809	9.993861	14.069002	Spo75p
SPP1	10.271919	15.301282	22.405012	21.244282	Spp1p
SPR1	0	0	0.209662	0	hypothetical protein MG
SPR28	5.221523	6.698219	25.828663	21.687012	hypothetical protein ME
SPR3	0.155438	0	0.542594	0.921011	septin
SPS20	45.140514	49.521587	49.069828	54.824459	Sps20p
SPT10	13.681704	11.98843	28.325155	27.693592	Spt10p
SPT14	58.418652	69.157143	61.806065	49.380234	phosphatidylinositol N-a
SPT20	13.023471	12.328221	26.605162	25.634672	transcription factor SPT
SPT23	175.005173	177.464935	124.188568	110.34124	hypothetical protein W5
SPT3	34.518238	35.879948	80.886963	66.716026	transcriptional regulator

SPT5	78.242241	70.131142	83.113457	74.774963	transcription elongation f
SPT6	57.646328	44.016171	83.256424	74.784218	transcription elongation f
SPT7	17.267876	14.180638	27.147451	22.963501	SAGA histone acetyltran
SRB1	354.10379	378.389618	764.268799	683.735046	mannose-1-phosphate g
SRB8	5.684346	4.485915	7.693557	6.411871	Srb8p
SRB9	6.4119	6.555249	11.371765	12.248783	Srb9p
SRD1	31.950565	28.757648	25.14938	25.725668	Srd1p
SRO77	15.392363	12.300406	29.886143	33.963604	putative Rab GTPase-bi
SRP101	22.1528	26.022392	30.609005	26.065069	Signal recognition particl
SRP40	139.786545	146.341339	42.789066	49.70192	hypothetical protein MG
SRP54	62.070324	69.52285	69.435028	70.383354	signal recognition partic
SRR1	234.343704	330.977386	56.93214	74.210693	Srr1p
SRT1	9.69608	12.747619	20.901508	14.872549	ditrans,polycis-polypreny
SRV2	86.76049	94.977524	135.812561	132.29155	adenylate cyclase-bindin
SSA2	522.896057	501.847809	391.686523	512.669128	Hsp70 family chaperone
SSB1	924.433716	982.671387	799.690125	874.483215	hsp75-like protein
SSC1	315.266632	343.27652	646.16156	624.313843	Hsp70 family ATPase
SSD1	54.076653	52.918591	33.792137	38.181076	hypothetical protein MG
SSF1	130.085464	141.568146	34.283142	39.340836	rRNA-binding ribosome
SSH1	53.45118	53.341541	62.846264	72.594383	Ssh1p
SSK1	28.573334	27.968077	36.83432	35.665089	mitogen-activated protei
SSK2	29.920189	28.518446	40.378399	44.116238	mitogen-activated protei
SSN3	11.510659	14.278049	19.010181	16.740685	cyclin-dependent serine/
SSN6	73.492722	70.413025	125.122086	143.911728	transcription regulator
SSN8	10.635308	12.684003	15.855916	17.964262	cyclin-dependent protein
SSO2	127.740562	145.71138	233.775208	243.87294	syntaxin
SSP96	17.462379	14.698507	20.015667	16.67548	Ssp96p
SSR1	340.524536	394.898041	680.174438	785.276123	hypothetical protein ME
SST2	5.12316	10.228054	6.641164	5.139135	hypothetical protein MG
SSU1	257.746429	271.345093	40.699642	53.351246	Ssu1p
SSU72	30.920507	34.664738	60.625957	65.167938	RNA polymerase II subu
SSU81	57.304379	57.260593	56.741211	50.660156	osmosensor
SSY1	27.914501	31.826576	21.574131	18.907784	Ssy1p
SSY5	28.150791	33.67614	26.451475	27.270582	Ssy5p
SSZ1	217.727859	236.72403	178.950073	177.009979	Ssz1p
STB3	321.780182	318.014954	170.150986	177.898483	Stb3p
STB5	12.310019	14.839559	15.474097	17.419559	Stb5p
STD1	181.708313	178.853394	94.055336	107.406273	Std1p
STE11	40.890591	39.021648	38.71368	37.918232	mitogen-activated protei
STE13	4.532943	5.883383	8.983842	10.205112	Ste13p
STE18	46.14769	42.042637	79.967079	115.605339	Ste18p
STE2	26.359112	34.235832	4.16903	5.506951	pheromone alpha factor
STE23	78.94931	77.37928	9.99282	7.910316	metalloendopeptidase
STE24	61.561554	63.361736	151.919434	153.03273	zinc metalloprotease
STE3	2.663253	1.974745	2.844727	7.655716	Ste3p
STE4	37.170536	42.392616	31.800413	37.055252	G protein subunit beta
STE50	16.569035	13.413301	24.59153	28.465487	Ste50p
STF2	6385.371094	5568.710449	6185.019531	5369.660156	Stf2p
STI1	126.412544	120.302559	77.168648	81.706024	Hsp90 cochaperone
STN1	1.145773	0.946589	2.049262	5.72224	Stn1p
STP1	23.711111	25.347486	19.72616	27.564016	hypothetical protein MG
STP2	930.630432	891.835266	663.087158	740.510986	hypothetical protein ME
STP4	272.536743	254.108292	348.89502	392.633667	Stp4p
STR2	19.288128	27.47751	29.857941	26.917461	cystathionine gamma-sy
STT3	49.583141	41.839512	59.427612	58.58754	dolichyl-diphosphooligos
STT4	17.177332	20.76779	25.692463	28.728218	1-phosphatidylinositol 4-
STV1	25.188324	23.863674	36.218174	39.191597	Stv1p
SUA71	684.609436	722.107483	353.410553	346.272736	transcription factor TFIIB
SUA72	11.43773	9.734925	19.834793	15.723501	Sua72p
SUB2	149.219955	152.593872	289.456573	296.038422	ATP-dependent RNA he
SUC1	8.797333	8.170038	9.89397	10.972391	transcription factor
SUI1	1006.313599	1200.054199	739.309509	782.569214	translation initiation facto
SUI2	158.664749	169.566711	110.870415	100.753784	translation initiation facto
SUI3	300.082581	342.341827	168.523163	147.870316	translation initiation facto

SUL2	469.524506	350.231018	8.948871	13.489562	sulfate permease
SUN41	1084.817261	872.515198	2388.817383	2349.238037	putative glucosidase
SUP35	99.804909	89.00589	88.420525	80.792496	translation termination fa
SUR2	1657.710815	1874.221191	429.600708	428.392059	sphingosine hydroxylase
SUR7	791.459229	855.580627	673.687378	661.562622	Sur7p
SUT1	125.019127	132.988541	85.491669	100.670998	Sut1p
SUV3	19.506577	24.938614	17.224926	22.41452	ATP-dependent RNA he
SVF1	141.230484	155.255234	138.716446	122.183929	Svf1p
SWC4	22.626284	22.295164	40.070084	48.31765	SWR1-complex protein
SWD1	13.216792	18.53533	30.618128	26.719805	COMPASS subunit prote
SWD2	21.623024	20.411522	47.195671	40.585228	WD-repeat containing pr
SWD3	9.822083	11.402333	29.660412	28.974876	Swd3p
SWE1	22.098963	19.601154	58.947769	57.341274	tyrosine protein kinase
SWI1	24.2917	23.575994	56.117737	57.951885	Swi1p
SWI4	15.658484	18.117956	34.826977	35.84761	SBF complex DNA-bindi
SWI6	11.569782	13.411353	33.995022	41.840496	transcriptional regulator
SWR1	11.772826	10.090057	20.801323	21.27948	chromatin-remodeling pr
SYG1	15.746578	15.479997	10.139047	10.663323	Syg1p
SYN8	14.215322	13.191847	26.559689	27.617292	syntaxin
SYS1	60.11871	77.132385	116.352776	108.155556	Sys1p
SYS3	12.695299	8.317552	18.275316	20.912973	Sys3p
TAC1	13.815409	15.105681	16.180445	19.107656	Tac1-21p
TAF14	116.063255	106.911072	237.613174	232.809799	TATA-binding protein-as
TAF145	18.870502	18.915407	31.362904	34.304916	Taf145p
TAF19	18.311436	28.746929	60.448608	65.748161	Taf19p
TAF4	60.641373	66.180443	89.004852	76.639999	Taf4p
TAF60	19.071516	19.440758	65.154366	59.28117	Taf60p
TAL1	446.412537	486.637665	667.565674	672.914062	sedoheptulose-7-phosp
TAR1	709.779724	842.917236	1767.998657	1334.385376	Tar1p
TAZ1	25.758394	20.596764	10.002351	11.237304	lysophosphatidylcholine
TBF1	47.042065	44.226357	30.872362	36.01778	Tbf1p
TBP1	202.867371	209.786133	243.314407	194.558853	TATA-binding protein
TCC1	161.842896	128.951767	97.613739	121.834831	Tcc1p
TCO89	18.542755	20.377403	11.82783	18.202984	hypothetical protein L15
TCP1	54.462463	59.170658	58.397812	63.699852	chaperonin-containing T
TDH3	6015.503418	6453.962402	3509.842041	3195.653809	glyceraldehyde-3-phosp
TEA1	15.267901	14.097538	14.4328	17.345411	Tea1p
TEC1	39.812073	48.391911	32.548004	39.849525	Tec1p
TEF1	2911.140869	3216.479004	2670.804688	2386.815918	translation elongation fa
TEF2	3548.485352	3985.56958	3249.095459	2874.904785	elongation factor 1-alpha
TEF4	8.28805	8.52717	0	0	Tef4p
TEL1	4.681322	4.760199	7.325024	5.523938	DNA-binding protein kin
TEM1	19.833536	20.061726	65.680229	44.56316	Ras family GTPase
TEN1	8.69067	5.445008	12.217985	13.082714	Ten1p
TEP1	2.363377	4.650468	6.293464	6.416165	putative phosphatidylino
TERT	6.473666	6.60677	17.866699	14.593341	Tertp
TES1	6.14976	6.330717	13.678278	8.404407	Tes1p
TES15	53.402096	71.89502	59.962421	53.28735	Tes15p
TFA1	16.96032	16.721195	40.689426	41.149181	transcription factor TFIIE
TFB3	20.783991	29.595627	30.974096	28.653849	TFIIH/NER complex sub
TFC4	6.93681	7.614551	25.462574	27.29315	transcription factor TFIII
TFG1	114.910179	95.353752	96.518318	88.820099	transcription factor IIF s
TFP1	87.645111	86.915558	92.977226	98.202019	H(+)-transporting V1 se
TFS1	269.537476	287.196655	280.642334	296.170135	Tfs1p
TGL99	9.543532	17.057465	18.887381	17.764462	Tgl99p
THG1	10.774098	12.39502	14.109975	15.53637	tRNA guanylyltransferas
THI13	12.597644	19.573322	10.678736	11.285038	4-amino-5-hydroxymeth
THI20	8.901422	11.538007	15.784159	14.850015	trifunctional hydroxymet
THI4	4.367672	8.485552	2.439382	2.897186	thiamine thiazole syntha
THI6	17.792925	19.133858	13.482944	13.742293	bifunctional hydroxyethyl
THR1	25.46138	40.562859	29.534262	28.031704	homoserine kinase
THR4	43.734379	37.206223	43.074135	45.39769	threonine synthase
THS1	80.280632	83.824844	129.733383	115.30899	threonine--tRNA ligase
TIF	435.316132	478.734131	504.265106	501.038208	translation initiation fact

TIF11	268.529694	252.351028	279.99707	248.591171	Tif11p
TIF3	157.158875	167.364105	150.174591	140.904602	Tif3p
TIF34	161.208435	170.755386	151.198334	126.713921	translation initiation facto
TIF35	173.223846	191.04538	138.799026	97.897072	translation initiation facto
TIF4631	110.055229	111.626793	70.921837	72.610832	translation initiation facto
TIF5	52.302605	78.289124	71.718155	59.06324	translation initiation facto
TIM10	105.22258	104.419945	229.176804	217.344543	protein transporter
TIM12	34.570679	35.356342	106.542099	89.390121	Tim12p
TIM13	31.598232	27.183273	116.759842	109.725288	mitochondrial import inne
TIM17	261.414368	287.015594	120.211769	109.595352	protein transporter
TIM21	25.781399	25.84124	105.052528	98.833313	Tim21p
TIM22	171.440002	178.347	114.562935	119.06488	translocation channel pro
TIM23	118.465874	121.670807	131.506653	117.71003	mitochondrial import inne
TIM44	70.121666	91.664185	167.799561	117.433022	protein translocase subu
TIM50	91.045464	109.598526	146.949844	170.300995	protein translocase subu
TIM54	33.05682	38.456867	67.006012	48.399452	Tim54p
TIM8	67.478737	47.618847	130.200592	112.135292	mitochondrial import inne
TIM9	95.104378	101.910912	148.706299	183.330582	protein transporter
TIP1	41.130302	35.811569	92.943504	76.570152	transporter
TIP120	13.851715	12.076866	12.079757	14.136635	hypothetical protein MEU
TIP20	15.436095	16.892313	27.762516	23.716602	Tip20p
TIP41	12.152981	16.319387	38.229145	31.950624	Tip41p
TKL1	520.928711	541.528259	377.112701	404.668579	transketolase
TLG2	9.404577	7.894168	22.104946	32.704651	Tlg2p
TLO1	41.037357	38.921055	30.08334	22.983725	Tlo1p
TLO10	92.541924	99.442757	126.49958	114.700768	Tlo10p, partial
TLO11	18.446564	21.249458	23.783844	26.394388	Tlo11p
TLO13	41.033081	49.348339	52.215797	55.88731	hypothetical protein CAW
TLO16	64.366219	69.598457	75.361809	56.746284	Tlo16p
TLO34	73.149399	71.655853	56.172928	46.358662	Tlo34p
TLO4	46.980434	51.780773	79.940552	57.479836	hypothetical protein MGK
TLO5	21.828232	25.973656	31.756268	29.158543	Tlo5p
TLO7	18.290262	19.33708	14.562623	9.332952	Member of a family of tel
TLO8	57.476646	62.011597	77.731636	66.235916	Tlo8p
TLO9	30.674526	32.433483	44.511772	35.607925	Tlo9p
TMA19	956.55304	946.663025	1165.807617	1083.640503	Tma19p
TNA1	3.77272	4.841505	0.472248	0.65777	Tna1p
TOA2	66.780182	67.922752	77.142624	56.76049	transcription initiation fac
TOK1	30.145012	31.428482	17.142179	20.22275	Tok1p
TOM1	20.454231	18.642952	31.677887	34.339729	e3 ubiquitin protein ligas
TOM20	122.049042	134.77153	310.291412	294.16803	Tom20p
TOM22	177.042618	185.639664	342.184753	357.800659	hypothetical protein CAW
TOM40	164.352203	187.791138	291.0672	289.220245	Tom40p
TOM6	177.234283	149.193939	296.563507	278.278961	mitochondrial import rec
TOM7	201.541321	224.528198	404.541107	349.473175	Tom7p
TOM70	76.709572	88.249352	123.47187	113.569092	hypothetical protein L15
TOP1	28.589836	31.742825	38.398796	32.046261	DNA topoisomerase 1
TOP2	10.718163	10.101556	32.491085	37.063564	DNA topoisomerase 2
TOR1	11.893539	12.687112	16.783934	17.972572	FKBP12-rapamycin com
TOS1	552.645264	492.568604	1872.448853	2076.938721	Tos1p
TOS4	113.307472	119.763481	181.024811	187.172806	Tos4p
TPD3	43.993572	52.746609	65.023483	67.871437	protein phosphatase 2A
TPI1	427.481171	439.358734	411.700012	386.978119	triose-phosphate isomer
TPK1	192.388397	222.611038	113.328384	109.510628	cAMP-dependent protei
TPK2	71.903595	72.865074	96.458923	81.670799	cAMP-dependent protei
TPM2	465.625671	484.352966	986.64502	1087.69104	hypothetical protein CPA
TPO2	3.031273	2.304066	4.447542	3.01119	Tpo2p
TPO3	38.06097	45.791019	246.888992	215.479935	spermine transporter
TPO4	20.046284	20.99411	82.821304	72.587776	Tpo4p
TPO5	6.228004	4.934015	9.101394	8.157622	Tpo5p
TPS1	129.48941	142.840561	63.013725	72.081436	alpha,alpha-trehalose-ph
TPS2	59.571743	65.607445	36.926323	33.435818	trehalose-phosphatase
TPS3	46.682594	57.013153	31.705864	23.387896	trehalose 6-phosphate sy
TPT1	27.145744	38.610577	30.74984	28.811903	tRNA 2'-phosphot

TRA1	12.766251	11.946436	25.791544	29.715857	histone acetyltransferase
TRK1	28.504694	28.333969	26.150789	22.697865	trk family potassium upta
TRM1	7.241153	6.601499	12.970392	9.482486	tRNA (guanine26-N2)-di
TRM12	19.767891	17.23107	32.930634	35.735954	Trm12p
TRM2	26.095802	21.242638	9.872859	19.195885	Trm2p
TRM9	30.717495	24.579849	34.452702	20.672049	tRNA (carboxymethyluric
TRP1	45.474827	49.815563	52.93541	40.406857	phosphoribosylanthranila
TRP2	25.035011	25.58724	26.349543	27.666349	anthranilate synthase
TRP3	15.727109	17.05047	28.339359	25.121328	bifunctional anthranilate
TRP4	20.347334	19.694885	27.537031	30.150991	anthranilate phosphoribo
TRP5	53.753616	54.722572	35.443642	31.679108	tryptophan synthase, par
TRP99	145.539246	134.565262	164.216934	172.959045	Trp99p
TRR1	109.475266	114.760048	1005.810242	949.017273	thioredoxin-disulfide redu
TRS20	8.324149	8.399549	12.911769	18.71373	TRAPP subunit
TRS33	53.719341	48.410381	52.646935	67.682526	Trs33p
TRX1	600.322876	627.61554	4671.248535	4713.486328	thioredoxin
TRX2	5.499036	10.025886	9.578614	23.985264	Trx2p
TRY2	17.051077	16.994892	26.232689	30.072901	Try2p
TRY3	107.209709	114.688095	22.24308	24.942476	Try3p
TRY4	109.082123	94.394135	26.557819	32.964046	hypothetical protein L150
TRY5	6.988062	5.426551	4.699359	2.854654	Try5p, partial
TRY6	26.438236	28.864166	4.873784	5.333868	Try6p
TSA1	756.857056	856.491089	2460.35083	2228.192627	thioredoxin peroxidase
TSA1B	749.474792	851.463806	2437.363525	2205.23999	thioredoxin peroxidase
TSC11	3.505767	2.740569	8.244444	11.271828	TORC2 complex subunit
TSC2	8.373673	9.604925	8.553503	9.424633	Tsc2p
TSM1	17.925224	16.645605	28.419426	33.034271	Tsm1p
TSR1	71.301079	63.133099	31.610949	31.816822	Tsr1p
TSR2	61.775497	54.218159	30.344589	38.714706	pre-rRNA-processing pro
TTR1	147.180679	209.040482	534.102722	488.309326	dithiol glutaredoxin
TUB1	227.93782	281.040253	710.521851	672.582886	tubulin alpha chain, puta
TUB2	180.48262	211.412201	513.457947	507.061249	beta-tubulin
TUB4	12.781597	11.585343	64.272148	59.254883	RecName: Full=Tubulin
TUF1	362.186737	364.646667	801.243713	780.565918	translation elongation fac
TUP1	285.338501	253.439148	532.271606	546.552551	transcriptional repressor
TUS1	20.399448	18.944777	29.648243	33.958687	hypothetical protein MEM
TVP18	111.836563	118.344788	157.628342	133.837967	Tvp18p
TYE7	744.857239	827.143799	70.69854	75.206573	Tye7p
TYR1	9.386926	20.147114	24.664614	29.098034	prephenate dehydrogena
TYS1	114.991608	119.282974	78.654678	74.42112	tyrosine--tRNA ligase
UAP1	82.617279	100.751152	29.697849	28.0224	UDP-N-acetylglucosamin
UBA1	46.588043	47.345943	59.429218	72.481094	ubiquitin-activating enzy
UBA2	13.104291	14.15864	26.049088	28.49246	E1 ubiquitin-activating pr
UBA4	12.004144	15.685619	26.925165	19.880016	Uba4p
UBC15	65.464645	60.103817	63.932106	75.457832	Ubc15p
UBC4	261.547485	245.986679	305.000336	368.692291	ubiquitin-conjugating enz
UBC8	108.962051	109.017723	204.832214	227.180573	E2 ubiquitin-conjugating
UBI3	1549.849243	1633.10498	1747.561523	1529.252319	polyubiquitin
UBI4	5514.288574	5843.355469	3040.8396	3394.841797	ubiquitin
UBP1	22.260824	22.049295	16.161055	19.900055	ubiquitin-specific proteas
UBP13	17.127537	13.567992	30.343872	32.547173	ubiquitin-specific proteas
UBP6	53.754105	52.248108	70.23085	69.302849	ubiquitin-specific proteas
UBR1	12.861572	12.56876	14.675081	16.407097	E3 ubiquitin-protein ligas
UCF1	11591.79297	13701.92481	9929.823242	9532.81543	Ucf1p
UEC1	11.030628	7.742646	10.93179	10.514467	Uec1p
UFE1	57.98782	56.563965	90.092751	84.947021	Ufe1p
UGA1	35.220505	30.961849	46.394405	46.636486	4-aminobutyrate transam
UGA11	42.892845	36.165871	18.386465	14.828798	4-aminobutyrate aminotr
UGA2	39.427025	42.100922	46.629601	40.595497	Uga2p
UGA3	95.280334	103.256683	41.765594	51.786789	Uga3p
UGA32	4.826499	8.422114	12.204889	14.737142	Uga32p
UGA33	8.279806	11.175026	18.049688	18.672163	Uga33p
UGA4	3.712486	1.585632	1.209897	0.997514	Uga4p
UGA6	4.229203	4.682409	5.400059	2.726248	Uga6p

UGP1	108.926117	121.12973	72.881477	68.025574	UTP glucose-1-phospha
UGT51C1	10.000834	9.117546	6.502256	8.474937	sterol 3-beta-glucosyltra
ULP1	19.03536	19.728216	16.673216	18.81563	Ulp1p
ULP2	18.957222	25.746759	29.096622	28.035448	SUMO protease
ULP3	9.226706	5.541598	9.272317	15.291697	SUMO protease
UME1	33.379364	38.720406	71.906311	62.507462	Ume1p
UME6	0.396631	0.67479	3.369357	2.951061	Ume6p
UME7	0.992969	1.597572	1.359146	2.230152	DNA-binding transcriptio
UPC2	45.553265	42.139515	50.394493	46.064964	Upc2
URA1	86.085114	74.55101	120.475151	107.098816	dihydroorotate dehydrog
URA2	16.528219	19.971992	16.435322	18.579338	bifunctional carbamoylph
URA3	30.757524	29.799826	43.917107	45.858959	orotidine-5'-phosp
URA4	43.247036	53.217827	62.373791	60.875847	dihydroorotase
URA5	44.969296	54.723785	41.800205	60.394569	orotate phosphoribosyltr
URA6	38.694057	54.268284	43.643482	54.876289	bifunctional uridylate/ade
URA7	121.130684	123.217598	84.167587	77.919685	CTP synthase
URE2	54.58408	53.157761	43.644642	56.432735	protein URE2
URK1	19.07403	27.461348	11.234238	10.652897	uridine kinase
USO1	7.250327	6.820182	10.354805	10.704562	hypothetical protein MEM
USO5	9.452153	8.437295	25.932291	36.673851	Uso5p
USO6	19.143009	17.375933	29.426029	31.689901	Uso6p
UTP13	28.702545	29.442883	18.506367	22.89604	Utp13p
UTP15	70.269867	80.7883	40.962353	38.474773	snoRNA-binding rRNA-p
UTP18	112.265053	105.625465	36.892982	42.978897	Utp18p
UTP20	6.997444	7.647772	7.551357	7.611613	Utp20p
UTP21	71.841797	72.142937	32.009327	28.912304	rRNA-processing protein
UTP22	52.004509	46.783123	31.368738	38.256336	rRNA-processing protein
UTP4	66.544601	58.49564	25.704313	28.37641	Utp4p
UTP5	46.10503	44.252312	28.054344	31.842312	Utp5p
UTP8	91.205261	89.888779	39.605106	38.82571	Utp8p
UTP9	132.730728	138.268005	62.838692	59.550106	Utp9p
UTR2	478.494843	423.672516	156.145355	144.578232	hypothetical protein MEQ
VAC7	10.368428	12.223123	9.347231	12.235474	Vac7p
VAC8	144.533127	160.934692	89.943336	87.111366	protein anchor
VAM3	9.474667	13.261288	44.558434	38.194302	SNAP receptor
VAN1	46.401043	52.799458	35.586449	33.386318	vanadate resistance prot
VAS1	32.329338	33.065979	59.556511	56.599422	valine--tRNA ligase
VCX1	52.754593	52.022175	31.108419	27.243134	Vcx1p
VID21	42.656532	29.784637	72.59391	67.436783	Vid21p
VID27	64.265968	82.331482	134.797256	80.867332	hypothetical protein MG9
VMA10	241.035294	237.638443	296.128021	282.936157	H(+)-transporting V1 sec
VMA11	96.392303	79.378876	108.381561	116.841423	H(+)-transporting V0 sec
VMA13	57.200905	56.199692	58.527462	62.503223	V-type H+-transporting A
VMA2	176.753754	168.847	167.01593	168.240311	H(+)-transporting V1 sec
VMA22	6.447453	7.208882	16.105579	25.377325	Vma22p
VMA4	138.927567	143.781906	175.497589	158.819595	H(+)-transporting V1 sec
VMA5	46.052341	51.006348	66.110374	81.914597	H(+)-transporting V1 sec
VMA7	79.510048	69.128189	118.763191	125.490791	V-ATPase F subunit, put
VMA8	81.832664	75.744797	115.109474	118.831055	H(+)-transporting V1 sec
VPH1	47.584396	43.764084	52.310848	48.201454	H(+)-transporting V0 sec
VPH2	16.436081	10.411374	29.977072	41.267056	Vph2p
VPS1	88.4757	84.066666	162.473984	150.941818	dynamin-like GTPase
VPS11	10.637843	9.32786	15.410715	20.154903	hypothetical protein MEK
VPS13	7.920505	7.189667	13.058419	10.785919	membrane morphogenes
VPS15	4.70157	5.540934	9.478291	8.806326	ubiquitin-binding serine/t
VPS16	10.721582	9.021301	15.975737	16.780432	tethering complex subun
VPS17	16.185631	16.514605	25.926357	26.627346	hypothetical protein MG7
VPS2	25.298416	30.763792	51.840752	51.615437	ESCRT-III subunit protei
VPS20	52.478683	52.967205	24.748678	19.822626	ESCRT-III subunit protei
VPS21	423.610596	391.739136	297.08728	233.957504	Rab family GTPase
VPS22	7.257738	9.642697	12.163329	9.694662	ESCRT-II subunit protein
VPS23	11.128092	9.447502	15.398221	22.742611	ubiquitin-binding ESCRT
VPS24	167.718262	197.59227	341.854401	294.523987	charged multivesicular b
VPS27	28.930653	30.454605	31.361889	28.448689	vacuolar protein sorting-

VPS28	56.657284	58.049026	64.879242	76.922333	ESCRT-I complex subur
VPS33	6.574856	7.249442	18.670019	16.269232	tethering complex ATP-b
VPS34	6.596653	5.860888	11.75599	9.281057	phosphatidylinositol 3-kir
VPS35	15.754017	21.469488	30.558395	36.621758	retromer subunit
VPS36	6.810626	9.851522	15.236026	14.483116	ESCRT-II subunit proteir
VPS4	31.620392	29.548246	55.157799	38.811848	vacuolar protein sorting-
VPS41	8.642412	9.154938	13.702059	14.721985	Vps41p
VPS51	6.04888	7.633988	20.15601	22.3039	Vps51p
VPS52	14.554355	18.144239	25.004915	25.146812	Vps52p
VPS53	20.687695	24.277111	53.09259	45.71196	hypothetical protein MG1
VPS70	21.530672	19.480137	7.192024	10.449512	putative zinc metalloprot
VPS8	3.444132	3.882551	10.540107	9.375777	CORVET complex mem
VRG4	112.680328	116.315788	160.141907	169.49025	GDP-mannose transport
VRP1	24.685204	23.247107	27.261694	29.036421	hypothetical protein MG1
VTC3	172.308243	148.896088	24.456663	25.227615	vacuolar transporter cha
VTC4	254.759964	224.053757	119.0196	108.218498	Vtc4p
VTI1	94.984879	93.750061	144.116669	131.268005	v-SNARE protein
WAL1	42.22559	35.92168	56.013748	57.553932	hypothetical protein MEU
WAR1	11.142288	11.672554	10.881077	15.197623	War1p
WBP1	85.625351	72.673401	109.087479	118.287178	dolichyl-diphosphooligos
WH11	142.510147	123.726082	4.217437	3.004082	white colony protein, put
WHI3	155.095459	143.68718	206.737106	226.68924	mRNA-binding protein
WOR1	24.351059	29.188322	16.734482	15.661661	hypothetical protein MG
WOR2	229.168869	245.148575	31.129986	30.969669	Wor2p
WOR3	9.382634	8.786388	1.429381	1.822156	Wor3p
WOR4	48.673031	52.258495	13.401878	9.071218	Wor4p
WRS1	15.792123	22.541447	26.982899	42.023232	tryptophan--tRNA ligase
WSC1	142.183899	154.75296	70.005997	68.328278	conserved hypothetical
WSC2	102.588516	101.422455	7.1178	6.703017	cell wall integrity and str
WSC4	24.442545	20.8773	15.353105	11.63227	hypothetical protein MEV
XKS1	17.448467	17.338108	16.300915	23.513285	xylulokinase
XOG1	49.107746	54.167187	46.635616	44.932125	glucan 1,3-beta-glucosid
XUT1	1.936782	2.809378	1.398188	1.80889	Xut1p
XYL2	752.628235	706.833923	740.881409	557.201416	L-iditol 2-dehydrogenase
YAE1	18.053728	25.283998	36.969112	40.808384	Yae1p
YAF9	25.692932	33.762642	50.14529	53.42878	Yaf9p
YAH1	36.042938	58.192482	64.476967	78.039352	adrenodoxin
YAK1	49.58971	48.690884	24.45694	28.860117	serine/threonine protein
YBL053	4.423805	4.130941	17.738522	16.553127	Ybl053p
YBN5	167.883682	161.747742	208.016937	204.691895	Obg-like ATPase
YBP1	17.770903	22.490751	30.182232	32.008961	Ybp1p
YCF1	47.650768	48.593983	32.706333	38.699673	ATP-binding cassette gl
YCG1	4.065008	3.716784	13.060053	12.985372	condensin subunit
YCK2	159.949005	192.337433	156.126877	163.434235	casein kinase 1
YCP4	102.047066	99.907532	70.257988	62.537792	flavodoxin-like fold famil
YCS4	8.229587	8.252257	32.375607	30.366957	condensin subunit
YDC1	33.6553	37.607212	35.749569	36.347118	alkaline dihydroceramid
YDJ1	407.381866	431.046936	232.280289	189.493454	chaperone DnaJ
YEA4	5.446702	7.374176	6.399129	4.302702	Yea4p
YFH1	51.493698	47.978588	131.077682	96.325653	ferroxidase
YHB1	14278.18262	15022.04004	4066.991211	4073.736328	conserved hypothetical
YHB4	14.371196	17.780483	14.0787	14.673796	Yhb4p
YHB5	44.15028	51.332588	6.966789	11.187621	Yhb5p
YHM1	111.870438	120.713943	177.958054	172.805374	Yhm1p
YHM2	111.492958	115.988853	87.223839	77.042946	mitochondrial DNA replic
YIM1	78.894997	86.779907	47.12051	52.573589	Yim1p
YKE2	150.590286	159.772766	65.479515	65.686775	hypothetical protein MEV
YKT6	57.412861	76.778488	101.384171	78.949486	palmitoyltransferase
YKU80	10.656392	9.87172	17.643085	20.757654	ATP-dependent DNA he
YMC1	24.159409	32.013275	9.370605	10.785024	organic acid transporter
YMC2	14.10546	15.322455	5.831547	7.759429	Ymc2p
YME1	269.096924	282.551178	425.132324	327.108124	i-AAA protease
YML6	43.36504	49.847885	81.244751	79.582085	hypothetical protein MG
YMX6	2.2986	2.619568	4.091014	6.008839	NADH dehydrogenase

YNK1	349.861176	384.354065	406.632538	291.99234	nucleoside diphosphate
YOR1	14.088752	15.185257	12.789138	13.487244	hypothetical protein MGE
YOX1	26.278933	30.602888	195.163208	223.611176	Yox1p
YPD1	62.334389	56.898518	177.465744	135.58374	Ypd1p
YPS7	16.96427	19.330612	45.575027	38.558571	hypothetical protein W5C
YPT1	336.302338	356.903137	520.293884	454.746948	hypothetical protein JA1_
YPT31	156.22377	160.016525	143.704773	152.92218	GTP-binding protein, put
YPT52	64.717773	71.025337	60.017166	73.366035	Rab family GTPase
YPT53	72.482552	77.166435	55.157799	41.663094	Rab family GTPase
YPT7	18.042744	16.500607	38.917534	28.420153	small GTP-binding prote
YPT72	82.555038	75.503685	122.36187	121.983528	Rab family GTPase
YRB1	227.314911	224.740585	210.255325	252.245239	ran-binding protein 1
YSA1	32.177921	26.378597	56.695892	79.986496	ADP-ribose diphosphata
YST1	978.755371	993.946899	943.368652	925.065613	Yst1 predicted ribosome
YTA6	22.545918	20.287519	13.191785	17.65596	putative AAA family ATP
YTH1	580.631897	604.430359	575.873474	622.717041	cleavage polyadenylatio
YTM1	84.448921	71.675713	38.340912	37.237091	Ytm1p
YUH2	43.207935	36.830654	79.609741	92.940941	ubiquitin carboxyl-termin
YVC1	33.267597	33.930546	17.083897	15.150817	Yvc1p
YVH1	30.259321	41.616501	24.143349	28.013983	tyrosine protein phospha
YWP1	65.23217	67.326836	75.560837	95.789192	Ywp1p
ZCF1	5.101785	6.700003	6.3598	4.370404	Zcf1p
ZCF10	6.720707	5.721849	15.052579	16.759779	putative transcription fac
ZCF11	10.827899	10.618724	14.885381	15.456145	hypothetical protein MG
ZCF13	10.954396	11.346054	6.179813	7.514512	Zcf13p
ZCF14	2.049349	2.029753	6.558828	5.52486	Zcf14p
ZCF15	10.299324	9.325943	7.047698	8.344589	hypothetical protein MEV
ZCF16	11.254557	10.340508	17.261063	23.209188	Zcf16p
ZCF17	18.148985	20.424015	6.992419	9.94662	Zcf17p
ZCF18	10.211889	10.06252	15.523666	12.096718	Zcf18p
ZCF19	1.484241	1.0699	2.244109	2.008345	Zcf19p
ZCF2	101.02684	125.5979	28.430614	33.006721	Zcf2p
ZCF20	12.762973	12.312633	19.681787	17.858463	hypothetical protein MG
ZCF21	112.440926	111.501404	35.813812	46.127277	Zcf21p
ZCF22	1.637564	2.012225	0.139525	0.934054	Zcf22p
ZCF23	22.183191	24.655781	43.965931	46.203888	Zcf23p
ZCF24	4.270597	7.020598	9.57308	11.903823	Zcf24p
ZCF25	5.363149	6.426888	0.976468	2.301811	Zcf25p
ZCF26	5.671046	3.577922	2.870168	3.515775	hypothetical protein MEV
ZCF27	9.599334	11.538088	5.955278	7.023252	hypothetical protein MEV
ZCF28	7.193803	4.286727	15.552907	16.408466	Zcf28p, partial
ZCF29	73.636902	73.232864	64.156136	60.782627	Zcf29p
ZCF3	333.10257	322.760773	75.579796	97.8078	conserved hypothetical p
ZCF30	19.615803	19.178713	8.194871	8.046665	Zcf30p
ZCF31	16.841034	17.921698	12.152243	12.96486	hypothetical protein I503
ZCF32	9.327533	10.774552	12.713509	12.349737	Zcf32p
ZCF35	6.55831	5.217796	7.887665	7.581808	Zcf35p
ZCF38	13.538812	14.171306	14.302931	10.676511	hypothetical protein MG7
ZCF39	47.662888	55.827206	55.91745	55.533176	Zcf39p
ZCF4	3.186133	3.075614	1.218783	1.843135	hypothetical protein MG3
ZCF5	5.858248	5.599063	7.935024	9.557094	Zcf5p
ZCF6	7.722052	8.637337	10.481792	14.401351	hypothetical protein I503
ZCF7	4.094266	3.578763	11.48401	15.412467	Zcf7p
ZCF8	9.159908	10.617517	21.7094	25.816467	Zcf8p
ZCF9	40.203625	37.515064	8.496638	11.871173	Zcf9p
ZDS1	16.230055	15.398592	19.873837	27.269098	Zds1p
ZFU2	28.871824	37.454269	4.386928	6.910871	Zfu2p
ZNC1	11.143922	11.013956	22.991774	24.727955	Znc1p
ZPR1	77.438568	88.202637	65.230217	53.091084	zinc finger-containing pr
ZRT1	511.562317	477.087006	0.157051	1.725055	ZIP zinc/iron transporter
ZRT2	5438.933105	5899.486816	95.687103	72.997322	low-affinity Zn(2+) transp
ZSF1	307.929596	354.799591	1060.037842	1003.151306	Zsf1p
ZUO1	152.920609	171.10994	109.174606	101.025024	zuotin
ZWF1	72.223549	102.968979	62.531063	69.557114	glucose-6-phosphate de

Function_annotation
Vacuolar aspartic proteinase; transcript equivalent in yeast-form and mycelial cells but is elevated at lower g
Septin, required for wild-type invasive growth in vitro but not required for virulence in a mouse model of syst
Possible regulatory protein; possible adhesin-like; Glu-rich domain; production in S. cerevisiae increases er
Adenine deaminase; purine salvage and nitrogen catabolism; colony morphology-related regulation by Ssn6
Putative amino acid permease; fungal-specific; possibly essential, disruptants not obtained by UAU1 metho
Aspartate aminotransferase; soluble protein in hyphae; macrophage-induced protein; alkaline upregulated;
Putative aspartate aminotransferase; stationary phase enriched protein; Gcn4-regulated; Spider biofilm indu
Aspartate aminotransferase; nitrogen metabolism; similar but not orthologous to S. cerevisiae Aat2; clade-a
Putative ubiquinol-cytochrome-c reductase; induced upon adherence to polystyrene; flow model biofilm indu
SAM-dependent RNA methyltransferase; methylates mRNA 5' cap; binds phosphorylated RNA Pol II C-term
Vacuolar membrane protein; depletion causes abnormal vacuolar morphology, cell separation defect, sensi
Ortholog of S. cerevisiae Abp1; actin-binding protein of the cortical actin cytoskeleton; caspofungin induced
Ortholog of S. cerevisiae actin-binding protein Abp140; Hap43-induced; F-12/CO2 early biofilm induced
Putative alpha-actinin-like protein; induced by alpha pheromone in SpiderM medium
Ortholog(s) have 4-amino-4-deoxychorismate synthase activity and role in para-aminobenzoic acid biosynth
Protein similar to a region of acyl-coenzyme-A-binding protein; amphotericin B repressed; regulated by Nrg1
Putative acetyl-coenzyme-A carboxylases; regulated by Efg1; amphotericin B repressed; caspofungin repre
Transcription factor; similar to S. cerevisiae Ace2 and Swi5; regulates morphogenesis, cell separation, adhe
Putative endo-1,3-beta-glucanase; fungal-specific (no human or murine homolog)
Acetyl-coA hydrolase; acetate utilization; nonessential; soluble protein in hyphae; antigenic in human; induc
Aconitase; induced in high iron; 2 upstream CCAAT motifs; amino acid starvation (3-AT), amphotericin B, p
Putative aconitate hydratase 2; induced in high iron; regulated by Gcn4; repressed by amino acid starvation
Putative mitochondrial acyl carrier protein involved in fatty acid biosynthesis; shows colony morphology-rela
Putative mitochondrial acyl carrier protein
Acetyl-CoA synthetase; induced by human neutrophils; fluconazole-repressed; regulated by Nrg1/Mig1; colo
Acetyl-CoA synthetase; antigenic during human and murine infection; induced by Efg1; macrophage-induce
Actin; gene has intron; transcript regulated by growth phase, starvation; at polarized growth site in budding a
Zinc finger and homeodomain transcriptional coactivator; role in cell wall integrity and in sensitivity to caspo
Protein of unknown function; transcription is specific to white cell type
Phosphoribosylaminoimadazole succinocarboxamide synthetase, enzyme of adenine biosynthesis; not indu
Adenylosuccinate synthase; upregulated in biofilm; decreased expression in hyphae vs yeast-form cells; no
Adenylosuccinate lyase; enzyme of adenine biosynthesis; soluble protein in hyphae; not induced during GC
5-Aminoimidazole-4-carboxamide ribotide transformylase, enzyme of adenine biosynthesis; antigenic in hur
Phosphoribosylaminoimadazole carboxylase; role in adenine biosynthesis; required for normal growth and v
Putative phosphoribosylpyrophosphate amidotransferase; flucytosine induced
Phosphoribosylamine-glycine ligase and phosphoribosylformylglycinamidine cyclo-ligase; interacts with Vps
5-Phosphoribosylformyl glycinamidine synthetase; adenine biosynthesis; not induced in GCN response, in c
Putative phosphoribosylglycinamide formyl-transferase, enzyme of amino acid biosynthesis pathway; upreg
Alcohol dehydrogenase; oxidizes ethanol to acetaldehyde; at yeast cell surface; immunogenic in humans/m
Alcohol dehydrogenase; soluble in hyphae; expression regulated by white-opaque switching; regulated by S
Putative NAD-dependent (R,R)-butanediol dehydrogenase; regulated by white-opaque switch; induced by n
Predicted 3-hydroxyacyl-CoA dehydrogenase; transcript is increased in azole-resistant strain overexpressin
Putative alcohol dehydrogenase; regulated by white-opaque switch; fluconazole-induced; antigenic in murin
Putative adenylate kinase; repressed in hyphae; macrophage-induced protein; adenylate kinase release use
Adenosine kinase; heterozygous null mutant is resistant to cordycepin in C. albicans fitness test; ketoconaz
Putative PDR-subfamily ABC transporter; similar to WHITE subfamily proteins; gene used for strain identific
C2H2 transcription factor; ortholog of S. cerevisiae Adr1 but mutant phenotype suggests a different set of ta
Putative mitochondrial ATPase of the AAA family; similar but not orthologous to S. cerevisiae Afg1; mutant
Similar to S. cerevisiae Afg3p, a subunit of the mitochondrial inner membrane m-AAA protease; likely to be
Predicted inositol polyphosphate kinase, involved in autophagy, energy metabolism, virulence
Agmatinase, involved in metabolism of agmatine; downregulated upon adherence to polystyrene; regulated
Putative Aft domain transcription factor; role in regulation of iron metabolism, oxidative stress, adhesion, hy
Protein with some similarity to agglutinin subunit; expression regulated upon white-opaque switch; Spider bi
Putative mitochondrial carrier protein; transcript is alkaline upregulated rat catheter biofilm induced
Putative GTPase activator; induced in low iron; rat catheter biofilm repressed
Ortholog(s) have GTPase activator activity and role in endoplasmic reticulum to Golgi vesicle-mediated tran
Putative ADP-ribosylation factor GTPase activating protein, functional ortholog of S. cerevisiae GCS1; muta
Phosphoacetylglucosamine mutase (N-acetylglucosamine-phosphate mutase); enzyme of UDP-N-acetylglu
Putative Argonaute protein involved in RNA silencing; hyphal-induced expression; regulated by Cyr1, Ras1,
Amino acid permease; hyphal repressed; white-opaque switch regulated; induced in core caspofungin respo
Putative serine transporter; possible role in assimilation of sulfur; F-12/CO2 early biofilm induced
Putative Hsp90p co-chaperone; Hap43-repressed; heavy metal (cadmium) stress-induced; oxidative stress

Alkyl hydroperoxide reductase; immunogenic; fluconazole-induced; amphotericin B, caspofungin, alkaline re
Putative thiol-specific peroxiredoxin; macrophage-downregulated gene
Zn(II)2Cys6 transcription factor; involved in regulation of adhesion genes; involved in white-opaque switch;
Putative actin interacting protein; regulated by Gcn4; induced in response to amino acid starvation (3-AT); r
Putative serine/threonine protein kinase; induced during the mating process
Ankyrin-repeat protein; induced by fluphenazine
Alanyl-tRNA synthetase; translational regulation generates cytoplasmic and mitochondrial forms; Gcn4p-reg
NAD-aldehyde dehydrogenase; decreased expression in fluconazole-resistant isolate, or in hyphae; biofilm
Putative aldehyde dehydrogenase; stationary phase enriched protein; expression regulated upon white-opa
Protein similar to S. cerevisiae Alg1p, a mannosyltransferase involved in N-linked protein glycosylation; likel
Alpha-1,2-mannosyltransferase; catalyzes sequential addition of 2 terminal alpha 1,2-mannose residues to
Putative mannosyltransferase involved in cell wall mannan biosynthesis; transcription is elevated in chk1, ni
Putative glucosyltransferase involved in cell wall mannan biosynthesis; possibly an essential gene, disrupta
Putative glucosyltransferase involved in cell wall mannan biosynthesis; transcription is elevated in chk1, nik
Protein involved in cell wall mannan biosynthesis; mutation confers hypersensitivity to tunicamycin; transcrip
Putative glucosyltransferase involved in cell wall mannan biosynthesis; transcription is elevated in nik1 and
Putative mannosyltransferase; similar to S. cerevisiae Alg9p; has HKEXRF motif
Putative NADH-ubiquinone oxidoreductase; in detergent-resistant membrane fraction (possible lipid raft cor
N-Alkane inducible cytochrome P450
Putative cytochrome P-450 of N-alkane-induced detoxification; macrophage-induced gene
Alkane-inducible cytochrome P450; catalyzes hydroxylation of lauric acid to hydroxylauric acid; overproduct
D-Arabinono-1,4-lactone oxidase involved in biosynthesis of dehydro-D-arabinono-1,4-lactone, which has a
Cystine transporter; present in pathogenic yeasts (no human or murine homolog); Spider biofilm induced
Putative transporter of divalent cations; hyphal-induced expression; rat catheter biofilm induced
Cell-surface adhesin; adhesion, virulence, immunoprotective roles; band at hyphal base; Rfg1, Ssk1, Spide
ALS family protein; role in adhesion, biofilm formation, germ tube induction; expressed at infection of huma
Cell wall adhesin; epithelial adhesion, endothelial invasion; alleles vary in adhesiveness; immunoprotective
GPI-anchored adhesin; role in adhesion, germ tube induction; growth, temperature regulated; expressed du
ALS family adhesin; highly variable; expression in S. cerevisiae causes adhesion to human epithelium, end
ALS family protein; expression in S. cerevisiae confers adhesion to gelatin; macrophage-induced gene; N-te
ALS family protein; hypermutable contingency gene; growth-regulated, downregulated in biofilm; two variab
ALS family cell-surface glycoprotein; expressed during infection of human epithelial cells; confers laminin a
Putative alanine transaminase; mutation confers hypersensitivity to 5-fluorocytosine (5-FC); rat catheter an
Putative negative regulator of exit from mitosis; Plc1-regulated; rat catheter biofilm induced
Putative peroxisomal copper amine oxidase
Protein similar to A. niger predicted peroxisomal copper amino oxidase; mutation confers hypersensitivity to
Putative alpha-mannosidase; transcript regulated by Nrg1; induced during cell wall regeneration; flow mode
Translation initiation factor eIF-5A; repressed in hyphae vs yeast cells; downregulated upon phagocytosis b
Putative mannosyltransferase of Golgi; member of Mnn9p family; similar to S. cerevisiae Anp1p; fungal-spe
Peroxisomal adenine nucleotide transporter; role in beta-oxidation of medium-chain fatty acid and peroxiso
Alternative oxidase; low abundance; constitutively expressed; one of two isoforms (Aox1p and Aox2p); invo
Alternative oxidase; cyanide-resistant respiration; induced by antimycin A, oxidants; growth; Hap43, chlamy
Putative ATP adenylyltransferase II; regulated by Gcn4; repressed by amino acid starvation (3-AT); induce
Putative Anaphase-Promoting Complex/Cyclosome subunit; essential for growth; periodic mRNA expressio
Neutral arginine, alanine, leucine specific metallo-aminopeptidase; purified from cell wall/intracellular fractio
Putative vacuolar aminopeptidase Y,; regulated by Gcn2 and Gcn4; rat catheter and Spider biofilm represse
Ortholog(s) have Atg12 activating enzyme activity, Atg8 activating enzyme activity
Phosphorylated protein of unknown function; mutation confers hypersensitivity to toxic ergosterol analog
Predicted gamma-adaptin, large subunit of the clathrin-associated protein (AP-1) complex; that binds clathr
Ortholog of S. cerevisiae and S. pombe Apl5; subunit of the AP-3 adaptor complex involved in Golgi-to-vac
Ortholog of S. cerevisiae/S. pombe Apm1; a clathrin-associated protein complex (AP-1) subunit; phosphory
Cargo-binding subunit of the clathrin associated protein complex (AP-2), involved in endocytosis; regulates
Ortholog of S. cerevisiae Apn1; an AP endonuclease; transcript induced by interaction with macrophages; f
Putative class II abasic (AP) endonuclease; flucytosine induced
Component of the adaptor complex AP-3, which is involved in vacuolar protein sorting
Adenine phosphoribosyltransferase; flucytosine induced; repressed by nitric oxide; protein level decreased
Aquaporin water channel; osmotic shock resistance, WT freeze tolerance; virulent in mice; flucytosine repre
D-Arabinose dehydrogenase; dehydro-D-arabinono-1,4-lactone synthesis; active on D-arabinose, L-fucose,
Putative G4 nucleic acid binding protein; macrophage/pseudohyphal-repressed; protein enriched in stationa
Putative ARP2/3 complex subunit; mutation confers hypersensitivity to cytochalasin D
Putative ARP2/3 complex subunit; mutation confers hypersensitivity to cytochalasin D
Putative ARP2/3 complex subunit; Hap43-induced gene; mutation confers hypersensitivity to cytochalasin D
Putative ARP2/3 complex subunit; shows colony morphology-related gene regulation by Ssn6p; mutation co
Protein similar to S. cerevisiae Arc40; involved in actin filament organization in S. cerevisiae; transposon mu

D-arabitol dehydrogenase, NAD-dependent (ArDH); enzyme of D-arabitol and D-arabinose catabolism; D-a
Acyl CoA:sterol acyltransferase; uses cholesterol and oleoyl-CoA substrates; protoberberine derivative drug
Golgi-localized ADP-ribosylation factor involved in regulation of the ER-mitochondria encounter structure (E
Essential protein, putative ADP-ribosylation factor; involved in invasive growth; mutation confers hypersensi
Similar to but not orthologous to S. cerevisae Arf3; transcript filament induced; Tup1 regulated; rat catheter
Argininosuccinate synthase; arginine synthesis; Gcn4, Rim101 regulated; induced by amino acid starvation
Putative ornithine transporter of the mitochondrial inner membrane; induced during the mating process
Putative enzyme of arginine biosynthesis; transcription of genes of arginine biosynthesis pathway, except fo
Putative ornithine carbamoyltransferase; Gcn4-regulated; Hap43-induced; repressed in alkalinizing medium
Argininosuccinate lyase, catalyzes the final step in the arginine biosynthesis pathway; alkaline downregulate
Arginine biosynthetic enzyme; processed in S. cerevisiae into 2 polypeptides with acetylglutamate kinase (A
Putative acetylornithine aminotransferase; Gcn2, Gcn4 regulated; rat catheter biofilm induced; Spider biofilr
Zn(II)2Cys6 transcription factor; required for utilization of ornithine as a nitrogen source and for wild-type res
GAL4-like Zn(II)2Cys6 transcription factor; clade-associated expression; null shows abnormal regulation of
Putative adrenodoxin-NADPH oxidoreductase; role in heme biosynthesis
Putative GTPase in the late Golgi involved in regulation of polarized growth and secretion; mutation confers
Putative Ras superfamily GTPase; induced by nitric oxide independent of Yhb1p
Putative pentafunctional arom enzyme; required for aromatic amino acid biosynthesis; involved in cell wall i
Aromatic decarboxylase; Ehrlich fusel oil pathway of aromatic alcohol biosynthesis; alkaline repressed; prot
Putative chorismate synthase; fungal-specific (no human or murine homolog); protein level decreased in sta
3-deoxy-D-arabinoheptulosonate-7-phosphate synthase; aromatic amino acid synthesis; GCN-regulated; fe
3-deoxy-D-arabinoheptulosonate-7-phosphate synthase; aromatic amino acid biosynthesis; GCN-regulated
Putative chorismate mutase; fungal-specific (no human or murine homolog); alkaline upregulated
Aromatic transaminase of the Ehrlich fusel oil pathway of aromatic alcohol biosynthesis; Rim101 independe
Zn(II)2Cys6 transcription factor; transcriptional activator of aromatic amino acid catabolism; regulator of aro
Aromatic transaminase; Ehrlich fusel oil pathway of aromatic alcohol biosynthesis; Rim101-dependent pH-r
Putative centractin; induced upon adherence to polystyrene
Component of the Arp2/3 complex; required for virulence, hyphal growth, cell wall/cytoskeleton organizatior
Protein with Myo5p-dependent localization to cortical actin patches at hyphal tip; mutation confers hypersen
Subunit of the NuA4 histone acetyltransferase complex
Putative chromatin-remodeling enzyme complex protein; mutation confers hypersensitivity to toxic ergostero
Component of the RSC chromatin remodeling complex; similar to S. cerevisiae Arp3p, a component of the
Ortholog of S. cerevisiae Arr3; arsenite transporter of the plasma membrane required for resistance to arse
Lipid transporter involved in sterol trafficking and transport of glycosylphosphatidylinositol and sphingolipid p
Putative ribosomal large subunit biogenesis protein; repressed in core stress response; repressed by prosta
40S ribosomal subunit similar to G-beta subunits; glucose or N starvation induced filamentation; required fo
Putative microtubule-associated protein; member of conserved Mcm1p regulon; periodic mRNA expression
Protein similar to S. cerevisiae Asf1p, a chromatin assembly complex component; likely to be essential for g
Gal4p family zinc-finger transcription factor with similarity to S. cerevisiae Asg1p
a-cell specific protein of unknown function; two predicted transmembrane domains; member of conserved M
GATA-like transcription factor; localizes to daughter cell, hyphal tip cell nuclei; mRNA localization mediated
Ortholog(s) have histone methyltransferase activity (H3-K4 specific) activity
Essential subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kineto
Putative secreted acid sphingomyelin phosphodiesterase; possible Kex2 substrate; transcript increased in a
Putative asparagine synthetase; soluble protein in hyphae; regulated by Rim101; decreased expression at p
Heat shock protein; transcript regulated by cAMP, osmotic stress, ciclopirox olamine, ketoconazole; repress
Adenylyl cyclase and stress responsive protein; induced in cyr1 or ras1 mutant; stationary phase enriched p
Adenylyl cyclase and stress responsive protein; induced in cyr1 or ras1 mutant; Spider biofilm induced
Cell wall acid trehalase; catalyzes hydrolysis of the disaccharide trehalose; similar to S. cerevisiae vacuolar
Putative alcohol acetyltransferase; caspofungin repressed; expression depends on Tac1p
Putative protein serine/threonine kinase; predicted role in vesicle formation in autophagy and the cytoplasm
Putative lipase; fungal-specific (no human or murine homolog); Hap43p-repressed gene
Protein similar to S. cerevisiae Atg9; required for early step in autophagy; required for cytoplasm to vacuole
Member of MDR subfamily of ABC family; ortholog of S. cerevisiae ABC transporter, Atm1; induced in low i
Putative fungal-specific transmembrane protein; induced by Rgt1; Spider biofilm induced
Putative fungal-specific transmembrane protein; rat catheter and Spider biofilm induced
Putative fungal-specific transmembrane protein; fluconazole repressed, Hap43-repressed; flow model biofil
Putative fungal-specific transmembrane protein
Putative fungal-specific transmembrane protein
Putative fungal-specific transmembrane protein
Putative fungal-specific transmembrane protein
ATP synthase alpha subunit; antigenic in human/mouse; at hyphal surface; ciclopirox, ketoconazole, flucyto
Putative mitochondrial F1F0 ATP synthase subunit; macrophage/pseudohyphal-induced
Subunit of the mitochondrial F1F0 ATP synthase; sumoylation target; protein newly produced during adapta

Mitochondrial ATPase complex subunit; downregulated by Efg1p; flucytosine induced; caspofungin represse
F1F0 ATP synthase complex subunit; fungal-specific; gene has intron
Subunit k of the mitochondrial F1F0 ATP synthase; a large enzyme complex required for ATP synthesis; Sp
F1 beta subunit of F1F0 ATPase complex; antigenic in human, mice; induced by ciclopirox olamine; caspof
Putative mitochondrial ATP synthase; shows colony morphology-related gene regulation by Ssn6p; flucytos
F1-ATP synthase complex subunit; caspofungin repressed; flucytosine and macrophage/pseudohyphal-indu
Putative F0-ATP synthase subunit 4; macrophage/pseudohyphal-induced; present in exponential and statio
Putative F0-ATP synthase FO subunit B; caspofungin repressed; protein level decreased in stationary phas
Putative subunit of the F1F0-ATPase complex; colony morphology-related gene regulation by Ssn6; farneso
Protein required for modification of wobble nucleosides in tRNA; induced upon adherence to polystyrene; re
Putative cytosolic copper metallochaperone; flucytosine induced; Ssr1-repressed; rat catheter biofilm induc
Inositolphosphorylceramide (IPC) synthase; catalyzes the key step in sphingolipid biosynthesis; antifungal d
Putative autophagosome protein; acts synergistically with Ysy6p to regulate unfolded protein response and
Putative vacuolar transporter; promoter bound by a1p and alpha2p by ChIP-chip analysis
Putative vacuolar transporter of large neutral amino acids; induced by alpha pheromone in SpiderM mediun
Ortholog of S. cerevisiae Avt7 transporter; repressed upon adherence to polystyrene; constitutive expressio
Putative endoprotease; induced by alpha factor; transcript is upregulated in an RHE model of oral candidias
Ortholog of S. cerevisiae Axl2; a plasma membrane protein involved in determination of budding pattern; O-
Putative oxidoreductase; transcriptionally induced by interaction with macrophage; rat catheter biofilm repre
Putative NADPH-dependent 1-acyl dihydroxyacetone phosphate reductase; shows colony morphology-relat
Putative Myb-like transcription factor; ortholog S. cerevisiae Bas1, a regulator of purine biosynthetic genes;
Putative branched chain amino acid aminotransferase; regulated by Gcn4, Gcn2; induced in response to ar
Putative branched chain amino acid aminotransferase; regulated by Gcn4p; induced by farnesol treatment,
Putative SH3-domain-containing protein
Ortholog of S. cerevisiae Bck1; MAP kinase kinase kinase of cell integrity pathway; mutant is hypersensitive
Transcription factor; regulates a/alpha biofilm formation, matrix, cell-surface-associated genes; confers adh
Protein kinase A regulatory subunit; involved in regulation of filamentation, phenotypic switching and mating
Essential chromatin-binding bromodomain protein; repressed upon adherence to polystyrene; reduced mRN
Protein required for wild-type budding, hyphal growth, and virulence in a mouse systemic infection; suppres
Putative Rho1p GTPase activating protein (GAP); serum-induced transcript; Spider biofilm induced; flow mo
Putative GTPase-activating protein (GAP) for Rho-type GTPase Cdc42p; involved in cell signaling pathways
Putative Type II geranylgeranyltransferase beta subunit; transcript regulated by Mig1
Ortholog(s) have Rab geranylgeranyltransferase activity and role in endoplasmic reticulum to Golgi vesicle-
Ortholog(s) have GDP-dissociation inhibitor activity, GTPase activator activity, role in mitotic spindle orienta
Protein involved in the maintenance of normal ploidy; S. cerevisiae ortholog cofers Brefeldin A resistance; s
Cell wall 1,3-beta-glucosyltransferase; mutant has cell-wall and growth defects, but wild-type 1,3- or 1,6-bet
Putative glucanase; induced during cell wall regeneration
Endoplasmic reticulum (ER) protein; ortholog of S. cerevisiae Big1; required for beta-1,6-glucan synthesis,
Putative biotin synthase; induced by high iron; repressed by ciclopirox olamine; upregulated in clinical isolat
Putative class III aminotransferase with a predicted role in biotin biosynthesis; Spider biofilm induced
Putative proteasome activator; binds core proteasome and stimulates proteasome-mediated protein degrad
Protein of unknown function, serum-induced
Sole 14-3-3 protein in C. albicans; role in hyphal growth; possibly regulated by host interaction; localizes to
Putative GTPase; Hap43-induced gene; mutation confers resistance to 5-fluorocytosine (5-FC); flucytosine
Beta-mannosyltransferase, required for addition of the 1st beta-mannose residue to acid-stable fraction of c
Beta-mannosyltransferase; adds 2nd beta-mannose to the acid-stable fraction of cell wall phosphopeptidom
Beta-mannosyltransferase; for elongation of beta-mannose chains on the acid-labile fraction of cell wall pho
Putative beta-mannosyltransferase involved in beta-1,2-mannosylation of phospholipomannan; 9-member f
Beta-mannosyltransferase; beta-1,2-mannosylation of phospholipomannan; member of a 9-member family
Beta-mannosyltransferase, member of a 9-gene family that includes characterized genes BMT1, BMT2, BM
Putative beta-mannosyltransferase, member of a 9-gene family including characterized BMT genes with rol
Beta-mannosyltransferase, 9-gene family that includes characterized genes BMT1, BMT2, BMT3, and BMT
Putative kynurenine 3-monooxygenase, involved in NAD biosynthesis; transposon mutation affects filament
Formin; role in cytoskeletal organization, cell polarity; role in systemic virulence in mouse; cell-cycle regulate
Protein required for wild-type cell wall chitin distribution, morphology, hyphal growth; not essential; similar to
Formin; probable role in hyphal cytoskeletal polarity; synthetic lethality if Bnr1p and Bni1p are absent
Putative SH3-domain-containing protein; mutation confers hypersensitivity to toxic ergosterol analog; Spide
Ortholog of S. cerevisiae Bph1; a putative ortholog of human Chediak-Higashi syndrome protein and murine
Putative E3 ubiquitin ligase with RING-type zinc finger domain; involved in ubiquitination of histone H2B dur
Component of the general transcription factor for RNA polymerase III (TFIIIB); possibly an essential gene, c
Transcription factor; recruits Hda1 to hypha-specific promoters; Tn mutation affects filamentation; Hap43-re
Putative condensin complex subunit; cell-cycle regulated periodic mRNA expression
Class E vacuolar protein sorting factor; role in transport from multivesicular body to vacuole; not involved in
Ortholog of C. dubliniensis CD36 : Cd36_10780, C. parapsilosis CDC317 : CPAR2_208080, C. auris B8441

Putative geranylgeranyl diphosphate synthase; repressed by benomyl treatment; Spider biofilm induced
Putative cell cycle checkpoint kinase; mutation confers increased sensitivity to nocodazole
Ortholog(s) have GTPase activator activity
Protein similar to S. cerevisiae Bub3; a kinetochore checkpoint component; induced by hydroxyurea treatm
Putative SH3-domain-containing protein; predicted role in bud-site selection; Spider biofilm induced
Putative pyridoxal kinase; a key enzyme in pyridoxal 5'-phosphate synthesis, the active form of vitamin B6;
GTPase activating protein (GAP) for Rsr1; negative regulator of filament branching, acts in hyphal growth g
Protein similar to S. cerevisiae Bud20p, which affects bud site selection; transposon mutation affects filame
Small-subunit processome component; repressed by prostaglandins
Protein with a predicted role in 18S rRNA maturation and small ribosomal subunit biogenesis; repressed in
Putative methyltransferase; Hap43-induced; repressed by prostaglandins
Bud31 ortholog; not subject to mating-type regulation, in contrast to S. cerevisiae Bud31 which has a role in
Predicted GTP/GDP exchange factor for Rsr1; rat catheter biofilm induced
Protein required for Spitzenkorper formation in hyphal cells (wild-type localization of Mlc1p to the Spitzenko
Ortholog(s) have small GTPase binding activity and role in Golgi to plasma membrane protein transport, G
Protein similar but not orthologous to S. cerevisiae Bul1; a protein involved in selection of substrates for ubi
Protein with a predicted BUL1 N-terminal and C-terminal domains; Bul1 binds the ubiquitin ligase Rsp5 in S
Protein with similarity to S. cerevisiae Bur2p, contains a cyclin domain; not required for wild-type hyphal gro
Protein similar to S. cerevisiae Bzz1p, which is an SH3 domain protein involved in the regulation of actin po
Protein of unknown function; transcript detected on high-resolution tiling arrays
Protein of unknown function; transcript detected on high-resolution tiling arrays
Ortholog(s) have role in ascospore formation, ascospore wall assembly, ascospore-type prospore membra
Cardiolipin synthase; ortholog of S. cerevisiae Crd1; transcript is upregulated in clinical isolates from HIV+
Putative nucleolar protein with a predicted role in pre-rRNA processing and ribosome biogenesis; represse
Protein of unknown function; flow model biofilm induced; Spider biofilm induced
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
Ortholog(s) have unfolded protein binding activity, role in protein folding, protein localization to cell surface
Predicted ORF in retrotransposon Tca8 with similarity to the Gag region encoding nucleocapsid-like protein
Putative protein of unknown function; shows colony morphology-related gene regulation by Ssn6p
Ortholog(s) have cargo adaptor activity, role in intracellular protein transport, retrograde transport, endosom
Putative CCR4-Not complex transcription factor; ortholog of S. cerevisiae Cdc36; Hap43-repressed gene
Protein of unknown function
Ortholog(s) have peptide alpha-N-acetyltransferase activity and role in N-terminal peptidyl-methionine acety
Hexadecenal dehydrogenase; involved in the conversion of sphingosine 1-phosphate breakdown product h
RNA polymerase II holoenzyme/mediator subunit; regulated by Mig1, Tup1; amphotericin B, caspofungin re
Ortholog(s) have phosphatidylinositol-3,5-bisphosphate binding, phosphatidylinositol-3-phosphate binding,
Mitochondrial protein; component of the mitochondrial inner membrane organizing system ; role in maintena
Putative TIM23 translocase complex subunit; membrane-localized; Hap43-repressed
Ortholog(s) have role in N-acylethanolamine metabolic process, N-acylphosphatidylethanolamine metabolic
Ortholog(s) have 3-methyl-2-oxobutanoate hydroxymethyltransferase activity, role in pantothenate biosynth
Ortholog(s) have phosphatase activity and role in dephosphorylation
Ortholog of C. dubliniensis CD36 : Cd36_00460, C. parapsilosis CDC317 : CPAR2_800010, Candida tenui
Protein with a Bul1 domain; binds the ubiquitin ligase Rsp5 and is involved in intracellular trafficking of a ge
Ortholog(s) have protein kinase activator activity and role in chromosome segregation, protein phosphoryla
Protein of unknown function; Spider biofilm induced
Has domain(s) with predicted UDP-N-acetylmuramate dehydrogenase activity, catalytic activity, flavin aden
Ortholog(s) have SNAP receptor activity
Protein of unknown function; repressed by nitric oxide
Protein of unknown function; transcript detected on high-resolution tiling arrays
Ortholog of C. dubliniensis CD36 : Cd36_00740, C. parapsilosis CDC317 : CPAR2_110170, C. auris B8441
Ortholog(s) have N-acetylglucosaminyldiphosphodolichol N-acetylglucosaminyltransferase activity and role
Ortholog of C. dubliniensis CD36 : Cd36_00770, C. auris B8441 : B9J08_004942, Candida tenuis NRRL Y-
Protein with a predicted multidrug transporter domain; Hap43-repressed gene
Ortholog(s) have Atg8 ligase activity
Protein of unknown function; Spider biofilm induced
Putative outer mitochondrial membrane GTPase, subunit of the ERMES complex; required for mitochondri
Has domain(s) with predicted DNA binding activity
Ortholog(s) have phosphatidylinositol-4,5-bisphosphate binding, phosphatidylserine binding activity and role
Ortholog of C. dubliniensis CD36 : Cd36_00920, Debaryomyces hansenii CBS767 : DEHA2F20724g, Pichi
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit, mito
Phosphorylated protein of unknown function
Plasma membrane-localized protein; repressed by nitric oxide; Hap43p-repressed gene
Ortholog(s) have peptide-methionine (R)-S-oxide reductase activity, role in cellular response to oxidative st
Putative enoyl reductase involved in very long chain fatty acid elongation; possibly an essential gene, disrup

Has domain(s) with predicted role in cell division, chromosome segregation and MIS12/MIND type complex
Ortholog of C. dubliniensis CD36 : Cd36_01020, C. parapsilosis CDC317 : CPAR2_110130, C. auris B8441
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Putative ubiquitin ligase complex component; induced by heavy metal (cadmium) stress; Hog1-induced; tra
Putative type-1 protein phosphatase targeting subunit; transcript repressed by yeast-hyphal switch; transcrip
Ortholog(s) have tRNA methyltransferase activity and role in tRNA methylation, wybutosine biosynthetic pro
Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in the nucleus a
Ortholog(s) have four-way junction DNA binding activity and role in homologous chromosome pairing at me
Flavin-containing monooxygenase; catalyzes oxidation of biological thiols to maintain the ER redox buffer ra
Ortholog of Candida tropicalis NEW ASSEMBLY : CTRG1_04422, Candida tropicalis MYA-3404 : CTRG_0
Protein of unknown function; Hap43-repressed; rat catheter and Spider biofilm induced
Protein of unknown function; flow model and Spider biofilm repressed
Ortholog(s) have lipid droplet, peroxisome localization
Putative thioredoxin; Spider biofilm repressed
Ortholog of C. dubliniensis CD36 : Cd36_01240, C. parapsilosis CDC317 : CPAR2_109140, C. auris B8441
Putative glycogen synthesis initiator; regulated by Efg1 and Efh1; Hog1-repressed; colony morphology-relat
Putative transcription factor; required for inhibition of filamentous growth by farnesoic acid and for expressio
Ortholog(s) have sphingosine-1-phosphate phosphatase activity, role in calcium-mediated signaling and en
Ortholog of Bre4 in S. cerevisiae has a role in brefeldin A resistence; a drug that affect intracellular transpo
Ortholog(s) have 5S rRNA binding, 7S RNA binding, poly(A) binding, ribonuclease P RNA binding, tRNA bi
Plasma membrane protein of unknown function; colony morphology-related gene regulation by Ssn6; repres
Protein of unknown function; merged with orf19.3338; rat catheter, flow and Spider model biofilm induced;
Putative tRNA-Arg synthetase; essential; genes encoding ribosomal subunits, translation factors, and tRNA
Ortholog(s) have role in positive regulation of protein autoubiquitination, protein deubiquitination
Ortholog(s) have structural constituent of ribosome activity and fungal-type vacuole, mitochondrial large ribo
Putative RNA polymerase II subunit B150; heterozygous null mutant exhibits resistance to parnafungin in th
Protein of unknown function; Hap43-induced; Spider biofilm induced
Has domain(s) with predicted oxidoreductase activity and role in metabolic process
Protein similar to a mitochondrial complex I intermediate-associated protein; fluconazole-repressed; Spider
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit, mito
Protein of unknown function; flow model biofilm induced; Spider biofilm induced
Predicted MFS membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) family; fl
Component of the RSC chromatin remodeling complex; only present in CTG clade
Ortholog(s) have cyclin-dependent protein kinase activating kinase regulator activity, cyclin-dependent prote
Protein with a Rho GDP-dissociation inhibitor domain; Hap43-repressed gene; Spider biofilm induced
Ortholog(s) have mRNA binding activity, role in mRNA polyadenylation, pre-mRNA cleavage required for po
Ortholog(s) have RNA polymerase II complex binding, RNA polymerase II complex recruiting activity
Putative UBX-domain (ubiquitin-regulatory domain) protein; macrophage-downregulated gene
Ortholog(s) have RNA binding activity and role in rRNA processing
Protein of unknown function; present in exponential and stationary growth phase yeast cultures
Protein of unknown function; regulated by Nrg1, Tup1; Spider and flow model biofilm induced
Ortholog of Srp21, signal recognition particle subunit, functions in protein targeting to the endoplasmic retic
Ortholog(s) have role in vacuolar protein processing
Protein of unknown function
Ortholog(s) have endoplasmic reticulum, nuclear envelope localization
Ortholog(s) have 5-formyltetrahydrofolate cyclo-ligase activity and role in folic acid-containing compound bi
Ortholog(s) have role in cellular response to DNA damage stimulus
Putative deubiquitinating enzyme; induced by Mnl1 under weak acid stress
Predicted plasma membrane protein; gene has intron
Predicted debranching enzyme-associated ribonuclease; rat catheter biofilm induced
Has domain(s) with predicted ATP binding, ATP-dependent microtubule motor activity, microtubule binding
Ortholog(s) have role in chromosome organization, endoplasmic reticulum to Golgi vesicle-mediated transp
Ortholog(s) have Atg8 ligase activity, cargo receptor ligand activity, enzyme activator activity
Ortholog of C. dubliniensis CD36 : Cd36_02060, C. parapsilosis CDC317 : CPAR2_106200, Candida tenuis
Putative protein of unknown function; stationary phase enriched protein
Ortholog(s) have protein-containing complex binding activity
Putative oxidoreductase; Spider biofilm induced
Ortholog(s) have protein domain specific binding activity, role in mitochondrial proton-transporting ATP synt
Ortholog(s) have unfolded protein binding activity, role in cytoskeleton organization, positive regulation of tra
Ortholog(s) have chromatin DNA binding activity and role in cell wall mannoprotein biosynthetic process, po
Putative protein similar to 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase; expression downregulate
Ribosomal 60S subunit protein; Spider biofilm repressed
Ortholog of C. dubliniensis CD36 : Cd36_02210, C. parapsilosis CDC317 : CPAR2_106350, C. auris B8441
Ortholog(s) have role in protein folding, tubulin complex assembly

Putative nuclease required for DNA single- and double-strand break repair; rat catheter biofilm induced
Has domain(s) with predicted role in retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum
Predicted translation initiation factor; role in translational initiation; Spider biofilm repressed
Ortholog(s) have thiol-dependent deubiquitinase activity and role in protein deubiquitination, regulation of tra
Similar to S. cerevisiae Bud20; predicted role in cellular bud site selection; rat catheter and Spider biofilm in
Ortholog of C. dubliniensis CD36 : Cd36_02330, C. parapsilosis CDC317 : CPAR2_106450, Candida tropic
Putative mitochondrial inner membrane protein with a predicted role in the assembly of respiratory complex
Ortholog(s) have role in mitochondrial cytochrome c oxidase assembly and mitochondrion localization
Putative v-SNARE of the endoplasmic reticulum membrane; possibly an essential gene, disruptants not obt
Protein of unknown function; Hap43-repressed gene; repressed by nitric oxide
Protein required for transfer of mannosylphosphate; induced by alpha pheromone in SpiderM medium
Planktonic growth-induced gene
Predicted ORF from Assembly 19; removed from Assembly 20; subsequently reinstated in Assembly 21 ba
Gene induced by hypoxia and ketoconazole; oral infection upregulated; mutants have reduced capacity to d
Putative transcription factor with zinc finger DNA-binding motif
Protein of unknown function; Spider biofilm induced
Has domain(s) with predicted NAD+ binding activity
Component of the RSC chromatin remodeling complex
Putative guanyl-nucleotide exchange factor; Spider biofilm repressed
Protein of unknown function; similar to human SERF2; gene has an alternatively spliced intron
Predicted dienelactone hydrolase domain; clade-associated gene expression; farnesol-downregulated; rat c
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_02630, C. parapsilosis CDC317 : CPAR2_108390, C. auris B8441
Ortholog(s) have RNA binding, flap-structured DNA binding activity and role in nuclear-transcribed mRNA c
Protein of unknown function; Hap43-repressed gene
Ortholog(s) have RNA helicase activity and role in generation of catalytic spliceosome for first transesterifica
Ortholog(s) have SNARE binding, molecular adaptor activity, protein kinase activator activity
Protein of unknown function; Hap43-repressed gene
Ortholog of C. dubliniensis CD36 : Cd36_02750, C. parapsilosis CDC317 : CPAR2_106015, C. auris B8441
Ortholog(s) have role in cellular ion homeostasis, mitochondrion inheritance, mitochondrion organization, re
Predicted aminotransferase based on S. pombe ortholog SPBC660.12c; flow model biofilm induced
Protein of unknown function; induced by nitric oxide; rat catheter and Spider biofilm induced
Ortholog of S. cerevisiae : ECM30, C. glabrata CBS138 : CAGL0M00924g, C. dubliniensis CD36 : Cd36_02
Putative lipid-binding protein with a predicted role in calcium-dependent phospholipid-binding
Ortholog of S. cerevisiae : YDR262W, C. glabrata CBS138 : CAGL0M08734g, C. dubliniensis CD36 : Cd36
Ortholog(s) have role in endosome organization, regulation of protein localization and BLOC-1 complex loca
Ortholog of C. dubliniensis CD36 : Cd36_02950, C. parapsilosis CDC317 : CPAR2_108520, C. auris B8441
Ortholog(s) have nucleus-vacuole junction localization
Putative lipoyl ligase; role in modification of mitochondrial enzymes by attachment of lipoic acid groups; rat
Ortholog of C. dubliniensis CD36 : Cd36_03040, C. parapsilosis CDC317 : CPAR2_108610, C. auris B8441
Putative DNA-dependent ATPase; transcription may be increased in an azole-resistant strain that overexpre
Putative protein of unknown function; Hap43-repressed gene; Spider biofilm induced
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Component of the RSC chromatin remodeling complex; putative DNA translocase; Spider biofilm repressed
Ortholog(s) have phosphatidylinositol-3,5-bisphosphate binding, phosphatidylinositol-3-phosphate binding,
Ortholog(s) have ATPase, acting on DNA, DNA binding, chromatin DNA binding, methylated histone binding
Putative poly(A)-binding protein; regulated by Gcn4p; induced in response to amino acid starvation (3-AT tr
Ortholog(s) have ubiquitin protein ligase binding activity
Protein of unknown function; Hap43-induced; rat catheter biofilm induced
Ortholog(s) have triglyceride lipase activity, role in triglyceride catabolic process and mitochondrion localizat
Predicted aldehyde dehydrogenase domain; virulence-group-correlated expression
Protein kinase-related protein, required for normal sensitivity to caspofungin
Protein of unknown function; repressed by alpha pheromone in SpiderM medium
Ortholog(s) have role in ascospore formation, ascospore wall assembly, ascospore-type prospore membran
Protein of unknown function; S. pombe ortholog SPAC17A2.02c plays a role in resistance to cadmium; colo
Protein of unknown function; present in exponential and stationary phase yeast; identified in extracts from b
Ortholog(s) have role in mitochondrial genome maintenance
OPutative dolichyl-diphosphooligosaccharide-protein glycotransferase; role in protein N-linked glycosylation
Ortholog of S. cerevisiae Rps22Ap and Rps22Bp; gene contains 5' UTR intron
Ortholog(s) have role in chromatin remodeling and ASTRA complex, TTT complex localization
Ortholog of C. parapsilosis CDC317 : CPAR2_108915, C. auris B8441 : B9J08_004667, Candida tenuis NF
Ortholog(s) have protein-containing complex binding activity, role in endoplasmic reticulum to Golgi vesicle-
Protein of unknown function; rat catheter biofilm repressed
Protein with a predicted cytochrome b5-like Heme/Steroid binding domain; Hap43, caspofungin repressed;

Putative peptidyl-prolyl cis-trans isomerase					
Ortholog(s) have role in exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rR					
Ortholog of C. dubliniensis CD36 : Cd36_03580, C. parapsilosis CDC317 : CPAR2_105090, C. auris B8441					
Predicted heme-binding stress-related protein; Tn mutation affects filamentous growth; induced during chla					
Ortholog of Candida albicans WO-1 : CAWG_01004					
Protein of unknown function; Spider biofilm induced					
Ortholog(s) have palmitoyltransferase activity, protein-cysteine S-palmitoyltransferase activity and role in pr					
Mitochondrial protein required for expression of mitochondrial respiratory chain complex I (NADH:ubiquinon					
Putative succinate dehydrogenase; localized to the mitochondrial membrane; Hap43p-repressed gene					
Protein of unknown function; Hap43-repressed gene					
Ortholog(s) have role in TOR signaling, re-entry into mitotic cell cycle after pheromone arrest and endoplas					
Ortholog(s) have proteasome binding activity and role in cellular response to arsenic-containing substance,					
Protein with a NADP-dependent oxidoreductase domain; transcript induced by ketoconazole; rat catheter a					
Ortholog(s) have aspartate-tRNA ligase activity, role in mitochondrial aspartyl-tRNA aminoacylation and mit					
Putative U3-containing 90S preribosome subunit; Hap43-induced; repressed in core stress response; Spide					
Ortholog(s) have cyclin-dependent protein serine/threonine kinase activator activity					
Ortholog(s) have lysophosphatidic acid acyltransferase activity, role in cellular triglyceride homeostasis, lipi					
Putative U2 snRNP protein; Hap43p-induced gene; mutation confers hypersensitivity to 5-fluorocytosine (5-					
Predicted NUDIX hydrolase domain; Hap43-induced					
Ortholog of S. cerevisiae : YMR087W, C. glabrata CBS138 : CAGL0J01397g, C. dubliniensis CD36 : Cd36_					
Predicted histone H2B; Hap43-induced gene; Spider biofilm repressed					
Inositol deacylase involved in attachment of GPI-anchored proteins to cell wall; required for host invasion a					
Ortholog(s) have role in endoplasmic reticulum tubular network membrane organization, nuclear envelope c					
Ortholog of C. dubliniensis CD36 : Cd36_03980, C. parapsilosis CDC317 : CPAR2_107050, C. auris B8441					
Subunit of the 19S regulatory base of the proteasome					
Ortholog of C. dubliniensis CD36 : Cd36_04020, C. parapsilosis CDC317 : CPAR2_107000, C. auris B8441					
Ortholog(s) have alpha-1,6-mannosyltransferase activity, mannosyltransferase activity and role in GPI anch					
Ortholog(s) have role in phospholipid translocation, retrograde transport, endosome to Golgi and endosome					
Protein of unknown function; Hap43-induced gene					
Has domain(s) with predicted ATPase inhibitor activity, role in negative regulation of ATPase activity, negati					
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali					
Putative protein of unknown function; clade-associated gene expression					
Ortholog of Candida albicans WO-1 : CAWG_00951					
Putative protein of unknown function, transcript upregulated in clinical isolates from HIV+ patients with oral					
Protein of unknown function; transcript detected in high-resolution tiling arrays; transcription induced by alph					
Ortholog(s) have role in CENP-A containing nucleosome assembly, chromatin maintenance and nucleoplas					
Putative transcription factor with bZIP DNA-binding motif; rat catheter biofilm induced					
Putative tRNA U44 2'-O-methyltransferase; virulence-group-correlated expression; induced during oral infe					
Putative transcription factor with C3HC4 zinc finger DNA-binding motif; mutants are viable					
Ortholog of Rmd6 involved in S. cerevisiae sporulation; flow model biofilm induced					
Protein of unknown function; Spider biofilm induced					
Protein of unknown function; Spider biofilm repressed					
Ortholog of C. dubliniensis CD36 : Cd36_04370, C. parapsilosis CDC317 : CPAR2_105410, C. auris B8441					
Ortholog(s) have role in endocytosis, phospholipid translocation, retrograde vesicle-mediated transport, Gol					
Ortholog(s) have hydrolase activity, acting on ester bonds, triglyceride lipase activity, role in lipid homeostas					
Protein involved in control of chromosome stability and homologous recombination during meiosis-like cond					
Ortholog of C. dubliniensis CD36 : Cd36_04450, C. parapsilosis CDC317 : CPAR2_105460, C. auris B8441					
Protein similar to S. cerevisiae Rsa3 predicted nucleolar protein involved in maturation of pre-60S ribosoma					
Ortholog of C. parapsilosis CDC317 : CPAR2_105440, Lodderomyces elongisporus NRLL YB-4239 : LELG					
Ortholog(s) have role in negative regulation of TORC1 signaling and cytoplasm localization					
Small subunit of the heterodimeric cap binding complex; component of the spliceosomal commitment comp					
Ortholog of C. parapsilosis CDC317 : CPAR2_105580, C. dubliniensis CD36 : Cd36_04550, Lodderomyces					
Ortholog(s) have role in ribosome biogenesis					
Ortholog(s) have signal sequence binding activity, role in vacuolar transport and late endosome localization					
Ortholog of S. cerevisiae : YPR089W, C. glabrata CBS138 : CAGL0K08008g, C. dubliniensis CD36 : Cd36_					
Has domain(s) with predicted methyltransferase activity and role in metabolic process					
Ortholog of C. dubliniensis CD36 : Cd36_04660, Candida tropicalis NEW ASSEMBLY : CTRG1_04484, Ca					
Protein of unknown function; exogenously expressed protein is a substrate for Kex2p processing in vitro					
Ortholog(s) have role in SCF-dependent proteasomal ubiquitin-dependent protein catabolic process, cellula					
Ortholog(s) have RNA binding activity, role in cellular response to osmotic stress and cytoplasmic stress gr					
Ortholog(s) have role in cellular iron ion homeostasis and mitochondrion localization					
Ortholog(s) have role in mRNA cis splicing, via spliceosome and U2-type prespliceosome, U2AF complex,					
Ortholog(s) have role in cellular zinc ion homeostasis					
Protein of unknown function; clade-associated gene expression					

Ortholog(s) have role in arginine transport, lysine transport, regulation of intracellular pH and cell division si
Protein of unknown function
Putative phosphatidyl synthase; stationary phase enriched protein; transcript repressed by yeast-hypha swi
Protein with a NADH-ubiquinone oxidoreductase B18 subunit domain; gene has intron
Protein with a NADH-ubiquinone oxidoreductase B18 subunit domain; gene has intron
Protein of unknown function; constitutive expression independent of MTL or white-opaque status; upregula
Protein of unknown function; repressed by prostaglandins
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III, transcriptio
Ortholog of Candida guilliermondii ATCC 6260 : PGUG_05525, Candida lusitaniae ATCC 42720 : CLUG_0
Ortholog(s) have DNA binding, DNA strand exchange activity, single-stranded DNA binding, structural cons
Has domain(s) with predicted membrane localization
Ortholog(s) have role in cellular protein-containing complex assembly, intra-Golgi vesicle-mediated transpo
Predicted SCF ubiquitin ligase complex protein; Spider biofilm induced; rat catheter biofilm induced
Putative non-canonical poly(A) polymerase; repressed by nitric oxide; Spider biofilm induced
Putative serine/threonine kinase; induced during planktonic growth; rat catheter biofilm repressed
Ortholog(s) have telomeric DNA binding activity
Ortholog of C. dubliniensis CD36 : Cd36_05120, C. parapsilosis CDC317 : CPAR2_107740, C. auris B844
Ortholog(s) have mitochondrial large ribosomal subunit localization
Ortholog(s) have enzyme activator activity, mRNA binding activity, role in deadenylation-dependent decapp
Protein of unknown function; flow model biofilm induced; Spider biofilm induced
Protein of unknown function
Ortholog of C. dubliniensis CD36 : Cd36_05200, C. parapsilosis CDC317 : CPAR2_107660, C. auris B844
Putative protein of unknown function; Hap43p-repressed gene
Protein of unknown function; induced by Sfu1; Spider biofilm induced
Protein similar to GTPase regulators; induced in low iron; transcript activated by Mnl1 under weak acid stre
Ortholog(s) have glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity, role in glutaminyl-tRNAGln bios
Putative karyopherin beta; repressed by nitric oxide
Protein with a predicted phosphoribulokinase/uridine kinase domain; Spider biofilm induced
Ortholog(s) have chromatin binding, promoter-specific chromatin binding, protein-containing complex bindi
Has domain(s) with predicted peptidase activity and role in proteolysis
Protein of unknown function; Spider biofilm induced
60S ribosomal protein L7; snoRNA snR39b encoded within the 2nd intron
Ortholog of C. dubliniensis CD36 : Cd36_05410, C. parapsilosis CDC317 : CPAR2_107480, C. auris B844
Ortholog(s) have histone demethylase activity (H3-trimethyl-K4 specific) activity
Component of the RSC chromatin remodeling complex; decreased transcription is observed upon fluphena
Ortholog of C. dubliniensis CD36 : Cd36_61610, C. parapsilosis CDC317 : CPAR2_107530, C. auris B844
Ortholog of S. pombe replication termination factor Rtf2; Spider biofilm induced
Ortholog(s) have trans-aconitate 3-methyltransferase activity and cytosol localization
Protein of unknown function; substrate for Kex2 processing in vitro; repressed by alpha pheromone in Spid
Protein of unknown function; mRNA binds to She3; Hap43 repressed gene; Spider biofilm induced
Protein of unknown function; induced during chlamydospore formation in both C. albicans and C. dublinien
Ortholog(s) have glutathione hydrolase activity, omega peptidase activity, peptidase activity, role in glutathi
Protein of unknown function; induced in high iron; repressed in core caspofungin response; ketoconazole-r
Putative adhesin-like protein; macrophage-induced gene
Putative Type II phosphatidylinositol 4-kinase; Ssr1-repressed; flow model biofilm repressed
Has domain(s) with predicted 2-dehydropantoate 2-reductase activity, NADP binding, oxidoreductase activi
Putative dicarboxylic amino acid permease; fungal-specific (no human or murine homolog); induced by alp
Ortholog of S. cerevisiae Shg1; a COMPASS (Set1C) complex subunit that methylates histone H3 on lysine
Ortholog(s) have ubiquinol-cytochrome-c reductase activity, role in aerobic respiration, mitochondrial electr
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Predicted protein serine/threonine kinase; Spider biofilm induced
Has domain(s) with predicted flap-structured DNA binding activity and role in double-strand break repair via
Ortholog of Candida albicans WO-1 : CAWG_00792
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Ortholog of Pichia stipitis Pignal : PICST_29216 and Candida albicans WO-1 : CAWG_00788
Protein of unknown function; flow model biofilm induced; induced by alpha pheromone in SpiderM medium
Protein of unknown function; mutants are viable; filament induced; regulated by Nrg1, Rfg1, Tup1
Predicted membrane protein; transcript repressed by ciclopirox olamine
Has domain(s) with predicted phosphatidylinositol binding activity and role in cell communication
Ortholog of C. dubliniensis CD36 : Cd36_05920, C. parapsilosis CDC317 : CPAR2_803860, C. auris B844
Protein of unknown function; rat catheter biofilm repressed
Ortholog(s) have protein serine/threonine kinase activity, ribosomal protein S6 kinase activity, role in TORC
Ortholog of C. dubliniensis CD36 : Cd36_05960, C. parapsilosis CDC317 : CPAR2_301790, C. auris B844

Putative ubiquitin C-terminal hydrolase; regulated by Gcn2p and Gcn4p
Ortholog(s) have role in mRNA splicing, via spliceosome and transcriptionally active chromatin localization
Ortholog of C. dubliniensis CD36 : Cd36_05990, C. auris B8441 : B9J08_000600, Candida tenuis NRRL Y-
Putative cohesin complex subunit; expression downregulated in an ssr1 null mutant
Ortholog of C. dubliniensis CD36 : Cd36_06020, C. parapsilosis CDC317 : CPAR2_803380, C. auris B8441
Protein of unknown function; Spider biofilm induced
Ortholog of S. cerevisiae Rpl39; a component of the 60S ribosomal subunit; Hap43-induced; Spider biofilm
Ortholog(s) have role in endoplasmic reticulum to Golgi vesicle-mediated transport and COPII-coated ER to
Ortholog of C. dubliniensis CD36 : Cd36_06080, C. parapsilosis CDC317 : CPAR2_803360, C. auris B8441
Predicted MFS membrane transporter; member of the monocarboxylate porter (MCP) family; Spider biofilm
Ubiquitin-specific protease; cleaves ubiquitin from ubiquitinated proteins; Spider biofilm induced
Exosome non-catalytic core component; involved in 3'-5' RNA processing and degradation in the nucleus ai
Putative protein of unknown function; Hap43p-repressed gene
Ortholog(s) have RNA polymerase II complex binding activity
Ortholog(s) have eukaryotic initiation factor 4G binding, mRNA binding activity, role in P-body assembly, ne
Ortholog of C. dubliniensis CD36 : Cd36_06210, Candida tropicalis NEW ASSEMBLY : CTRG1_04227, Ca
Ortholog(s) have chromatin binding activity
Ortholog(s) have protein transmembrane transporter activity and role in mitochondrial outer membrane tran
Ortholog(s) have peptide alpha-N-acetyltransferase activity and role in N-terminal peptidyl-methionine acety
Protein of unknown function; regulated by osmotic stress via Hog1 and oxidative stress (Hog1- and Cap1-ir
Ortholog of C. dubliniensis CD36 : Cd36_06250, C. parapsilosis CDC317 : CPAR2_206820, C. auris B8441
SH3-domain protein; role in barrier septum assembly involved in cell cycle cytokinesis; activates the Chs2 c
Putative serine/threonine protein kinase, involved in control of filamentous growth; possibly an essential ger
Has domain(s) with predicted oxidoreductase activity
Protein of unknown function; Spider biofilm induced
Has domain(s) with predicted oxidoreductase activity and role in metabolic process
Ortholog(s) have GDP binding, RNA NAD-cap (NAD-forming) hydrolase activity, RNA pyrophosphohydrolas
Ortholog of C. dubliniensis CD36 : Cd36_06390, C. parapsilosis CDC317 : CPAR2_209040, C. auris B8441
Ortholog(s) have role in mitochondrial cytochrome c oxidase assembly and extrinsic component of matrix si
RTA domain protein; predicted role in response to stress; Spider biofilm induced
Ortholog of C. parapsilosis CDC317 : CPAR2_208910, Candida tenuis NRRL Y-1498 : CANTEDRAFT_114
Ribosomal 60S subunit protein; Spider biofilm repressed
Ortholog(s) have role in positive regulation of transcription elongation from RNA polymerase II promoter and
Ortholog of C. dubliniensis CD36 : Cd36_06470, C. parapsilosis CDC317 : CPAR2_208960, Candida tenuis
Protein of unknown function; protein newly produced during adaptation to the serum
Predicted membrane transporter; monocarboxylate porter (MCP) family, major facilitator superfamily (MFS)
Ortholog of C. dubliniensis CD36 : Cd36_06550, C. parapsilosis CDC317 : CPAR2_209030, C. auris B8441
Pry family pathogenesis-related protein; oral infection upregulated gene; mutant has reduced capacity to da
Ortholog(s) have 5'-3' DNA helicase activity and DNA helicase A complex, nuclear replisome localization
Ortholog of S. cerevisiae : YIL156W-B, C. glabrata CBS138 : CAGL0H06732g, C. dubliniensis CD36 : Cd3
Component of the SWI/SNF and RSC chromatin remodeling complexes; suggested role in chromosome ma
Ortholog(s) have 3'-5'-exoribonuclease activity
Ortholog of C. dubliniensis CD36 : Cd36_06640, C. parapsilosis CDC317 : CPAR2_208220, C. auris B8441
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_06690, C. auris B8441 : B9J08_002288, Debaryomyces hansenii
Protein conserved among the CTG-clade; 2 adjacent upstream SRE-1 elements; highly up-regulated in cec
Protein similar to ammomium permeases that is probably inactive, as a mep2 mep3 double homozygous nu
Protein of unknown function; Plc1p-regulated; expression induced early upon infection of reconstituted hum
Ortholog(s) have DNA replication origin binding, double-stranded DNA binding, single-stranded DNA bindin
Ortholog(s) have role in nucleotide-excision repair, phosphorylation of RNA polymerase II C-terminal domai
Ortholog(s) have ATPase, DNA binding, nucleosome binding, rDNA binding activity
Ortholog(s) have beta-tubulin binding, kinetochore binding, microtubule binding activity and role in attachme
Ortholog(s) have ubiquitin binding activity and role in proteasome-mediated ubiquitin-dependent protein cata
Ortholog of C. dubliniensis CD36 : Cd36_06910, C. parapsilosis CDC317 : CPAR2_208560, C. auris B8441
Putative glucosyltransferase; localized to the mitochondrial membrane
Putative helicase; fungal-specific (no human or murine homolog)
Has domain(s) with predicted ATP binding, DNA binding, helicase activity, hydrolase activity, nucleic acid bi
Ortholog(s) have DNA-directed DNA polymerase activity, role in DNA replication initiation, telomere capping
Putative non-specific single-domain racemase; regulated by Gcn4p; repressed in response to amino acid st
Ortholog of Candida albicans WO-1 : CAWG_00667
Ortholog of C. dubliniensis CD36 : Cd36_07040, C. parapsilosis CDC317 : CPAR2_208700, C. auris B8441
Has domain(s) with predicted RNA binding, pseudouridine synthase activity and role in pseudouridine synth
Ortholog(s) have AP-2 adaptor complex, cellular bud neck localization
Ortholog of C. dubliniensis CD36 : Cd36_07090, C. auris B8441 : B9J08_003145, Candida tenuis NRRL Y-

Ortholog(s) have 2 iron, 2 sulfur cluster binding, disulfide oxidoreductase activity, glutathione disulfide oxido
Protein with predicted serine/threonine kinase and tyrosine kinase domains; possibly an essential gene, dis
Protein of unknown function; Hap43-repressed gene
Protein of unknown function; transcript is upregulated in clinical isolates from HIV+ patients with oral candid
Ortholog(s) have role in protein export from nucleus, snRNA import into nucleus and nuclear envelope, nuc
Ortholog of C. dubliniensis CD36 : Cd36_07300, C. parapsilosis CDC317 : CPAR2_208300, C. auris B8441
Putative U3-containing 90S preribosome processome complex subunit; Hap43-induced gene; rat catheter a
Has domain(s) with predicted protein heterodimerization activity
Ortholog of S. cerevisiae : YFR045W, C. glabrata CBS138 : CAGL0C02013g, C. dubliniensis CD36 : Cd36_
Putative acetyltransferase
Putative quinolinate phosphoribosyl transferase, involved in NAD biosynthesis; Hap43p-repressed gene
Ortholog(s) have enzyme regulator activity, ubiquitin protein ligase activity and role in anaphase-promoting c
Ortholog of C. dubliniensis CD36 : Cd36_07380 and Candida albicans WO-1 : CAWG_00634
Ortholog of C. dubliniensis CD36 : Cd36_07450, C. parapsilosis CDC317 : CPAR2_208450, Candida tenuis
Putative pre-60S pre-ribosomal particle subunit; essential gene; S. cerevisiae ortholog RRP17 is essential;
Predicted nuclear exosome-associated nucleic acid binding protein; rat catheter and Spider biofilm induced
Ortholog of S. cerevisiae Sae3; meiosis specific protein involved in DMC1-dependent meiotic recombination
Similar to cell-wall mannoproteins; induced in low iron; induced in cyr1 homozygous null; regulated by osmo
Ortholog of C. parapsilosis CDC317 : CPAR2_804320, Candida tenuis NRRL Y-1498 : CANTEDRAFT_114
Subunit of mitochondrial respiratory chain complex I; Hap43-repressed gene; repressed by nitric oxide
Ortholog of C. dubliniensis CD36 : Cd36_07590, C. parapsilosis CDC317 : CPAR2_206680, C. auris B8441
Ortholog(s) have nuclear localization sequence binding activity
Ortholog(s) have tRNA-specific adenosine deaminase activity, tRNA-specific adenosine-34 deaminase activ
Has domain(s) with predicted kinetochore localization
Component of the RSC chromatin remodeling complex
Putative oxysterol-binding protein; caspofungin induced; possibly an essential gene, disruptants not obtaine
Protein with a predicted phosphoglycerate mutase family domain; Hap43-repressed; clade-associated gene
Sorting nexin; role in maintaining late-Golgi resident enzymes in their proper location by recycling molecules
Ortholog of C. dubliniensis CD36 : Cd36_02630, C. parapsilosis CDC317 : CPAR2_206910, Candida tenuis
Ortholog of S. cerevisiae : YPL247C, C. glabrata CBS138 : CAGL0H00781g, C. dubliniensis CD36 : Cd36_
Protein of unknown function; Hap43-induced gene
Ortholog(s) have role in mitochondrial respiratory chain complex III assembly and integral component of mit
Putative kynureninase; predicted role in NAD biosynthesis; Hap43-repressed gene; flow model biofilm induc
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali:
Ortholog of C. dubliniensis CD36 : Cd36_08040, C. parapsilosis CDC317 : CPAR2_207180, C. auris B8441
Putative serine/threonine protein kinase; possibly an essential gene, disruptants not obtained by UAU1 met
Ortholog of S. cerevisiae Aim38/Rcf2, cytochrome c oxidase subunit; plasma membrane localized; Hap43-r
Ortholog(s) have RNA binding activity, role in mRNA processing, mitochondrial translation and mitochondria
Ortholog(s) have RNA binding activity, role in spliceosomal complex assembly and U2-type prespliceosome
Ortholog(s) have 1-phosphatidylinositol 4-kinase activator activity, calcium ion binding, enzyme activator act
Ortholog(s) have role in mitochondrial respiratory chain complex II assembly, tricarboxylic acid cycle and mi
Ortholog(s) have role in histone deacetylation and Set3 complex localization
Ortholog of S. cerevisiae : YNL050C, C. glabrata CBS138 : CAGL0G01276g, C. dubliniensis CD36 : Cd36_
Ortholog(s) have role in cytoplasm to vacuole transport by the Cvt pathway, intra-Golgi vesicle-mediated tra
Protein of unknown function; Hap43-repressed
Ornithine cyclodeaminase family protein; Sef1, Sfu1, and Hap43-regulated; ortholog of S. cerevisiae YGL15
Ortholog(s) have alkaline phosphatase activity, zinc ion sensor activity, role in nicotinamide nucleotide meta
Ortholog(s) have integral component of endoplasmic reticulum membrane localization
Ortholog(s) have aminoacyl-tRNA hydrolase activity and role in mitochondrial translation
Protein of unknown function; C. albicans- and C. dubliniensis specific gene; rat catheter biofilm repressed
Putative SH3-domain-containing protein
Putative phosphatidylinositol 3-phosphate (PI3P) phosphatase; repressed by alpha pheromone in SpiderM r
Putative U2B'' component of the U2 snRNP, involved in splicing; contains an RNA recognition motif (RRM);
Protein of unknown function; hyphal-induced expression, regulated by Cyr1, Ras1, Efg1; Hap43-induced ge
Ortholog of C. dubliniensis CD36 : Cd36_08410, C. parapsilosis CDC317 : CPAR2_301700, C. auris B8441
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Has domain(s) with predicted NADH dehydrogenase (ubiquinone) activity, role in electron transport chain ar
Ortholog of S. cerevisiae : YTP1, C. dubliniensis CD36 : Cd36_08490, C. parapsilosis CDC317 : CPAR2_80
Putative reductase or dehydrogenase; Hap43-repressed gene; alkaline repressed
Protein of unknown function; possibly membrane bound; mutants are viable; rat catheter biofilm repressed
Ortholog(s) have poly(A)-specific ribonuclease activity, role in nuclear-transcribed mRNA poly(A) tail shorten
Protein of unknown function; Spider biofilm induced
Protein of unknown function; Spider biofilm induced
Putative transporter; slightly similar to the Sit1p siderophore transporter; Gcn4p-regulated; fungal-specific; i

Predicted MFS family membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) fa
Protein of unknown function; induced during chlamydospore formation in both C. albicans and C. dubliniens
Ortholog of S. cerevisiae : JJJ2, C. glabrata CBS138 : CAGL0I06226g, C. dubliniensis CD36 : Cd36_0875
Has domain(s) with predicted metal ion binding activity
Protein of unknown function; Spider biofilm induced
Protein with a regulator of G-protein signaling domain; Plc1-regulated; Spider biofilm induced; rat catheter b
Putative ribosome-associated protein; ortholog of S. cerevisiae Tma16; Hap43-induced gene; Spider biofilm
Protein of unknown function; Sef1-, Sfu1-, and Hap43 regulated; Spider biofilm induced
Putative eIF-4E-binding repressor of CAP-dependent translation; stationary phase enriched protein
Ortholog(s) have role in protein localization to plasma membrane and plasma membrane localization
Ortholog(s) have tRNA binding, tRNA dimethylallyltransferase activity, role in tRNA modification, transfer RN
Putative membrane protein; induced by alpha pheromone in SpiderM medium; Hap4-induced gene; Spider
Ortholog(s) have inorganic diphosphatase activity, role in aerobic respiration and mitochondrion localization
Putative tricarboxylate carrier family protein; localized to the mitochondrial membrane
Ortholog of C. dubliniensis CD36 : Cd36_08960, C. parapsilosis CDC317 : CPAR2_301680, Candida tenuis
Protein of unknown function; induced by nitric oxide
Protein of unknown function; Spider biofilm induced
Protein of unknown function; transcript detected on high-resolution tiling arrays; rat catheter biofilm induced
Ortholog of S. cerevisiae : YKL162C, C. dubliniensis CD36 : Cd36_09010, C. parapsilosis CDC317 : CPAR
Planktonic growth-induced gene
Mitochondrial matrix protein; required for assembly/stability of the F1 sector of mitochondrial F1F0 ATP syn
WD repeat domain protein; Hap43-repressed gene; flow model biofilm induced
Has domain(s) with predicted DNA binding activity, role in DNA recombination, DNA repair, DNA replication
Ortholog of C. dubliniensis CD36 : Cd36_09140, C. parapsilosis CDC317 : CPAR2_804920, Debaryomyces
Ortholog(s) have role in endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S
Ortholog of C. parapsilosis CDC317 : CPAR2_804880, Candida tenuis NRRL Y-1498 : CANTEDRAFT_111
GET complex subunit; expression downregulated in an ssr1 null mutant
Protein of unknown function; Spider biofilm induced
Putative iron/copper reductas; involved in iron homeostasis; rat catheter and Spider biofilm induced
Ortholog(s) have 3'-5' RNA helicase activity, RNA binding, polynucleotide adenylyltransferase activity, prote
GlcNAc-induced protein
Protein required for localizing proteasomes to the nucleus; involved in ubiquitin-mediated protein degradatio
Ortholog of S. cerevisiae : CUB1, C. dubliniensis CD36 : Cd36_09270, C. parapsilosis CDC317 : CPAR2_8
Protein with a dual-specificity phosphatase domain; Hap43-induced gene
Protein of unknown function; rat catheter biofilm repressed
Protein of unknown function
Putative integral membrane protein; S. cerevisiae ortholog Tvp23 localizes to late Golgi vesicles; rat cathete
Ortholog(s) have acylglycerol lipase activity, role in triglyceride metabolic process and lipid droplet, membra
Protein of unknown function; induced by Mnl1 under weak acid stress; Hap43-induced; mutant is viable
Protein of unknown function; transcript regulated by white-opaque switch; flow model biofilm induced; Spide
Ortholog(s) have role in mRNA splicing, via spliceosome and U2-type spliceosomal complex localization
Protein of unknown function; Hap43-repressed; rat catheter biofilm repressed
Protein of unknown function; flow model biofilm induced
TFIIE small subunit; involved in RNA polymerase II transcription initiation; Spider biofilm induced
Protein of unknown function; S. cerevisiae ortholog Cos111 confers resistance to the antifungal drug ciclopi
Putative adhesin-like protein; Hap43-repressed; rat catheter and Spider biofilm induced
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
Predicted MFS family membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) fa
Ortholog of C. dubliniensis CD36 : Cd36_09630, C. parapsilosis CDC317 : CPAR2_805080, C. auris B8441
Protein with similarity to S. cerevisiae Yer010cp, a protein of unknown function belonging to the prokaryotic
Ortholog of C. dubliniensis CD36 : Cd36_09650, C. parapsilosis CDC317 : CPAR2_805060, C. auris B8441
Putative protein of unknown function; induced by prostaglandins
Predicted methyltransferase; Spider biofilm induced
Ortholog(s) have N-acetylglucosaminylphosphatidylinositol deacetylase activity
Ortholog(s) have nucleosome binding activity, role in chromatin remodeling, histone exchange and Swr1 co
Putative MFS transporter; Hap43p-induced gene; also regulated by regulated by Sef1p and Sfu1p; represse
Putative adhesin-like protein; positively regulated by Tbf1; Spider biofilm induced
Putative protein of unknown function; Hap43p-repressed gene; increased transcription is observed upon flu
BED zinc finger protein; predicted DNA binding protein; Spider biofilm repressed
Ortholog(s) have ubiquitin protein ligase binding activity, role in positive regulation of receptor internalizatior
Ortholog of S. cerevisiae : YEL043W, C. glabrata CBS138 : CAGL0L01221g, C. dubliniensis CD36 : Cd36_
Protein of unknown function; oral infection upregulated gene; upregulated in strains from HIV+ patients with
Mitochondrial ribosomal protein of the small subunit; Spider biofilm repressed
Protein of unknown function; rat catheter biofilm repressed

Protein of unknown function; induced by Mnl1 under weak acid stress; flow model biofilm repressed
Protein with a predicted leucine-rich repeat domain; possibly an essential gene, disruptants not obtained by
Putative adapter protein; links synaptojanins Inp52 and Inp53 to the cortical actin cytoskeleton in S. cerevisi
Protein of unknown function; Hap43-repressed gene
Protein with predicted RNI-like domains; rat catheter biofilm induced
Protein of unknown function; Hap43-induced; rat catheter and Spider biofilm induced
Ortholog(s) have pseudouridine synthase activity
Has domain(s) with predicted role in mitotic sister chromatid cohesion
Predicted lipid-binding ER protein; involved in ER-plasma membrane tethering; Spider biofilm induced
Ortholog(s) have mitochondrion localization
Protein similar to S. cerevisiae Yor378w; MFS family transporter; transposon mutation affects filamentous g
Putative protein of unknown function, transcription is positively regulated by Tbf1p
Putative vacuolar H+ ATPase subunit e of the V-ATPase V0 subcomplex; added to Assembly 21 based on
Pry family pathogenesis-related protein; predicted to be extracellular
Putative aspartyl aminopeptidase; stationary phase enriched protein; mutation confers hypersensitivity to 5-
Ortholog(s) have role in retrograde transport, endosome to Golgi and cytoplasm, late endosome localizatior
Ortholog of C. dubliniensis CD36 : Cd36_10180, C. parapsilosis CDC317 : CPAR2_210560, Candida tropic
Putative U3 snoRNA-associated protein; Hap43-induced; transposon mutation affects filamentous growth; r
Ortholog of C. dubliniensis CD36 : Cd36_10220, C. parapsilosis CDC317 : CPAR2_210530, C. auris B8441
Ortholog(s) have role in double-strand break repair via homologous recombination, mitotic intra-S DNA dam
Ortholog(s) have RNA polymerase III general transcription initiation factor activity and RNA polymerase III t
Putative serine/threonine-protein kinase; possibly an essential gene, disruptants not obtained by UAU1 met
Ortholog(s) have inositol phosphoceramide synthase regulator activity, role in inositol phosphoceramide me
Putative nucleolar protein with a predicted role in pre-rRNA processing; Hap43-induced gene; repressed in
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Protein with a role in nucleolar integrity and processing of pre-rRNA; mutation confers hypersensitivity to 5-f
Putative ortholog of S. cerevisiae Pex32 a peroxisomal integral membrane protein with a role in negative re
Protein similar to ferric reductase Fre10p; possibly an essential gene, disruptants not obtained by UAU1 me
Predicted single-stranded nucleic acid binding protein; flow model biofilm induced
Putative 6-phosphofructo-2-kinase; catalyzes synthesis of fructose-2,6-bisphosphate; Hap43-repressed; flo
Ortholog(s) have role in mRNA 3'-end processing, mRNA polyadenylation, pre-mRNA cleavage required for
Ortholog(s) have acireductone dioxygenase (Ni2+-requiring) activity and role in L-methionine salvage from r
Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and cytoplasm, prefoldin complex
Protein similar to S. cerevisiae Gvp36p; transposon mutation affects filamentous growth
Ortholog(s) have enzyme regulator activity, role in cellular calcium ion homeostasis, glycosphingolipid biosy
Ortholog(s) have role in proteasome regulatory particle assembly and cytoplasm, cytosol, nucleus localizatio
Ortholog(s) have protein tag activity
Predicted mucin-like protein; ketoconazole-induced; fluconazole-repressed; induced in cyr1 mutant; colony
Microtubule-binding protein of the cortical microtubule; delays exit from mitosis when the spindle is abnorma
Putative adhesin-like protein
Cell wall protein; induced in core stress response and core caspofungin response; iron-regulated; amphoter
Ortholog(s) have U6 snRNA binding activity and role in mRNA cis splicing, via spliceosome, mRNA splicing
Has domain(s) with predicted FMN binding, catalytic activity, oxidoreductase activity
Ortholog(s) have RNA binding, first spliceosomal transesterification activity, role in mRNA 5'-splice site reco
Protein of unknown function; hypoxia, Hap43-repressed; ketoconazole induced; induced in oralpharyngeal c
Essential protein required for the DNA integrity checkpoint pathway; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_10680, Debaryomyces hansenii CBS767 : DEHA2E14058g, Pichia
Predicted ORF from original SGTC Assembly 19 annotation, removed from the reduced ORF set by the SG
Protein of unknown function; mRNA binds She3
Putative DnaJ-like molecular chaperone; Spider biofilm induced
Ortholog(s) have sulfonate dioxygenase activity and role in sulfur compound catabolic process
Has domain(s) with predicted GTP binding activity
Ortholog of S. cerevisiae : YJR112W-A, C. glabrata CBS138 : CAGL0C04829g, C. dubliniensis CD36 : Cd3
Protein of unknown function; transcript upregulated by benomyl treatment
Ortholog(s) have COPII receptor activity and role in endoplasmic reticulum to Golgi vesicle-mediated transp
Protein similar to A. nidulans CysA serine O-trans-acetylase; suggests that C. albicans uses an O-acetyl-se
Ortholog of S. cerevisiae Yft2 required for normal ER membrane biosynthesis; Hap43-repressed gene
Protein of unknown function; induced in core stress response; Gcn2 and Gcn4 regulated; flow model biofilm
Ortholog of C. dubliniensis CD36 : Cd36_10990, C. parapsilosis CDC317 : CPAR2_804585, C. auris B8441
GATA-like transcription factor; oral infection induced; mutant has reduced capacity to damage oral epithelia
Ortholog of C. dubliniensis CD36 : Cd36_11020 and Candida albicans WO-1 : CAWG_00266
Ortholog of Candida albicans WO-1 : CAWG_00265
Protein with SEL-1 like protein domain; early-stage flow model biofilm induced
Ortholog of Pichia stipitis Pignal : PICST_30878, Candida tropicalis NEW ASSEMBLY : CTRG1_01052, Sp

Protein of unknown function; Spider biofilm repressed
Protein of unknown funtion; S. cerevisiae ortholog Svl3 plays a role in endocytosis and is localized to the bu
Thymidylate kinase of unknown role; forms a dimer; potential target for antifungal drugs
Ortholog(s) have AP-2 adaptor complex, clathrin-coated vesicle localization
Protein of unknown function; Hap43-repressed gene; mRNA binds to She3; repressed in hyphae; Efg1 and
Predicted essential RNA-binding G protein; ortholog an effector of mating response pathway in S. cerevisia
Ortholog(s) have structural constituent of ribosome activity and role in cellular respiration, regulation of mito
Protein of unknown function; Spider biofilm induced
Ortholog(s) have role in DNA recombination, nuclear-transcribed mRNA catabolic process, 3'-5' exonucleol
Putative nuclear pore-associated protein; Hap43p-induced gene; induced upon low-level peroxide stress; p
Ortholog(s) have ATPase activator activity, protein-macromolecule adaptor activity and role in late endosom
Ortholog of S. cerevisiae : SKG3, C. dubliniensis CD36 : Cd36_11180, C. parapsilosis CDC317 : CPAR2_2
Protein of unknown function; Hap43-induced gene
Protein of unknown function; rat catheter biofilm induced
Ortholog of S. cerevisiae : YPR170W-B, C. glabrata CBS138 : CAGL0I06457g, C. dubliniensis CD36 : Cd3
Ortholog of C. dubliniensis CD36 : Cd36_11210, C. parapsilosis CDC317 : CPAR2_805180, C. auris B8441
Putative cell wall adhesin-like protein; repressed in core caspofungin response and by alpha pheromone in
Planktonic growth-induced gene
Ortholog of C. dubliniensis CD36 : Cd36_11290, C. parapsilosis CDC317 : CPAR2_805090, C. auris B8441
Protein of unknown function; induced by nitric oxide
Protein of unknown function; Hap43-repressed gene; induced by alpha pheromone in SpiderM medium
Protein of unknown function; repressed by nitric oxide
Has domain(s) with predicted ATP binding, protein kinase activity, protein tyrosine kinase activity and role i
Ortholog of C. dubliniensis CD36 : Cd36_11370, C. parapsilosis CDC317 : CPAR2_207480, C. auris B8441
Ortholog(s) have role in autophagosome assembly, macroautophagy and Atg1/ULK1 kinase complex, phag
Has domain(s) with predicted protein tyrosine phosphatase activity
Protein of unknown function; Hap43-repressed gene
Predicted alanine-tRNA ligase; oxidative stress-induced via Cap1
Ortholog of C. dubliniensis CD36 : Cd36_11490, C. parapsilosis CDC317 : CPAR2_701040, C. auris B8441
Putative mitochondrial ribosomal protein of the large subunit; Hap43-induced; mutants are viable; protein le
Protein of unknown function; flow model biofilm induced
Ortholog(s) have 3'-5'-exoribonuclease activity, endoribonuclease activity, exoribonuclease activity, ribonucl
Chaperone component; involved in assembly of alpha subunits into the 20S proteasome; flow model biofilm
Ortholog of Candida albicans WO-1 : CAWG_00201
Ortholog(s) have phosphatidylinositol-4,5-bisphosphate binding, signaling adaptor activity
Putative RNA exonuclease; induced in a ssr1 null mutant
Protein of unknown function; induced by Mnl1 under weak acid stress
Ortholog of C. dubliniensis CD36 : Cd36_11670, C. parapsilosis CDC317 : CPAR2_201750, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_11710, C. auris B8441 : B9J08_003469, Candida tenuis NRRL Y-
Ortholog of C. dubliniensis CD36 : Cd36_11720, C. parapsilosis CDC317 : CPAR2_201890, C. auris B8441
Putative elongator complex subunit; for modification of wobble nucleosides in tRNA; Spider biofilm induced
Has domain(s) with predicted membrane localization
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Protein involved in pre-mRNA splicing; Spider biofilm induced
Ortholog(s) have role in mitochondrial respiratory chain complex assembly, proteolysis and mitochondrial in
Ortholog(s) have ubiquitin conjugating enzyme activity, ubiquitin-protein transferase activity and role in free
Ortholog(s) have protein-containing complex binding activity
Ortholog(s) have role in mRNA splicing, via spliceosome and U4/U6 snRNP, U4/U6 x U5 tri-snRNP comple
Ortholog(s) have unfolded protein binding activity, role in ribosome biogenesis and nucleolus localization
Ortholog of C. dubliniensis CD36 : Cd36_11870, C. parapsilosis CDC317 : CPAR2_201650, C. auris B8441
Ortholog of Candida albicans WO-1 : CAWG_00172
Ortholog of C. dubliniensis CD36 : Cd36_11880, C. auris B8441 : B9J08_002514, Candida tenuis NRRL Y-
Ortholog of C. dubliniensis CD36 : Cd36_11890 and Candida albicans WO-1 : CAWG_00170
Predicted cysteine proteinase domain; mutants are viable
Pre-mRNA splicing factor; important for catalytic step II of pre-mRNA splicing; possible role in cell cycle pro
Putative nuclear export protein; Hap43p-induced gene; decreased transcription is observed in an azole-resi
Ortholog of C. dubliniensis CD36 : Cd36_11980, C. parapsilosis CDC317 : CPAR2_201330, C. auris B8441
Ortholog(s) have 5-amino-6-(5-phosphoribosylamino)uracil reductase activity and role in riboflavin biosynth
Ortholog(s) have DNA-directed 5'-3' RNA polymerase activity, RNA polymerase I activity, RNA polymerase
Ortholog(s) have ubiquitin binding activity
Ortholog(s) have role in cellular response to DNA damage stimulus and FANCM-MHF complex localization
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Ortholog of Candida albicans WO-1 : CAWG_00155
Has domain(s) with predicted DNA binding, nucleic acid binding activity

Ortholog of C. dubliniensis CD36 : Cd36_12030 and Candida albicans WO-1 : CAWG_00152
Protein of unknown function; Spider biofilm repressed
Ortholog(s) have Golgi apparatus localization
Predicted membrane transporter; sugar porter (SP) family member, major facilitator superfamily; caspofung
Ortholog of C. parapsilosis CDC317 : CPAR2_801655, Candida tropicalis NEW ASSEMBLY : CTRG1_CG
Protein of unknown function; repressed in ssr1 mutant; Spider biofilm induced
Ortholog(s) have mRNA binding, translation regulator activity and role in mitochondrial cytochrome c oxidas
Putative tRNA-Cys synthetase; induced by alpha pheromone in SpiderM medium; ribosomal subunits, trans
Ortholog(s) have role in mitochondrial translation and mitochondrion localization
Putative adhesin-like protein; Spider biofilm induced
Putative histidine permease; fungal-specific (no human or murine homolog); Hap43p-induced gene
Ortholog of C. dubliniensis CD36 : Cd36_12240, C. parapsilosis CDC317 : CPAR2_801750, C. auris B8441
Mitochondrial membrane protein of unknown function; Spider biofilm induced
Protein of unknown function; Spider biofilm induced
Protein of unknown function; flow model biofilm induced; Spider biofilm induced
Ortholog(s) have FK506 binding, peptidyl-prolyl cis-trans isomerase activity and membrane localization
Putative ATPase; predicted role in ER-associated protein catabolism; induced during chlamydospore forma
Ortholog(s) have role in vacuolar acidification and integral component of membrane localization
Ortholog(s) have role in ascospore wall assembly and ascospore wall, prospore membrane localization
Protein of unknown function; Spider biofilm repressed
Ortholog(s) have spermine synthase activity and role in pantothenate biosynthetic process, spermine biosyn
Ortholog(s) have protein carrier activity, unfolded protein binding activity, role in ribosomal large subunit bio
Ortholog(s) have role in mRNA splicing, via spliceosome and RES complex, nucleus localization
Protein of unknown function; rat catheter biofilm induced
Protein of unknown function; Spider biofilm induced
Ortholog(s) have role in cellular calcium ion homeostasis, regulation of G0 to G1 transition
S. cerevisiae ortholog Sae2 is an endonuclease that processes hairpin DNA structures with the MRX compl
Ortholog of C. dubliniensis CD36 : Cd36_12580
Ortholog of S. cerevisiae : YBL029W, C. glabrata CBS138 : CAGL0F04125g, C. parapsilosis CDC317 : CP
Ortholog(s) have GTPase regulator activity and cytoplasm, nucleus localization
Ortholog(s) have SNAP receptor activity and role in Golgi to plasma membrane transport, ascospore-type p
Ortholog of S. cerevisiae : KEL3, C. glabrata CBS138 : CAGL0A01067g, C. dubliniensis CD36 : Cd36_127
Ortholog of C. dubliniensis CD36 : Cd36_12740, C. parapsilosis CDC317 : CPAR2_201620, C. auris B8441
Has domain(s) with predicted nucleic acid binding activity
Ortholog(s) have role in [4Fe-4S] cluster assembly, protein maturation by [4Fe-4S] cluster transfer and mito
Ortholog of C. dubliniensis CD36 : Cd36_12800, C. parapsilosis CDC317 : CPAR2_203460, C. auris B8441
Protein of unknown function; Hap43-induced; Spider biofilm induced
Ortholog(s) have inorganic cation transmembrane transporter activity and role in cellular cobalt ion homeos
C2H2 transcription factor; Spider biofilm induced
Ortholog(s) have Atg8 ligase activity, enzyme activator activity, protein tag activity
Putative Rho GDP dissociation inhibitor; induced by nitric oxide independent of Yhb1p
Protein of unknown function; Spider biofilm induced
Putative beta-adaptin, large subunit of the clathrin associated protein complex (AP-2); mutation causes dec
Putative ATP-dependent RNA helicase; fungal-specific (no human or murine homolog)
Glucan 1,3-beta-glucosidase; regulated by Nrg1, Tup1 and possibly Tac1; induced by NO and during cell w
Nucleolar protein; component of the small subunit processome containing the U3 snoRNA; involved in pre-
Ortholog(s) have chaperone binding, unfolded protein binding activity and role in chaperone-mediated prote
Ortholog(s) have protein-lysine N-methyltransferase activity, role in peptidyl-lysine monomethylation and cyt
Ortholog(s) have ubiquitin protein ligase activity and role in histone catabolic process, histone ubiquitination
Ortholog of C. dubliniensis CD36 : Cd36_13150, C. parapsilosis CDC317 : CPAR2_700610, C. auris B8441
Protein phosphatase inhibitor; Hap43-repressed; homozygous Tn insertion decreases colony wrinkling but c
Possible Golgi membrane protein; transcript positively regulated by Tbf1; mRNA binds She3
Component of the RSC chromatin remodeling complex; possibly an essential gene, disruptants not obtaine
Putative protein of unknown function; mutation confers hypersensitivity to amphotericin B
Ortholog(s) have arylformamidase activity and role in NAD biosynthetic process
Deoxycytidine monophosphate (dCMP) deaminase; role in dUMP and dTMP biosynthesis; Spider biofilm re
Putative fumarylacetoacetate hydrolase; induced by nitric oxide independent of Yhb1; regulated by Sef1, Sf
Ortholog(s) have tRNA-5-taurinomethyluridine 2-sulfurtransferase activity, role in mitochondrial tRNA wobbl
Protein of unknown function; rat catheter and Spider biofilm induced
Ortholog(s) have role in mRNA metabolic process, mitochondrial translational initiation and extrinsic compo
Ortholog of S. cerevisisae/S. pombe Lsm5; Lsm (Like Sm) protein involved in mRNA decay; Predicted ORF
Protein with a predicted NADP-dependent oxidoreductase or aldo-keto reductase domain; Hap43-represse
Putative X-Pro aminopeptidase; Spider biofilm repressed
Metalloprotease subunit of the 19S regulatory particle of the 26S proteasome lid; couples the deubiquitinati

Putative zinc-finger domain protein with a predicted role in pre-mRNA splicing; Hap43-repressed; Spider bio
Ortholog of Candida albicans WO-1 : CAWG_00007
Putative polyamine acetyltransferase; acetylates polyamines (e.g. putrescine, spermidine, spermine) and ar
Protein of unknown function; Spider biofilm repressed
Protein of unknown function; transcript detected on high-resolution tiling arrays
Protein of unknown function; transcript detected on high-resolution tiling arrays
Predicted ORF in retrotransposon Zorro2 with similarity to retroviral reverse transcriptase proteins
Predicted ORF in retrotransposon Zorro2 with similarity to zinc finger-containing retroviral nucleocapsid pro
Similar to a region of the Tca2 (pCal) retrotransposon, which is present in strain hOG1042 as 50 to 100 cop
Protein of unknown function; Spider biofilm repressed
Protein of unknown function; flow model biofilm induced
Predicted NADH-dependent flavin oxidoreductase; Hap43-repressed gene
Putative molybdopterin-converting factor; fungal-specific (no human or murine homolog)
Predicted uricase; ortholog of S. pombe SPCC1223.09; Spider biofilm induced
Putative integral peroxisomal membrane protein; Hap43p-repressed gene
snRNP U5 splicing factor component; involved in positioning the 3' splice site during the 2nd catalytic step o
Ortholog(s) have RNA polymerase II complex binding activity
Ortholog(s) have arginyltransferase activity and role in protein arginylation
Putative protein of unknown function; Hap43p-repressed gene
Putative pre-mRNA-splicing factor; possibly an essential gene, disruptants not obtained by UAU1 method
Ortholog(s) have ATPase activator activity, chaperone binding activity
Ortholog of Candida albicans WO-1 : CAWG_03811
Ortholog(s) have protein-membrane adaptor activity, role in mitophagy, protein insertion into ER membrane
Predicted DNA-dependent ATPase/helicase; Spider biofilm induced
Ortholog(s) have role in negative regulation of transcription from RNA polymerase II promoter in response t
Putative peroxisomal cystathionine beta-lyase; Gcn4p-regulated
Putative NADH dehydrogenase; repressed by nitric oxide, Hap43p-repressed
Ortholog of S. cerevisiae Ecm16, an essential DEAH-box ATP-dependent RNA helicase specific to the U3 s
Ortholog of Nyv1, v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion in S. cer
Ortholog(s) have role in Golgi to vacuole transport and early endosome, trans-Golgi network localization
Protein of unknown function; S. pombe ortholog SPAC7D4.05 encodes a predicted hydrolase; Hap43-repre
Protein with a multidrug and toxin extrusion protein domain; induced by Mnl1 under weak acid stress
Ortholog(s) have (R)-carnitine transmembrane transporter activity, choline transmembrane transporter activ
Component of the RSC chromatin remodeling complex
Ortholog of C. dubliniensis CD36 : Cd36_15550, C. parapsilosis CDC317 : CPAR2_213190, C. auris B8441
Protein with a predicted role in mitochondrial iron metabolism; Hap43-repressed; expression upregulated du
Ortholog(s) have protein-lysine N-methyltransferase activity and role in peptidyl-lysine trimethylation
Ortholog(s) have allantoicase activity and role in allantoin catabolic process
Putative transcription factor with zinc finger DNA-binding motif
Ortholog of C. dubliniensis CD36 : Cd36_15600, C. parapsilosis CDC317 : CPAR2_213140, C. auris B8441
Protein with homology to magnesium-dependent endonucleases and phosphatases; regulated by Sef1, Sfu
Ortholog(s) have ATP binding, ATPase, metallopeptidase activity and role in cellular protein-containing com
Ortholog of C. dubliniensis CD36 : Cd36_15670, C. parapsilosis CDC317 : CPAR2_213100, C. auris B8441
Ortholog(s) have sterol esterase activity, role in cellular lipid metabolic process, sterol metabolic process ar
Plasma membrane-associated protein; heterozygous null mutant displays sensitivity to virgineone; Spider b
Proten of unknown function; transcript positively regulated by Sfu1; Hap43 repressed; Spider biofilm induce
Putative protein of unknown function; Hap43p-repressed gene; mutation confers hypersensitivity to toxic erg
Ortholog(s) have diacylglycerol kinase activity and role in phosphatidic acid biosynthetic process, regulation
Has domain(s) with predicted ATP binding, ATPase, iron-sulfur cluster binding activity and role in iron-sulfur
Ortholog(s) have role in mitochondrial tRNA wobble uridine modification and mitochondrial inner membrane
Component of the RSC chromatin remodeling complex
Ortholog(s) have oxidoreductase activity, acting on NAD(P)H activity
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_15810, C. parapsilosis CDC317 : CPAR2_212950, C. auris B8441
Predicted dihydrodiol dehydrogenase; ortholog of S. pombe SPAC513.06c; flow model and rat catheter biof
Ortholog of C. dubliniensis CD36 : Cd36_15830, C. parapsilosis CDC317 : CPAR2_212930, Candida tropic
Ortholog of C. parapsilosis CDC317 : CPAR2_212925, C. dubliniensis CD36 : Cd36_15840, Candida tropic
Protein of unknown function; rat catheter biofilm induced
Plasma membrane-associated protein; induced in cyr1 or ras1 mutant; induced by hypoxia, ketoconazole a
Ortholog(s) have structural constituent of ribosome activity, role in mitochondrial translation and mitochondr
PProtein of unknown function; gene has intron; similar to human BLOC1S2
Ortholog of Candida tropicalis NEW ASSEMBLY : CTRG1_CGOB_00043 and Candida tropicalis MYA-340
Protein with a predicted DnaJ chaperone domain and a CSL-type zinc finger; Spider biofilm induced
Ortholog(s) have RNA polymerase I activity and role in nucleolar large rRNA transcription by RNA polymera

Ortholog of C. dubliniensis CD36 : Cd36_16030, C. parapsilosis CDC317 : CPAR2_213800, Debaryomyces
Ortholog(s) have S-methyl-5-thioribose-1-phosphate isomerase activity and role in L-methionine salvage fro
Ortholog(s) have role in Golgi to vacuole transport, ascospore wall assembly, cellular sphingolipid homeosta
Ortholog of S. cerevisiae : YPL162C, C. glabrata CBS138 : CAGL0M02057g, C. dubliniensis CD36 : Cd36_
Ortholog(s) have structural constituent of nuclear pore activity
Has domain(s) with predicted 2-oxoglutarate-dependent dioxygenase activity, L-ascorbic acid binding, iron i
Ortholog(s) have DNA helicase activity and role in DNA-dependent DNA replication maintenance of fidelity,
Protein of unknown function; transcript detected on high-resolution tiling arrays
Ortholog of C. dubliniensis CD36 : Cd36_16140, C. parapsilosis CDC317 : CPAR2_213870, C. auris B8441
Ortholog(s) have phosphatidylinositol binding, phosphatidylinositol-3-phosphate binding activity, role in retro
Subunit of the 19S regulatory particle lid of the proteasome
Has domain(s) with predicted integral component of membrane localization
Component of the RSC chromatin remodeling complex; only present in CTG clade
Ortholog(s) have phosphatidylinositol-4,5-bisphosphate binding activity, role in actin cortical patch assembly
Has domain(s) with predicted DNA-binding transcription factor activity, sequence-specific DNA binding activ
Ortholog(s) have plus-end-directed microtubule motor activity, protein-containing complex binding activity
Protein of unknown function; induced in azole-resistant strain that overexpresses MDR1; protein present in
Ortholog of C. dubliniensis CD36 : Cd36_16320, Candida tropicalis NEW ASSEMBLY : CTRG1_01238, Ca
Putative RNA polymerase transcription factor TFIIH core component; possibly an essential gene, disruptant
Ortholog of Candida albicans WO-1 : CAWG_03922
Ortholog(s) have tRNA-specific adenosine deaminase activity and role in tRNA modification
Putative glutamine-dependent NAD synthetase, involved in NAD salvage pathway
S. pombe ortholog SPCC576.01c is a predicted sulfonate dioxygenase; possibly transcriptionally regulated
Has domain(s) with predicted N-acetyltransferase activity
2-hydroxyacid dehydrogenase domain-containing protein; Hap43-repressed gene; induced by alpha pheron
Ortholog(s) have mRNA (N6-adenosine)-methyltransferase activity and role in mRNA methylation, meiotic
Protein of unknown function; possible ER protein; Hap43p-repressed; Spider biofilm induced
Ortholog of the mitochondria localized S. cerevisiae Pib2 protein of unknown function; has a FYVE zinc fing
Putative succinate dehydrogenase; enzyme of citric acid cycle; repressed by nitric oxide; Efg1, Hap43 repre
Ortholog(s) have copper ion binding activity, role in mitochondrial cytochrome c oxidase assembly and extri
Ortholog of S, cerevisiae Spc24; a component of the conserved kinetochore-associated Ndc80 complex inv
Mitochondrial ribosomal protein of the large subunit; rat catheter biofilm induced
Protein with a life-span regulatory factor domain; regulated by Sef1, Sfu1, and Hap43; flow model biofilm in
Ortholog of C. dubliniensis CD36 : Cd36_16630, C. parapsilosis CDC317 : CPAR2_210300, C. auris B8441
Predicted ORF in retrotransposon Tca16 with similarity to the Gag-Pol region of retrotransposons; added to
Ortholog(s) have RNA binding activity, role in mRNA splicing, via spliceosome and U1 snRNP, U2-type pres
Ortholog(s) have role in L-methionine salvage from methylthioadenosine
Putative transcription factor with zinc finger DNA-binding motif; Hap43p-repressed gene
Ortholog of C. dubliniensis CD36 : Cd36_16720, C. parapsilosis CDC317 : CPAR2_210210, C. auris B8441
Has domain(s) with predicted aminoacyl-tRNA hydrolase activity
Putative patatin-like phospholipase; fungal-specific (no human or murine homolog)
Ortholog of S. cerevisiae : YBR138C, C. dubliniensis CD36 : Cd36_16750, C. parapsilosis CDC317 : CPAR
Ortholog(s) have enzyme binding, phosphatidylinositol-4-phosphate binding activity
Ortholog(s) have thiol-dependent deubiquitinase activity and role in negative regulation of gluconeogenesis,
Protein of unknown function; Hap43-repressed gene
Ortholog of C. dubliniensis CD36 : Cd36_16850, C. parapsilosis CDC317 : CPAR2_211990, C. auris B8441
Ortholog(s) have role in nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
Protein of unknown function; Spider biofilm induced
Putative mitochondrial RNA polymerase specificity factor; possibly an essential gene, disruptants not obtain
Protein of unknown function; macrophage-induced gene
Protein of unknown function
Ortholog(s) have RNA binding activity and role in mRNA polyadenylation, pre-mRNA cleavage required for
Possible vacuolar protein; Hap43-induced gene
Ortholog of S. cerevisiae Zrt3, vacuolar membrane zinc transporter; predicted Kex2 substrate; induced in o
Protein of unknown function; Hap43-induced gene
Putative zinc transporter essential for tolerance to zinc; plays a role in zincosome formation; Hap43-induced
Protein of unknown function; F-12/CO2 early biofilm induced
Protein with a globin-like domain; repressed by alpha pheromone in SpiderM medium; Spider biofilm induce
Putative cis-golgi localized protein involved in ER to Golgi transport; Spider biofilm repressed
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Membrane-localized protein of unknown function
Ortholog(s) have double-stranded DNA binding, polynucleotide 3'-phosphatase activity and role in double-st
Ortholog(s) have role in mRNA splicing, via spliceosome and U4/U6 x U5 tri-snRNP complex localization
Plasma membrane-associated protein identified in detergent-resistant membrane fraction (possible lipid raf

Predicted protein of unknown function; overlaps CPR3/orf19.1552
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity and role in protein methylatio
Protein of unknown function; flow model biofilm induced; Spider biofilm induced; repressed by alpha pheron
Plasma membrane-localized protein of unknown function
Protein of unknown function
Putative component of vacuole-mitochondrion patches (vCLAMPs), involved in autophagy under nitrogen s
Ortholog(s) have fungal-type vacuole membrane, vacuole-mitochondrion membrane contact site localizatio
Putative TFIID subunit involved in RNA polymerase II transcription initiation; possibly an essential gene, dis
Ortholog(s) have nuclear localization sequence binding, ubiquitin binding activity and role in response to eth
Has domain(s) with predicted DNA-binding transcription factor activity, sequence-specific DNA binding, zinc
Ortholog of S. cereviaie Rrp5, an RNA binding protein involved in synthesis of 18S and 5.8S rRNAs; Hap43
Protein of unknown function; Spider biofilm induced
Predicted membrane transporter; member of the drug:proton antiporter (12 spanner) (DHA1) family, major
Predicted MFS membrane transporter; monocarboxylate porter family member; colony morphology-related
Putative mitochondrial protein of unknown function; regulated by Sef1p-, Sfu1p-, and Hap43p
Putative transcription factor component of the core factor (CF) rDNA transcription factor complex; Spider bi
Has domain(s) with predicted catalytic activity, pyridoxal phosphate binding activity and role in biosynthetic
Ortholog of C. dubliniensis CD36 : Cd36_17700, C. parapsilosis CDC317 : CPAR2_212340, C. auris B8441
Ortholog(s) have actin filament binding activity, role in negative regulation of actin filament polymerization a
Ortholog(s) have 4-amino-4-deoxychorismate lyase activity and role in folic acid biosynthetic process
Ortholog(s) have rRNA binding activity, role in rRNA processing, ribosomal small subunit assembly and CU
Ortholog(s) have role in mRNA export from nucleus, protein import into nucleus and cytoplasm, nucleus loc
Ortholog(s) have SUMO binding, polyubiquitin modification-dependent protein binding, ubiquitin binding acti
Ortholog of C. dubliniensis CD36 : Cd36_17620, C. parapsilosis CDC317 : CPAR2_212260, Candida tropic
Ortholog(s) have pre-mRNA branch point binding activity and role in mRNA branch site recognition, mRNA
Predicted amino acid transmembrane transporter; rat catheter biofilm repressed
Ortholog(s) have role in endoplasmic reticulum to Golgi vesicle-mediated transport and COPII-coated ER to
Protein of unknown function; rat catheter and Spider biofilm induced
Ortholog of S. cerevisiae : YML002W, C. dubliniensis CD36 : Cd36_17530, C. parapsilosis CDC317 : CPA
Ortholog(s) have role in cytoplasm to vacuole transport by the Cvt pathway, endoplasmic reticulum to Golgi
Protein of unknown function; Spider biofilm induced
Protein of unknown function
Putative adhesin-like protein; upregulated during growth in the mouse cecum; flow model, rat catheter and
Ortholog of S. cerevisiae Ett1, a nuclear protein that inhibits replication of Brome mosaic virus; early-stage
Putative arylformamidase, enzyme of the NAD biosynthesis pathway; Gcn4p-regulated
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity, protein-lysine N-methyltrans
Ortholog(s) have transferase activity, role in maturation of SSU-rRNA and cytoplasm localization
Ortholog of S. cerevisiae : TPH3, C. dubliniensis CD36 : Cd36_17790, C. parapsilosis CDC317 : CPAR2_2
Protein of unknown function; upregulated in a cyr1 or ras1 null mutant; induced by nitric oxide
Ortholog(s) have protein-arginine omega-N monomethyltransferase activity and role in peptidyl-arginine me
Ortholog(s) have phospholipase activity, role in cardiolipin metabolic process, phosphatidylethanolamine me
Putative protein of unknown function; Hap43p-repressed gene
Protein of unknown function; F-12/CO2 early biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_17965, C. parapsilosis CDC317 : CPAR2_211700, C. auris B8441
Ortholog(s) have cytoplasm, nucleus localization
Ortholog of C. dubliniensis CD36 : Cd36_18040, C. parapsilosis CDC317 : CPAR2_211790, C. auris B8441
Ortholog(s) have guanyl-nucleotide exchange factor activity and role in retrograde transport, endosome to
Putative AMP deaminase; possibly an essential gene, disruptants not obtained by UAU1 method
Ortholog(s) have role in COPII-coated vesicle cargo loading and COPII vesicle coat localization
Ortholog(s) have myosin binding activity, role in intracellular mRNA localization, mating type switching and
Protein required for respiratory growth
Predicted mitochondrial i-AAA protease supercomplex; degrades misfolded mitochondrial proteins; Hap43-
Ortholog of C. dubliniensis CD36 : Cd36_18230, C. auris B8441 : B9J08_004272, Debaryomyces hansenii
Ortholog(s) have GTPase activator activity, role in positive regulation of GTPase activity, positive regulation
Ortholog(s) have superoxide-generating NAD(P)H oxidase activity, role in apoptotic process, regulation of a
Ortholog(s) have role in DNA recombination, nuclear-transcribed mRNA catabolic process, 3'-5' exonucleol
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_18340, Candida tenuis NRRL Y-1498 : CANTEDRAFT_124631,
Protein of unknown function; repressed by Rim101; negatively modulates intracellular ATP levels during the
Ortholog(s) have protein-N-terminal asparagine amidohydrolase activity, protein-N-terminal glutamine amid
Ortholog(s) have enzyme activator activity and role in protein N-linked glycosylation, protein O-linked glycos
Predicted protein kinase similar to S. cerevisiae Nnk1; implicated in proteasome function in S. cerevisiae; ir
Putative DNA repair exonuclease; fungal-specific (no human or murine homolog)

Ortholog(s) have SNARE binding activity, role in Golgi vesicle docking, Golgi vesicle transport and Golgi me
Putative endoribonuclease; induced by nitric oxide independent of Yhb1p; mutation confers hypersensitivity
Ortholog(s) have U1 snRNP, U2 snRNP, U2-type prespliceosome, U4/U6 x U5 tri-snRNP complex, U5 snR
Protein likely to be essential for growth, based on an insertional mutagenesis strategy
Ortholog(s) have role in nucleosome mobilization and Ino80 complex, cytosol, nucleus localization
Ortholog(s) have carbohydrate binding, mannosyl-oligosaccharide 1,2-alpha-mannosidase activity
Subunit of SWI/SNF chromatin remodeling complex; involved in transcriptional regulation of carbon utilizatio
Putative ribosomal protein, large subunit, mitochondrial precursor; repressed by prostaglandins; Spider biof
Ortholog of C. dubliniensis CD36 : Cd36_18620, C. parapsilosis CDC317 : CPAR2_212480, C. auris B8441
Protein of unknown function; Spider biofilm induced
Protein of unknown function; mutants are viable; Hap43-induced gene; oxidative stress-induced via Cap1; r
Ortholog of C. dubliniensis CD36 : Cd36_18730, C. parapsilosis CDC317 : CPAR2_212510, C. auris B8441
Protein of unknown function; mutant is viable; Hap43-repressed
Ortholog(s) have DNA helicase activity, heteroduplex DNA loop binding activity
Ortholog(s) have rRNA binding activity, role in maturation of LSU-rRNA from tricistronic rRNA transcript (SS
Ortholog(s) have role in histone deacetylation, negative regulation of chromatin silencing at telomere and ne
Putative protein of unknown function; possibly mitochondrial; Hap43-repressed; Spider biofilm repressed
Ortholog of S. cerevisiae : YPR010C-A, C. dubliniensis CD36 : Cd36_02990, C. parapsilosis CDC317 : CP
Putative mitochondrial carrier family transporter; rat catheter biofilm induced
Ortholog(s) have protein serine/threonine kinase activity, protein serine/threonine/tyrosine kinase activity, pr
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_18970, C. parapsilosis CDC317 : CPAR2_212800, Debaryomyces
S. cerevisiae ortholog Env9 has similarity to oxidoreductases and is proposed to have vacuolar functions, fo
Putative gluconokinase; rat catheter biofilm induced
Protein kinase of unknown function; mutants are viable
Protein of unknown function; Hap43-induced gene
Ortholog(s) have tetrahydrofolylpolyglutamate synthase activity, role in one-carbon metabolic process and c
Predicted protein with similarity to cell wall proteins; possibly an essential gene, disruptants not obtained by
Protein of unknown function; mutants are viable; rat catheter and Spider biofilm induced
Ortholog of Candida albicans WO-1 : CAWG_04197
Protein of unknown function
Ortholog of Candida albicans WO-1 : CAWG_04200
Protein of unknown function; Hap43-repressed; rat catheter biofilm repressed
Has domain(s) with predicted oxidoreductase activity, zinc ion binding activity
Similar to HMG-box variant of S. pombe; Spider biofilm repressed
Ortholog(s) have ATPase, DNA binding, TBP-class protein binding activity
Ortholog of C. dubliniensis CD36 : Cd36_19120, C. parapsilosis CDC317 : CPAR2_103880, C. auris B8441
Ortholog(s) have role in nuclear division, rRNA processing, ribosomal large subunit biogenesis and nuclear
Predicted ortholog of S. cerevisiae Swi3, subunit of the SWI/SNF chromatin remodeling complex; possibly a
Protein of unknown function; transcript detected on high-resolution tiling arrays
Putative ortholog of S. cerevisiae Utp30; a U3-containing 90S preribosome complex protein; Hap43-induced
Ortholog of C. dubliniensis CD36 : Cd36_19300, C. parapsilosis CDC317 : CPAR2_209720, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_19310, C. parapsilosis CDC317 : CPAR2_209710, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_19320, C. parapsilosis CDC317 : CPAR2_209670, C. auris B8441
Ortholog(s) have role in chromatin remodeling, endoplasmic reticulum organization, histone exchange and
Ortholog of Candida albicans WO-1 : CAWG_04234
Ortholog(s) have structural constituent of ribosome activity, role in mitochondrial translation, mitochondrial t
Ortholog(s) have rRNA (guanine-N1-)-methyltransferase activity, role in rRNA modification and mitochondri
Ortholog of C. dubliniensis CD36 : Cd36_19390, C. parapsilosis CDC317 : CPAR2_209600, C. auris B8441
Ortholog(s) have actin filament binding activity, role in actin cortical patch localization, actin cytoskeleton org
Putative THO complex subunit; possibly an essential gene, disruptants not obtained by UAU1 method; prot
Protein of unknown function; Spider biofilm induced
Ortholog(s) have role in regulation of DNA-dependent DNA replication initiation and DNA replication preinitia
Ortholog(s) have role in mitochondrion organization
Ortholog(s) have cellular bud neck, fungal-type vacuole localization
Ortholog(s) have acetylglucosaminyltransferase activity, role in protein N-linked glycosylation and Golgi med
Putative sulfiredoxin; regulated by Tsa1, Tsa1B in minimal media at 37 degrees C; flow model biofilm induc
Predicted nucleolar S-adenosylmethionine-dependent rRNA methyltransferase; Spider biofilm induced
Putative protein of unknown function; Hap43p-repressed gene
Ortholog(s) have mRNA 3'-UTR binding, mRNA 5'-UTR binding, translation repressor activity, mRNA regula
Ortholog(s) have mitochondrial inner membrane localization
Ortholog(s) have structural constituent of nuclear pore activity
Transportin or cytosolic karyopherin beta; Spider biofilm induced
Has domain(s) with predicted role in transport and integral component of membrane localization

S. cerevisiae ortholog Mrps35p is a structural constituent of ribosome and localizes to mitochondrial small r
Ortholog of C. dubliniensis CD36 : Cd36_19810, C. parapsilosis CDC317 : CPAR2_206450, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_19830, C. parapsilosis CDC317 : CPAR2_206470, C. auris B8441
Protein of unknown function; S. cerevisiae YLR407W mutants have abnormal budding; constitutive express
Ortholog of C. dubliniensis CD36 : Cd36_19870, C. parapsilosis CDC317 : CPAR2_209420, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_19880, C. auris B8441 : B9J08_003635, Candida tenuis NRRL Y-
Ribosomal 60S subunit protein L31B; Spider biofilm repressed
Ortholog(s) have mitochondrial intermembrane space localization
Ortholog of C. dubliniensis CD36 : Cd36_19950, C. parapsilosis CDC317 : CPAR2_104135, Candida tenuis
Ortholog(s) have histone binding activity, role in DNA replication-dependent nucleosome assembly and CA
Ortholog(s) have protein-lysine N-methyltransferase activity and role in peptidyl-lysine dimethylation, peptid
Ortholog(s) have role in protein export from nucleus, regulation of chromatin silencing at telomere, ribosom
Putative U1-70K component of the U1 snRNP, involved in splicing; ortholog of S. cerevisiae SNP1; downre
Protein with a predicted cytochrome b5-like heme/steroid binding domain; repressed by alpha pheromone i
Putative NADPH-dependent methylglyoxal reductase; homozygous transposon insertion causes decreased
Putative lipid raft associated protein; Spider biofilm induced
Protein of unknown function; Hap43-induced; flow model biofilm repressed
Putative protein of unknown function; Hap43p-repressed gene
Putative helix-loop-helix (HLH) transcription factor with a role in filamentous growth
Ortholog(s) have tRNA-intron endonuclease activity, role in tRNA-type intron splice site recognition and clea
Ribosomal 60S subunit protein; Spider biofilm repressed
Putative oxysterol binding protein family; probable peripheral membrane protein of the Golgi complex; flow
Ortholog(s) have rRNA binding activity and role in maturation of LSU-rRNA from tricistronic rRNA transcript
Predicted ORF from Assembly 19; repressed by nitric oxide; removed from Assembly 20; subsequently rein
Zn(II)2Cys6 domain transcription factor; regulated by Mig1 and Tup1; rat catheter and Spider biofilm induce
Ortholog(s) have GTPase binding activity, role in endoplasmic reticulum to Golgi vesicle-mediated transport
Ortholog(s) have role in cellular response to methylmercury
Protein of unknown function; Hap43-repressed gene
Putative chaperone protein; role in the assembly of box H/ACA snoRNPs and thus for pre-rRNA processing
Predicted diphthamide biosynthesis protein; Spider biofilm induced
Ortholog(s) have role in cytoplasm to vacuole transport by the Cvt pathway, intra-Golgi vesicle-mediated tra
Putative Xbp1 transcriptional repressor; binds to cyclin gene promoters in S. cerevisiae; Hap43-repressed;
Protein conserved in C. dublinensis
Ortholog(s) have SUMO transferase activity, chromatin binding activity and role in homologous chromosom
Putative protein of unknown function; transcript is upregulated in clinical isolates from HIV+ patients with or
Ortholog of C. dubliniensis CD36 : Cd36_20380, C. parapsilosis CDC317 : CPAR2_209840, Candida tropic
Ortholog(s) have acyl-CoA hydrolase activity, role in fatty acid beta-oxidation, fatty acid oxidation and perox
Predicted thioesterase/thiol ester dehydrase-isomerase; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_20450, C. parapsilosis CDC317 : CPAR2_104160, C. auris B8441
Ortholog(s) have N-acetyltransferase activity, role in response to drug and nuclear envelope, plasma memb
Ortholog(s) have 8-oxo-dGDP phosphatase activity, thiamine diphosphokinase activity and role in thiamine
Ortholog of C. dubliniensis CD36 : Cd36_20490, C. parapsilosis CDC317 : CPAR2_104180, C. auris B8441
Exopolyphosphatase, hydrolyzes inorganic polyphosphate (poly P) into Pi residues; Spider biofilm represse
Ortholog(s) have ubiquitin conjugating enzyme binding activity
Ortholog of C. dubliniensis CD36 : Cd36_20540, C. parapsilosis CDC317 : CPAR2_104860, C. auris B8441
Ortholog of C. parapsilosis CDC317 : CPAR2_104840, C. auris B8441 : B9J08_001223, Candida tenuis N
Ortholog(s) have GTPase activity, mitochondrial ribosome binding activity, role in positive regulation of tran
Putative endoribonuclease; heterozygous null mutant exhibits hypersensitivity to parnafungin and cordycep
Ortholog(s) have mitochondrial inner membrane, mitochondrial large ribosomal subunit, mitochondrion loca
Ortholog of C. dubliniensis CD36 : Cd36_20660, C. parapsilosis CDC317 : CPAR2_104730, Candida tenuis
Ortholog of C. dubliniensis CD36 : Cd36_20670, C. parapsilosis CDC317 : CPAR2_104720, C. auris B8441
Ortholog(s) have mRNA binding, pre-mRNA 5'-splice site binding activity and role in mRNA 5'-splice site rec
Putative RNA-binding protein; induced by alpha pheromone in SpiderM medium
Ortholog(s) have 4-hydroxyphenylpyruvate dioxygenase activity and role in aromatic amino acid family bios
Ortholog(s) have role in ethanol metabolic process and mitochondrial inner membrane localization
Protein with homology to peroxisomal membrane proteins; Sef1p-, Sfu1p-, and Hap43p-regulated gene
Ortholog(s) have tRNA (guanine(9)-N(1))-methyltransferase activity, tRNA (guanine) methyltransferase acti
Putative peptide N-glycanase; induced by nitric oxide independent of Yhb1p
Ortholog of C. dubliniensis CD36 : Cd36_20860, C. parapsilosis CDC317 : CPAR2_104250, C. auris B8441
Putative thiamine transmembrane transporter; Spider biofilm induced
Ortholog of S. cerevisiae Tah11, a DNA replication licensing factor required for pre-replication complex ass
Ortholog of C. parapsilosis CDC317 : CPAR2_201960, C. dubliniensis CD36 : Cd36_20900, Candida meta
Predicted ORF from Assembly 19; removed from Assembly 20; restored based on transcription data; simila
Predicted kinase; rat catheter, flow model, Spider biofilm induced

Protein of unknown function
Component of the conserved oligomeric Golgi complex; predicted to mediate fusion of transport vesicles to
Ortholog of C. parapsilosis CDC317 : CPAR2_104640, Candida orthopsilosis Co 90-125 : CORT_0B05695
Ortholog(s) have role in spliceosomal snRNP assembly and U4/U6 x U5 tri-snRNP complex localization
Ortholog(s) have role in exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic r
Has domain(s) with predicted catalytic activity and role in cellular metabolic process
Protein of unknown function; possibly an essential gene, disruptants not obtained by UAU1 method
Ortholog of C. dubliniensis CD36 : Cd36_21050, C. parapsilosis CDC317 : CPAR2_104310, C. auris B8441
Protein of unknown function; flow model biofilm induced; nitric oxide-repressed
Ortholog(s) have actin filament binding, actin monomer binding activity
Ortholog(s) have ubiquitin-protein transferase activity, role in protein ubiquitination, response to ethanol, se
Putative pre-mRNA-splicing factor; decreased transcription is observed upon benomyl treatment
Protein of unknown function; Spider biofilm induced
Ortholog of Slx9 required for pre-rRNA processing; associated with 90S pre-ribosome and 43S small ribos
Similar to oxidoreductases and to S. cerevisiae Yjr096wp; Sfu1 repressed; induced by benomyl treatment,
Ortholog of S. cerevisiae : YPL199C, C. glabrata CBS138 : CAGL0G09108g, C. dubliniensis CD36 : Cd36_
Ortholog of C. dubliniensis CD36 : Cd36_21220, C. parapsilosis CDC317 : CPAR2_406700, Candida tenui
Putative metalloprotease of the mitochondrial inner membrane; expression downregulated in an ssr1 null m
Protein of unknown function; rat catheter biofilm repressed
Protein of unknown function; expression regulated by white-opaque switch; repressed by alpha pheromone
Ortholog of S. cerevisiae : YCR051W, C. glabrata CBS138 : CAGL0C03003g, C. dubliniensis CD36 : Cd36
Predicted ER protein involved in ER-nucleus signaling; Spider biofilm repressed
Ortholog of C. dubliniensis CD36 : Cd36_21310, C. parapsilosis CDC317 : CPAR2_406650, C. auris B8441
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Putative transcription factor with zinc finger DNA-binding motif
Ortholog(s) have RNA binding activity, role in mRNA splicing, via spliceosome and U2 snRNP, U2-type pre
Protein similar to quinone oxidoreductases; induced by benomyl treatment, nitric oxide; oxidative stress-ind
Ortholog of C. dubliniensis CD36 : Cd36_21360, C. parapsilosis CDC317 : CPAR2_406560, C. auris B8441
Component of the RSC chromatin remodeling complex
Ortholog(s) have ATPase, DNA binding, nucleosome binding activity, role in sister chromatid cohesion and
Putative 3-phosphoserine phosphatase; induced by benomyl or in azole-resistant strain that overexpresses
Ortholog of C. dubliniensis CD36 : Cd36_21450, Candida tropicalis NEW ASSEMBLY : CTRG1_01739, Ca
Putative mitochondrial ribosomal protein; predicted role in aerobic respiration; Spider biofilm repressed
Ortholog(s) have RNA-directed 5'-3' RNA polymerase activity
Putative 20S proteasome assembly protein; filament induced; induced by alpha pheromone in SpiderM me
Has domain(s) with predicted CoA-transferase activity and role in metabolic process
Has domain(s) with predicted catalytic activity, catechol 1,2-dioxygenase activity, ferric iron binding, iron ion
Protein with an FMN-binding domain; Hap43-repressed; flow model biofilm induced
Protein of unknown function; transcription induced by benomyl treatment
Putative deoxyhypusine hydroxylase; ketoconazole-induced; protein level decreases in stationary phase cu
Ortholog(s) have RNA methyltransferase activity and role in 7-methylguanosine cap hypermethylation, RNA
Ortholog of C. dubliniensis CD36 : Cd36_21640, C. parapsilosis CDC317 : CPAR2_105040, Candida tenui
Protein of unknown function; Spider biofilm repressed
Ortholog(s) have acylglycerol lipase activity, triglyceride lipase activity and role in medium-chain fatty acid b
Putative phosphoglycerate mutase family protein; stationary phase enriched protein; early-stage flow model
Putative nicotinamide riboside hydrolase; cleaves N-glycosidic bonds in nucleosides; pyrimidine salvage an
Ortholog(s) have sterol esterase activity, role in sterol metabolic process and integral component of membr
Has domain(s) with predicted nucleic acid binding activity
Ortholog(s) have mRNA binding activity and role in mRNA splice site selection, mRNA splicing, via spliceos
Ortholog(s) have protein serine/threonine kinase activity
Protein of unknown function; Hap43-repressed gene; repressed by nitric oxide
Plasma membrane protein; repressed by nitric oxide
Putative malate permease; induced during macrophage infection; regulated by Gcn2 and Gcn4; putative pe
Ortholog(s) have role in proteasome-mediated ubiquitin-dependent protein catabolic process, rescue of sta
Has domain(s) with predicted guanyl-nucleotide exchange factor activity, role in regulation of Rho protein si
Possible stress protein; increased transcription associated with CDR1 and CDR2 overexpression or flupher
BAR domain-containing protein, forms heterodimer with Rvs162p that binds liposomes in vitro; flow model
Ortholog(s) have extracellular region localization
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Ortholog(s) have role in negative regulation of telomere maintenance, positive regulation of helicase activity
Ortholog of C. dubliniensis CD36 : Cd36_21980, Debaryomyces hansenii CBS767 : DEHA2F19734g, Pichi
Ortholog of C. dubliniensis CD36 : Cd36_21990, C. parapsilosis CDC317 : CPAR2_103660, Debaryomyce
Protein of unknown function; Spider biofilm induced
Ortholog(s) have role in response to salt stress

Predicted membrane protein of unknown function; Spider biofilm induced
Ortholog of C. parapsilosis CDC317 : CPAR2_103590, C. auris B8441 : B9J08_004020, Debaryomyces ha
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Ortholog(s) have ribosome binding activity, role in mitochondrial respiratory chain complex III assembly, pos
Protein of unknown function; rat catheter biofilm repressed
Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine di
Ortholog(s) have ubiquitin binding activity
Ortholog of C. dubliniensis CD36 : Cd36_11730, C. parapsilosis CDC317 : CPAR2_104195, Candida tenuis
Ortholog(s) have diphthine methylesterase activity, role in endocytic recycling, peptidyl-diphthamide biosynt
Putative fumarylacetoacetate hydrolase; clade-associated gene expression; rat catheter and Spider biofilm
Ortholog(s) have calcium ion binding, zinc ion binding activity and role in axial cellular bud site selection, bip
Ortholog of Spathaspora passalidarum NRRL Y-27907 : spas_CGOB_00067 and Candida albicans WO-1 :
Protein of unknown function; Spider biofilm induced
Sef1p-, Sfu1p-, and Hap43p-regulated gene; overlaps IFM3/orf19.2176
Mitochondrial apoptosis-inducing factor; induced by nitric oxide; Spider biofilm induced; rat catheter biofilm
Ortholog(s) have role in ER-dependent peroxisome organization, endoplasmic reticulum inheritance, endop
Putative sterol deacetylase; flow model biofilm induced; rat catheter biofilm repressed
Ortholog(s) have role in ribosomal large subunit biogenesis, ribosomal small subunit biogenesis and nucleo
Predicted hydrolase; induced by nitric oxide
Predicted ORF in retrotransposon Tca3; similar to Gag-Pol; a-specific transcript, alpha-factor induced; rat c
Protein of unknown function; Hap43-repressed gene; by Rgt1; repressed in Spider biofilms by Bcr1, Tec1, E
Putative casein kinase; plasma membrane-localized
Ortholog of C. dubliniensis CD36 : Cd36_22440, C. parapsilosis CDC317 : CPAR2_407000, Candida tenuis
Protein with a thioredoxin domain; predicted role in cell redox homeostasis; rat catheter and Spider biofilm i
Ortholog of C. dubliniensis CD36 : Cd36_22470, Candida tropicalis NEW ASSEMBLY : CTRG1_01829, Ca
Ortholog of C. dubliniensis CD36 : Cd36_22500, Candida tropicalis NEW ASSEMBLY : CTRG1_01825, Ca
Ortholog(s) have DNA polymerase binding, protein kinase activator activity, signaling adaptor activity
Protein of unknown function; Hap43-repressed; colony morphology-related gene regulation by Ssn6; Spider
Ortholog of C. dubliniensis CD36 : Cd36_22550, Candida tropicalis NEW ASSEMBLY : CTRG1_01836, Ca
Ortholog(s) have DNA-3-methyladenine glycosylase activity, alkylbase DNA N-glycosylase activity, damage
Ortholog of C. dubliniensis CD36 : Cd36_22580, C. parapsilosis CDC317 : CPAR2_406960, C. auris B8441
Ortholog(s) have role in purine nucleobase catabolic process
Ortholog of C. dubliniensis CD36 : Cd36_22640, C. parapsilosis CDC317 : CPAR2_406910, C. auris B8441
Ortholog of C. parapsilosis CDC317 : CPAR2_406905, Candida tropicalis NEW ASSEMBLY : CTRG1_CG
Has domain(s) with predicted asparagine synthase (glutamine-hydrolyzing) activity and role in asparagine b
Has domain(s) with predicted zinc ion binding activity
Possible pseudogene; similar to Ywp1p; ORF extended upstream from the initiating Met of orf19.3621 has a
Protein of unknown function; induced in core caspofungin response; expression upregulated in an ssr1 null
Ortholog(s) have RNA polymerase II C-terminal domain phosphoserine binding, RNA polymerase II comple
Protein of unknown function; Hap43-repressed gene; repressed by nitric oxide
Protein of unknown function; upregulation correlates with clinical development of fluconazole resistance; reg
Ortholog of C. dubliniensis CD36 : Cd36_22860, C. parapsilosis CDC317 : CPAR2_806540, C. auris B8441
Ortholog of S. cereviae Sna4 vacuolar outer membrane protein that plays a role in sensitivity to NA+; induce
Ortholog(s) have Ino80 complex localization
Has domain(s) with predicted ATP binding, ATPase, nucleoside-triphosphatase activity, nucleotide binding a
Protein of unknown function; flow model biofilm induced
Putative adhesin-like protein; predicted ORF from Assembly 19; removed from Assembly 20; subsequently
Ortholog(s) have role in chitin localization, vesicle-mediated transport and integral component of endoplasm
Putative tRNA methyltransferase complex subunit; regulated by Gcn4; repressed in response to amino acid
Predicted 2-hydroxyacid dehydrogenase; Hap43-repressed gene
Putative serine/threonine protein kinase; Hap43-repressed; induced by prostaglandins; possibly an essentia
Ortholog(s) have DNA binding activity
Ortholog of C. parapsilosis CDC317 : CPAR2_806510, Candida tenuis NRRL Y-1498 : CANTEDRAFT_109
Protein with a metallo-dependent phosphatase domain; ketoconazole-induced; upregulation correlates with
Component of a complex containing the Tor2p kinase; possible a role in regulation of cell growth; Spider bio
Subunit of the 19S regulatory particle lid of the proteasome
Predicted homeodomain-like transcription factor; also has a metal-binding Ada DNA repair protein domain;
Ortholog(s) have role in mitotic division septum assembly, protein localization to bud neck and cell division s
Putative adhesin-like protein
Ortholog of C. dubliniensis CD36 : Cd36_23180, Candida tropicalis NEW ASSEMBLY : CTRG1_01968, Ca
Protein of unknown function; unmerged from orf19.202 in a revision of Assembly 21
Putative nuclear RNA-binding protein; Spider biofilm repressed
Protein of unknown function; hyphal-induced expression; upregulated in a cyr1 null mutant
Putative glycerol-3-phosphate acyltransferase; Hog1-repressed

Protein of unknown function; flow model biofilm induced
Protein of unknown function; repressed by alpha pheromone in SpiderM medium
Ortholog(s) have role in U1 snRNA 3'-end processing, U4 snRNA 3'-end processing and U5 snRNA 3'-end
Putative ribonuclease H2 subunit; required for RNase H2 activity; repressed in Spider biofilms by Bcr1, Tec
Protein of unknown function; transcript detected on high-resolution tiling arrays
Has domain(s) with predicted protein tyrosine phosphatase activity
Predicted membrane transporter, member of the fucose:proton symporter (FHS) family, major facilitator su
Ortholog(s) have role in vacuolar proton-transporting V-type ATPase complex assembly and endoplasmic r
Trimeric GatFAB AmidoTransferase(AdT) complex subunit; involved in the formation of Q-tRNAQ; represse
Ortholog of C. dubliniensis CD36 : Cd36_23450, C. parapsilosis CDC317 : CPAR2_407010, Candida tenuis
Ortholog of C. dubliniensis CD36 : Cd36_23460, C. parapsilosis CDC317 : CPAR2_407020, Debaryomyces
Ortholog of C. dubliniensis CD36 : Cd36_23480, C. parapsilosis CDC317 : CPAR2_407050, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_23530, C. parapsilosis CDC317 : CPAR2_406140, C. auris B8441
Predicted Gal4-like DNA-binding transcription factor; Spider biofilm induced
Ortholog(s) have DNA-directed DNA polymerase activity, role in error-free translesion synthesis, error-pron
Predicted tRNA dihydrouridine synthase; Spider biofilm induced
Ortholog(s) have ATP:ADP antiporter activity, calcium ion binding activity and role in ADP transport, ATP tr
Ortholog of C. dubliniensis CD36 : Cd36_23640, C. parapsilosis CDC317 : CPAR2_406130, C. auris B8441
Has domain(s) with predicted heme binding activity
Ortholog(s) have copper ion transmembrane transporter activity, inorganic phosphate transmembrane trans
Putative protein of unknown function; mutant is viable; protein level decreases in stationary phase cultures;
Ortholog(s) have NAD transmembrane transporter activity, pyruvate secondary active transmembrane trans
Ortholog(s) have protein disulfide isomerase activity, protein-disulfide reductase (glutathione) activity, unfol
Protein with similarity to trimeric LpxA-like enzymes; Hap43-repressed gene
Ortholog(s) have poly(A) binding activity, role in mRNA metabolic process and cytoplasm localization
Putative 66S pre-ribosomal particle component; Hap43-induced; F-12/CO2 early biofilm induced
Ortholog(s) have 4 iron, 4 sulfur cluster binding, ATPase activity, role in iron-sulfur cluster assembly, tRNA
Ortholog(s) have SNAP receptor activity and role in endoplasmic reticulum to Golgi vesicle-mediated transp
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Ortholog of S. cerevisiae/S. pombe Lsb5; predicted role in actin cortical patch localization, actin filament org
Ortholog of C. dubliniensis CD36 : Cd36_23840, Candida tenuis NRRL Y-1498 : CANTEDRAFT_104074, D
Protein of unknown function; transcript regulated by Mig1 and Tup1
Mitochondrial protein required for expression of respiratory chain complex IV (cytochrome c oxidase)
Protein of unknown function; expression regulated by white-opaque switch; repressed by alpha pheromone
Protein with predicted peptidase domains; Hap43-repressed gene
Protein of unknown function; flow model biofilm induced; Spider biofilm induced
Ortholog of C. parapsilosis CDC317 : CPAR2_407330, C. auris B8441 : B9J08_001010, Candida tenuis N
Has domain(s) with predicted 2-oxoglutarate-dependent dioxygenase activity
Putative monooxygenase; mutation confers hypersensitivity to toxic ergosterol analog; constitutive expressi
Ortholog of S. pombe Stm1 G-protein coupled receptor; PQ-loop domains; constitutive expression indepen
Putative protein of unknown function; Plc1-regulated; transcript induced by Mnl1 under weak acid stress; fl
Putative adhesin-like protein
Ortholog(s) have role in mitochondrial genome maintenance, mitochondrion organization
Ortholog(s) have protein-containing complex binding activity, role in sporulation resulting in formation of a c
Ortholog(s) have thiosulfate sulfurtransferase activity and role in tRNA wobble position uridine thiolation, tR
Putative protein of unknown function; stationary phase enriched protein
Protein with a PI31 proteasome regulator domain; Hap43-repressed; flow model biofilm induced
Ortholog of C. parapsilosis CDC317 : CPAR2_407200.1, C. dubliniensis CD36 : Cd36_24070, Candida me
Membrane-localized protein of unknown function
Has domain(s) with predicted catalytic activity and role in carbohydrate metabolic process
Ortholog(s) have deubiquitinase activity, endopeptidase activity, thiol-dependent deubiquitinase activity
Putative pantetheine-phosphate adenylyltransferase (PPAT); which catalyzes 4th step in coenzyme A biosy
Predicted dehydrogenase; transcript upregulated in an RHE model of oral candidiasis; virulence-group-corr
Ortholog of S. cerevisiae : MRX1, C. glabrata CBS138 : CAGL0J03278g, C. dubliniensis CD36 : Cd36_241
Ortholog(s) have G-protein beta/gamma-subunit complex binding, actin binding activity, role in positive regu
Ortholog of C. dubliniensis CD36 : Cd36_24170, C. parapsilosis CDC317 : CPAR2_407480, Candida tropic
Putative ubiquitin-specific protease, involved in histone H2B deubiquitination during hyphal development
Secreted protein; fluconazole-induced
Secreted protein; fluconazole-induced
Protein of unknown function; rat catheter and Spider biofilm induced
Predicted olichyl-diphosphooligosaccharide-protein glycotransferase; role in protein N-linked glycosylation;
Putative C2H2 transcription factor; expression upregulated in clinical isolates from HIV+ patients with oral c
Protein of unknown function; shows colony morphology-related gene regulation by Ssn6
Protein similar to S. cerevisiae meiosis-specific, spore-wall-localized protein Ssp2p, which is required for wi

Protein of unknown function; Hap43-repressed gene
Ortholog(s) have methylenetetrahydrofolate reductase (NAD(P)H) activity and role in methionine biosynthet
Ortholog(s) have phosphatidylinositol-3-phosphate binding activity
Transcription factor with zinc finger DNA-binding motif, involved in glucose repression; possible ortholog of
Ortholog of S. cerevisiae Spg5; required for proteasome assembly during quiescence; transcript detected o
Ortholog(s) have cytosol, extracellular region localization
Protein of unknown function; protein newly produced during adaptation to the serum
Putative ubiquitin-like polyubiquitin-binding protein; induced by nitric oxide independent of Yhb1; Spider biof
Ortholog(s) have role in transcription by RNA polymerase II and transcription factor TFIID complex localizat
Ortholog(s) have role in positive regulation of DNA-templated transcription, elongation, positive regulation o
Protein with a predicted magnesium transporter domain; mutants are viable
Ortholog of C. dubliniensis CD36 : Cd36_24630, C. parapsilosis CDC317 : CPAR2_407790, Candida tropic
Protein with a predicted role in cell wall integrity; repressed in core stress response
Phosphorylated protein of unknown function
Component of UDP-GlcNAc transferase; required for the 2nd step of dolichyl-linked oligosaccharide synthe
Putative pre-mRNA splicing factor; intron in 5'-UTR; possibly an essential gene, disruptants not obtained by
S. cerevisiae ortholog YMR259C interacts with Trm7 for 2'-O-methylation of C32 of substrate tRNAs; down
Ortholog of C. dubliniensis CD36 : Cd36_24540, C. parapsilosis CDC317 : CPAR2_407710, C. auris B8441
Ortholog of Vms1; component of a Cdc48-complex involved in protein quality control in S. cerevisiae; Spide
Uroporphyrinogen decarboxylase; catalyzes the 5th step in the heme biosynthetic pathway; flow model and
Ortholog(s) have fungal-type vacuole membrane localization
Protein of unknown function; induced by Mnl1 under weak acid stress; transcript detected on high-resolution
Protein with a predicted DEAD-like DNA/RNA helicase domain; shows colony morphology-related gene reg
Predicted ORF from Assembly 19; removed from Assembly 20; restored based on transcription data; almos
Ortholog(s) have first spliceosomal transesterification activity and role in generation of catalytic spliceosome
Protein of unknown function
mRNA polyadenylation regulating protein; Hap43-repressed; transcript is upregulated in RHE model of oral
Protein of unknown function
Ortholog of Candida albicans WO-1 : CAWG_02350
Ortholog(s) have lipid droplet localization
Ortholog(s) have GTPase regulator activity, mRNA binding activity
Predicted integral membrane protein; Spider biofilm induced
Putative protein of unknown function; transcript is upregulated in clinical isolates from HIV+ patients with ora
Ortholog of C. dubliniensis CD36 : Cd36_80240, C. parapsilosis CDC317 : CPAR2_504040, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_80270, C. parapsilosis CDC317 : CPAR2_504010, Pichia stipitis P
Putative ubiquitin-protein ligase; role in protein sumoylation, protein ubiquitination; Spider biofilm induced
Ortholog(s) have protein folding chaperone activity, role in mitochondrial respiratory chain complex III asser
Protein of unknown function; Hap43-repressed; Spider biofilm induced
Ortholog(s) have DNA replication origin binding, ubiquitin-protein transferase activity
Putative Golgi membrane protein with a predicted role in manganese homeostasis; Hap43p-repressed gene
Putative patatin-like phospholipase; macrophage-regulated gene; fungal-specific (no human or murine hom
Ortholog of Candida albicans WO-1 : CAWG_02376
Ortholog(s) have 3'-tRNA processing endoribonuclease activity
Ortholog of C. dubliniensis CD36 : Cd36_80400, Candida tropicalis NEW ASSEMBLY : CTRG1_06188, Ca
Ortholog(s) have structural constituent of ribosome activity, role in mitochondrial translation and mitochondr
Ortholog(s) have role in endoplasmic reticulum to Golgi vesicle-mediated transport
Ortholog(s) have role in mRNA splicing, via spliceosome and Prp19 complex, spliceosomal complex localiz
Ortholog of S. cerevisiae : ECM9, C. glabrata CBS138 : CAGL0L02255g, C. dubliniensis CD36 : Cd36_804
Ortholog(s) have NEDD8 transferase activity and role in protein neddylation
Ortholog(s) have microtubule binding, microtubule plus-end binding activity
Predicted plasma membrane associated protein phosphatase; required for normal filamentous growth; mRI
Ortholog of Candida albicans WO-1 : CAWG_02394
Putative conserved oligomeric Golgi complex subunit; decreased transcription is observed upon fluphenazi
Ortholog(s) have role in mitochondrial cytochrome c oxidase assembly and integral component of mitochon
Ortholog(s) have role in early endosome to late endosome transport, regulation of protein-containing compl
Putative cysteine sulfinate decarboxylase; transcript positively regulated by Tbf1; Spider biofilm induced
Predicted RNA splicing and ER to Golgi transport protein; Hap43-induced gene
Ortholog of Candida albicans WO-1 : CAWG_02403
Ortholog(s) have mRNA binding activity and role in negative regulation of translation, nuclear-transcribed m
Ortholog of S. cerevisiae Elm1; a serine/threonine protein kinase that regulates cellular morphogenesis, se
Ortholog(s) have DNA ligase (ATP) activity, DNA ligase activity
Ortholog of S. cerevisiae : AIM11, C. glabrata CBS138 : CAGL0I04928g, C. dubliniensis CD36 : Cd36_807
Ortholog(s) have role in eisosome assembly and eisosome, membrane raft localization
Ortholog of C. dubliniensis CD36 : Cd36_80810, C. parapsilosis CDC317 : CPAR2_101800, C. auris B8441

Ortholog of C. dubliniensis CD36 : Cd36_80830, Debaryomyces hansenii CBS767 : DEHA2F17930g, Cand
Predicted ubiquitin-protein ligase; Hap43-repressed gene; oxidative stress-induced via Cap1; flow model bi
Putative peptidyl-prolyl cis-trans isomerase
Mitochondrial protein involved in assembly of NADH ubiquinone oxidoreductase Complex I; required for bio
Ortholog of S. cerevisiae : YGL138C, C. glabrata CBS138 : CAGL0H08910g, C. dubliniensis CD36 : Cd36_
Protein of unknown function; opaque-specific transcript; induced during chlamydospore formation in both C
Ortholog of C. dubliniensis CD36 : Cd36_80970, C. parapsilosis CDC317 : CPAR2_401850, Candida tropic
Ortholog of C. dubliniensis CD36 : Cd36_29340, Candida tropicalis NEW ASSEMBLY : CTRG1_CGOB_00
Ortholog(s) have role in protein folding, tubulin complex assembly
Ortholog of C. parapsilosis CDC317 : CPAR2_103040, Candida tenuis NRRL Y-1498 : CANTEDRAFT_116
Ortholog of C. dubliniensis CD36 : Cd36_81000, C. parapsilosis CDC317 : CPAR2_103050, C. auris B8441
Protein required for expression of NADH:ubiquinone oxidoreductase (mitochondrial complex I)
Predicted methyltransferase; rat catheter biofilm induced
ZZ-type zinc finger protein; rat catheter and Spider biofilm induced
Has domain(s) with predicted role in cell redox homeostasis
Ortholog of S. cerevisiae Apd1; required for normal localization of actin patches and normal tolerance of so
Ortholog(s) have role in inner mitochondrial membrane organization and integral component of mitochondri
Protein of unknown function; induced by Mnl1 under weak acid stress
Ortholog of S. cerevisiae : RMD1, C. glabrata CBS138 : CAGL0M10483g, C. dubliniensis CD36 : Cd36_81(
HMG-box protein; Spider biofilm repressed
Putative transcription factor with zinc finger DNA-binding motif
Ortholog of C. dubliniensis CD36 : Cd36_81190, C. parapsilosis CDC317 : CPAR2_503840, Debaryomyces
Putative adhesin-like protein; highly expressed in white cells during pheromone response; required for adhe
Ortholog(s) have role in response to purine-containing compound
Ortholog(s) have role in mitotic recombination
Ortholog of C. dubliniensis CD36 : Cd36_81270, C. parapsilosis CDC317 : CPAR2_502880, C. auris B8441
Sterol carrier domain protein; alkaline downregulated; colony morphology-related gene regulation by Ssn6;
Protein of unknown function; Spider biofilm induced
Ortholog of Candida albicans WO-1 : CAWG_02476
Ortholog(s) have phosphatidate phosphatase activity, role in cellular lipid metabolic process and actin cortic
Ortholog(s) have role in cytoplasmic translation, poly(A)+ mRNA export from nucleus and cytoplasm localiz
Plasma-membrane-localized protein; filament induced; Hog1, ketoconazole, fluconazole and hypoxia-induc
Ortholog of S. cerevisiae Prp43, an RNA helicase in the DEAH-box family that functions in both RNA polym
Has domain(s) with predicted phosphotransferase activity, alcohol group as acceptor activity and role in car
Ortholog of C. dubliniensis CD36 : Cd36_81500, C. parapsilosis CDC317 : CPAR2_503620, C. auris B8441
Membrane protein; Hap43p-repressed gene; repressed by nitric oxide
Ortholog of C. dubliniensis CD36 : Cd36_81530, C. parapsilosis CDC317 : CPAR2_503590, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_81550, C. parapsilosis CDC317 : CPAR2_503570, C. auris B8441
Protein of unknown function; transcript detected on high-resolution tiling arrays
Protein of unknown function; transcript detected on high-resolution tiling arrays
Predicted potassium ion transporter; Spider biofilm induced
Ortholog(s) have role in positive regulation of catalytic activity
Alpha subunit of COPI vesicle coatomer complex; role in ER to Golgi vesicle-mediated transport, retrograde
Predicted ORF added to Assembly 21 based on sequence re-analysis
Centromeric chromatin (CENP-A) chaperone, involved in nuclear DNA replication; expression downregulate
Ortholog(s) have role in mitochondrial cytochrome c oxidase assembly, mitochondrial respiratory chain com
Protein with a predicted SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfam
Ortholog of Dig2, a MAP kinase-responsive inhibitor of Ste12; regulates mating-specific genes and invasive
Protein of unknown function; expression downregulated in an ssr1 null mutant
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Ortholog(s) have cell cortex localization
Protein with a predicted FYVE/PHD zinc finger domain; Hap43-repressed; Spider biofilm induced
Ortholog(s) have phosphatidic acid binding, phosphatidylinositol-3,5-bisphosphate binding, phosphatidylinos
Predicted membrane protein; induced by prostaglandins
Has domain(s) with predicted integral component of membrane localization
Ortholog of C. dubliniensis CD36 : Cd36_81960, Pichia stipitis Pignal : psti_CGOB_00163, Candida tropica
Ortholog(s) have role in ascospore wall assembly
Ortholog(s) have rRNA primary transcript binding activity
Ortholog(s) have serine-type endopeptidase activity, role in regulation of mitochondrion organization, signal
Ortholog of S. cerevisiae Loc1, a nuclear protein involved in asymmetric localization of ASH1 mRNA in S. c
Ortholog(s) have extracellular region localization
Has domain(s) with predicted oxidoreductase activity
Has domain(s) with predicted zinc ion binding activity, role in endoplasmic reticulum to Golgi vesicle-mediat
Ortholog of C. dubliniensis CD36 : Cd36_82070, C. parapsilosis CDC317 : CPAR2_202790, C. auris B8441

Has domain(s) with predicted fatty-acyl-CoA binding activity
Has domain(s) with predicted catalytic activity and role in carbohydrate metabolic process
Ortholog(s) have P-body localization
Deoxyhypusine synthase; catalyzes formation of deoxyhypusine, the first step in hypusine biosynthesis; Spi
Putative ubiquinone oxidoreductase; repressed by nitric oxide; Hap43p-repressed
Ortholog of C. parapsilosis CDC317 : CPAR2_405060, Candida tropicalis NEW ASSEMBLY : CTRG1_CG
Non-catalytic subunit of N-terminal acetyltransferase of the NatC type; flow model biofilm repressed
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Putative kinase subunit of RNA polymerase II carboxy-terminal domain kinase I; possibly an essential gene
Ortholog of C. dubliniensis CD36 : Cd36_82240, C. parapsilosis CDC317 : CPAR2_405130, C. auris B844
Protein similar to S. cerevisiae Ydr282cp; transposon mutation affects filamentous growth; Hap43p-repress
Protein of unknown function; Spider biofilm induced
Putative protein of unknown function, transcription is activated in the presence of elevated CO2
Ortholog(s) have role in endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU
Has domain(s) with predicted catalytic activity, sulfuric ester hydrolase activity and role in metabolic process
Protein of unknown function; Plc1-regulated
Ortholog(s) have ubiquitin-protein transferase activity, role in ubiquitin-dependent protein catabolic process
Putative ATP-dependent helicase; Component of the RSC chromatin remodeling complex; induced by nitric
Protein involved in ER stress response; acts synergistically with Aut7p to regulate unfolded protein respons
Predicted metalloendopeptidase; Spider biofilm induced
Ortholog(s) have role in endosome organization, regulation of protein localization and BLOC-1 complex loca
Protein of unknown function; S. cerevisiae ortholog Fmp37 which localizes to mitochondria; Hap43-repress
Protein of unknown function; Hog1p-repressed; Spider biofilm induced
Protein of unknown function; Spider biofilm induced
Protein with a predicted role in 60S ribosomal subunit assembly; flow model biofilm induced
Ortholog(s) have dolichol kinase activity, role in dolichyl monophosphate biosynthetic process and endoplas
Protein of unknown function; gene has intron; Spider biofilm induced
Has domain(s) with predicted protein kinase binding activity and role in regulation of cyclin-dependent prote
Protein with a ribonuclease III domain; flow model biofilm induced; Spider biofilm induced
Protein required for normal filamentous growth; mRNA binds She3
Ortholog(s) have role in DNA repair, transcription-coupled nucleotide-excision repair and Ddb1-Ckn1 compl
Ortholog of C. dubliniensis CD36 : Cd36_82780, C. parapsilosis CDC317 : CPAR2_102150, Pichia stipitis
Protein involved in regulation of C14-methylated sterol biosynthesis; mutations increase azole sensitivity
Ortholog(s) have RNA binding, ribonuclease MRP activity, ribonuclease P activity
Plasma membrane-associated protein; upregulated in an azole-resistant strain that overexpresses MDR1;
Protein of unknown function; required for adhesion to abiotic substrate; Spider biofilm induced
Protein with a predicted D-Tyr-tRNA(Tyr) deacylase domain; Hap43-repressed gene
Ortholog of C. dubliniensis CD36 : Cd36_82875 and Candida albicans WO-1 : CAWG_02609
Ortholog of C. dubliniensis CD36 : Cd36_82880, C. parapsilosis CDC317 : CPAR2_102370, Candida tenuis
Ortholog of C. dubliniensis CD36 : Cd36_82890, Debaryomyces hansenii CBS767 : DEHA2G01034g, Pichi
Ortholog of S. cerevisiae Igo2; role in mRNA stabilization of mRNA; Spider biofilm induced
Has a predicted autophagy-related protein domain; transcription repressed by fluphenazine treatment
Putative metalloprotease involved in repair of DNA-protein crosslinks; interacts with SUMO (Smt3p) and Cd
Ortholog of C. dubliniensis CD36 : Cd36_82960, C. parapsilosis CDC317 : CPAR2_102390, C. auris B844
Ortholog of C. dubliniensis CD36 : Cd36_82970, C. auris B8441 : B9J08_001198, Lodderomyces elongispo
Ortholog of C. dubliniensis CD36 : Cd36_82980, C. parapsilosis CDC317 : CPAR2_102360, Candida tenuis
Protein of unknown function; flow model biofilm induced
Ortholog(s) have role in endoplasmic reticulum to Golgi vesicle-mediated transport and TRAPPI protein co
Putative transporter similar to MDR proteins; fungal-specific; Spider biofilm induced
Protein of unknown function; upregulated in a cyr1 null mutant
Ortholog(s) have transcription coactivator activity, transcription coregulator activity and role in chromatin or
Ortholog(s) have role in nucleobase-containing compound transport, regulation of fungal-type cell wall orga
Putative mitochondrial protein with a predicted role in cell wall biogenesis; possibly an essential gene, disru
Ortholog of S. cerevisiae : STB6, C. glabrata CBS138 : CAGL0L05016g, C. dubliniensis CD36 : Cd36_831
Ortholog of C. dubliniensis CD36 : Cd36_83120, C. parapsilosis CDC317 : CPAR2_103220, C. auris B844
Ortholog(s) have role in protein maturation by [2Fe-2S] cluster transfer, protein maturation by [4Fe-4S] clus
Ortholog of S. cerevisiae : YDR286C, C. glabrata CBS138 : CAGL0H01111g, C. dubliniensis CD36 : Cd36_
Predicted short chain dehydrogenase; Spider biofilm induced
Ortholog(s) have L-methionine transmembrane transporter activity and role in methionine import across pla
Putative haloacid dehalogenase; localized to plasma membrane
Putative mRNA cleavage and polyadenylation factor; heterozygous null mutant exhibits hypersensitivity to
Protein of unknown function; Spider biofilm repressed
Putative pre-mRNA branch point binding protein; role in mRNA splicing via spliceosome; Spider biofilm repr
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity, protein methyltransferase ac

Member of a complex that contains Prp19; stabilizes U6 snRNA in catalytic forms of the spliceosome conta
Ortholog of C. dubliniensis CD36 : Cd36_83290, C. parapsilosis CDC317 : CPAR2_102640, Candida tenuis
Protein of unknown function; flow model biofilm induced; Spider biofilm induced; regulated by Sef1, Sfu1, ar
Sef1p-, Sfu1p-, and Hap43p-regulated gene
Putative glycoside hydrolase; stationary phase enriched protein; Hog1p-downregulated; shows colony morp
Ortholog(s) have role in ATP export, protein targeting to membrane, protein targeting to vacuole and ESCR
Putative spermidine export pump; fungal-specific (no human or murine homolog)
Protein of unknown function; upregulated by fluphenazine treatment or in an azole-resistant strain that over
Succinate semialdehyde dehydrogenase; for utilization of gamma-aminobutyrate (GABA) as a nitrogen sour
Ortholog(s) have role in aerobic respiration, mRNA metabolic process
Ortholog of S. cerevisiae : MAY24, C. glabrata CBS138 : CAGL0L08382g, C. dubliniensis CD36 : Cd36_83
Ortholog of C. dubliniensis CD36 : Cd36_83550, C. parapsilosis CDC317 : CPAR2_404510, C. auris B8441
Ortholog(s) have aminopeptidase activity, role in protein processing, protein stabilization and extrinsic comp
Has domain(s) with predicted oxidoreductase activity
Ortholog(s) have role in inner mitochondrial membrane organization, mitochondrion inheritance, mitochondr
Ortholog(s) have DNA binding, chromatin binding, histone deacetylase activity, role in gene silencing by RN
Ortholog(s) have sphinganine-1-phosphate aldolase activity and role in calcium-mediated signaling, cellular
Putative vacuolar membrane transporter for cationic amino acids; Spider biofilm induced
Predicted ORF from Assembly 19; removed from Assembly 20; subsequently reinstated in Assembly 21 ba
Putative diacylglycerol acyltransferase; catalyzes the terminal step of triacylglycerol formation; flow model b
Predicted ORF from Assembly 19; removed from Assembly 20; restored based on comparative genome an
Protein of unknown function
Ortholog(s) have role in protein insertion into mitochondrial inner membrane from matrix and integral compo
Ortholog(s) have peptidyl-prolyl cis-trans isomerase activity, protein phosphatase regulator activity, role in m
Putative cleavage factor I subunit; heterozygous null mutant exhibits hypersensitivity to parnafungin and cor
Ortholog(s) have acid phosphatase activity, protein tyrosine phosphatase activity, metal-dependent activity
Ortholog of C. parapsilosis CDC317 : CPAR2_502850, Candida tenuis NRRL Y-1498 : CANTEDRAFT_135
Ortholog(s) have chromatin binding activity, role in RNA polymerase II preinitiation complex assembly, trans
Protein of unknown function; Spider biofilm induced
Ortholog of subunit 6 of the ubiquinol cytochrome-c reductase complex, a component of the mitochondrial i
Ortholog of Candida albicans WO-1 : CAWG_02725
Membrane-localized protein of unknown function
Ortholog of C. dubliniensis CD36 : Cd36_84070, C. parapsilosis CDC317 : CPAR2_102720, Candida tenuis
Predicted ORF from Assembly 19; removed from Assembly 20; subsequently reinstated in Assembly 21 ba
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_84160, C. auris B8441 : B9J08_001714, Candida tenuis NRRL Y-
Ortholog(s) have ATPase, acting on RNA activity, role in generation of catalytic spliceosome for first transes
Ortholog(s) have role in metal ion transport, protein targeting to vacuole, ubiquitin-dependent protein catabo
Ortholog of C. dubliniensis CD36 : Cd36_84250, C. parapsilosis CDC317 : CPAR2_806160, Candida tenuis
Protein of unknown function; Cyr1-repressed; induced by alpha pheromone in SpiderM medium; rat cathete
Has domain(s) with predicted oxidoreductase activity and role in metabolic process
Putative voltage-gated chloride channel; predicted role in copper ion and iron ion homeostasis; flow model b
Putative nucleolar preribosomal-associated protein; decreased transcription is observed upon benomyl trea
Putative U3 snoRNP protein; flucytosine induced
Ortholog of C. dubliniensis CD36 : Cd36_84350, C. parapsilosis CDC317 : CPAR2_806070, C. auris B8441
Ortholog of S. cerevisiae Hul4; similar to hect domain E3 ubiquitin-protein ligases; Hap43-repressed gene
Ortholog of S. cerevisiae : YEL023C, C. glabrata CBS138 : CAGL0I03168g, C. dubliniensis CD36 : Cd36_8
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Ortholog(s) have role in positive regulation of TORC1 signaling and Seh1-associated complex, extrinsic cor
Protein of unknown function; Hap43-induced; F-12/CO2 early biofilm induced
Putative histone acetyltransferase complex subunit; induced upon low-level peroxide stress; Spider biofilm i
RNA binding protein required for export of poly(A)+ mRNA from the nucleus; Spider biofilm repressed
Ortholog of C. dubliniensis CD36 : Cd36_84570, C. parapsilosis CDC317 : CPAR2_404420, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_84580, C. parapsilosis CDC317 : CPAR2_404290, C. auris B8441
Ortholog of S. cerevisiae : AIM6, C. glabrata CBS138 : CAGL0C05533g, C. dubliniensis CD36 : Cd36_8461
Putative protein of unknown function, transcription is positively regulated by Tbf1p
Ortholog(s) have structural constituent of nuclear pore activity
Protein of unknown function; Spider biofilm induced
Protein of unknown function; transcript induced by benomyl treatment
Ortholog(s) have DNA topoisomerase activity, DNA topoisomerase type I (single strand cut, ATP-independe
Ortholog of C. dubliniensis CD36 : Cd36_84710, C. parapsilosis CDC317 : CPAR2_807470, C. auris B8441
Ortholog(s) have role in endoplasmic reticulum to Golgi vesicle-mediated transport and COPII-coated ER to
Zinc finger protein orthologous to S. cerevisiae Itt1; repressed by adherence to polystyrene; Spider biofilm in
Ortholog(s) have role in peroxisome organization and peroxisomal membrane localization

Protein of unknown function; transcript upregulated in an RHE model of oral candidiasis; rat catheter and S
Protein of unknown function; induced by nitric oxide independent of Yhb1; Sef1, Sfu1, and Hap43-induced;
Ortholog(s) have ubiquitin ligase activator activity
Ortholog(s) have proteasome regulatory particle binding activity, role in proteasome regulatory particle asse
Putative prenyltransferase; essential gene in S. cerevisiae; Spider biofilm induced
Ortholog(s) have ubiquitin-ubiquitin ligase activity
Putative DNA repair helicase; transcriptionally induced by interaction with macrophage; fungal-specific (no h
Ortholog of S. cerevisiae : MTC6, C. glabrata CBS138 : CAGL0I01892g, C. dubliniensis CD36 : Cd36_849
Protein of unknown function; ortholog of S. cerevisiae Urn1; downregulated by fluphenazine treatment, in az
Has domain(s) with predicted acyltransferase activity, transferring groups other than amino-acyl groups, oxi
Protein of unknown function; Hap43-repressed gene
Putative protein of unknown function; homozygous transposon insertion causes decreased colony wrinkling
Ortholog(s) have tubulin binding activity, role in tubulin complex assembly and cytoplasm, polysome, prefol
Ortholog(s) have tRNA (guanine-N2-)-methyltransferase activity, role in tRNA methylation and cytoplasm, t
Putative cleavage factor I subunit; required for the cleavage and polyadenylation of pre-mRNA 3' ends; Spi
Ortholog(s) have role in assembly of large subunit precursor of preribosome, maturation of 5.8S rRNA from
Protein of unknown function; role in intracellular signal transduction; Spider biofilm induced
Predicted fatty acid acyl transferase-related protein domain; repressed by prostaglandins
S. cerevisiae ortholog YLL032C interacts with ribosomes; repressed by alpha pheromone in SpiderM mediu
Ortholog(s) have choline kinase activity, ethanolamine kinase activity and role in phosphatidylcholine biosyn
Protein of unknown function; Hog1-repressed; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_85310, C. parapsilosis CDC317 : CPAR2_807370, C. auris B8441
ATP-dependent LON protease family member; Hap43-repressed gene; regulated by Gcn2 and Gcn4; Spide
Predicted MFS membrane transporter; member of the proton coupled folate transporter/heme carrier protei
Planktonic growth-induced gene
Ortholog(s) have role in cellular manganese ion homeostasis, mitochondrion organization
Ortholog(s) have cell periphery, cellular bud neck localization
Ortholog(s) have role in vacuole organization
Ortholog(s) have mitochondrial ribosome binding activity and role in mitochondrial translational initiation
Protein of unknown function; Hap43-repressed gene; repressed by nitric oxide; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_85460, C. parapsilosis CDC317 : CPAR2_405760, C. auris B8441
Has domain(s) with predicted intracellular anatomical structure localization
Putative U2 snRNP-associated protein; Spider biofilm induced
Putative peptidyl-prolyl cis-trans isomerase; predicted endoplasmic reticulum (ER) localization
Predicted oxidoreductase; rat catheter biofilm repressed
Ortholog of C. parapsilosis CDC317 : CPAR2_806990, Candida tenuis NRRL Y-1498 : CANTEDRAFT_122
Ortholog(s) have ubiquitin-protein transferase activity, role in protein monoubiquitination, protein polyubiquit
Ortholog of C. parapsilosis CDC317 : CPAR2_807080, C. dubliniensis CD36 : Cd36_85690, Candida meta
Ortholog(s) have phosphopantothenate--cysteine ligase activity, role in acetyl-CoA biosynthetic process fro
Ortholog(s) have enzyme activator activity, role in histone deubiquitination, regulation of transcription by RN
Ortholog(s) have tRNA-intron endonuclease activity, role in tRNA-type intron splice site recognition and clea
Has domain(s) with predicted N,N-dimethylaniline monooxygenase activity, NADP binding, flavin adenine di
Ortholog(s) have ubiquitin-protein transferase activity and role in negative regulation of apoptotic process, n
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity, rRNA (uridine-N3-)-methyltra
Ortholog(s) have mRNA binding, poly(U) RNA binding activity and role in nuclear-transcribed mRNA catabo
Possible G-protein coupled receptor; vacuolar membrane transporter for cationic amino acids; PQ-loop mot
Putative U1A component of the U1 snRNP, involved in splicing; contains two RNA recognition motifs (RRM
Ortholog of C. dubliniensis CD36 : Cd36_85880, C. parapsilosis CDC317 : CPAR2_806870, C. auris B8441
Putative phosphopantothenoylcysteine decarboxylase, binds to protein phosphatase Ppz1p and regulates it
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
CCCH zinc finger protein; Spider biofilm induced
Ortholog(s) have mitochondrial ribosome binding activity and role in inner mitochondrial membrane organiza
Predicted NAD+/NADH kinase; possible role in cellular iron ion homeostasis; Spider biofilm induced
Protein of unknown function; Spider biofilm induced; Hap43-repressed
Ortholog(s) have role in negative regulation of transcription by RNA polymerase II, positive regulation of tra
Predicted ORF identical to NSA2
Predicted ORF identical to orf19.7420
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localiz
Ortholog of C. dubliniensis CD36 : Cd36_86220, C. parapsilosis CDC317 : CPAR2_404490, C. auris B8441
Ortholog of Rad33; involved in nucleotide excision repair in S. cerevisiae; induced by Mnl1 under weak acid
Catabolic L-serine (L-threonine) deaminase;, catalyzes degradation of L-serine and L-threonine; required to
Ortholog of S. cerevisiae : YML020W, C. glabrata CBS138 : CAGL0G07062g, C. dubliniensis CD36 : Cd36_
Ortholog(s) have transcription coactivator activity, role in RNA polymerase II preinitiation complex assembly
Ortholog(s) have role in endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S

Protein of unknown function' Hap43-induced gene; repressed by prostaglandins
Ortholog(s) have uracil DNA N-glycosylase activity, role in DNA repair, base-excision repair and cytoplasm,
Ortholog(s) have protein-disulfide reductase activity, role in cellular protein-containing complex assembly, p
Has domain(s) with predicted integral component of membrane localization
Ortholog(s) have structural constituent of nuclear pore activity
Putative protein of unknown function; Hap43p-repressed gene; ortholog of S. cerevisiae YJL218W
Ortholog(s) have role in lipid homeostasis, nuclear envelope organization and nuclear envelope localization
Ortholog of C. dubliniensis CD36 : Cd36_86500, C. parapsilosis CDC317 : CPAR2_206120, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_86510, C. parapsilosis CDC317 : CPAR2_206110, C. auris B8441
Ortholog(s) have transcription factor TFIIH holo complex localization
Ortholog of S.c. Vid24; a peripheral membrane protein located at Vid (vacuole import and degradation) vesi
Ortholog(s) have role in mitochondrial genome maintenance, plasmid maintenance
Ortholog(s) have myosin II tail binding, protein-macromolecule adaptor activity, role in protein localization to
Ortholog(s) have chromatin binding activity and role in DNA replication initiation, DNA unwinding involved in
Ortholog of Candida albicans WO-1 : CAWG_02974
Ortholog of C. dubliniensis CD36 : Cd36_86630, Candida tropicalis NEW ASSEMBLY : CTRG1_05698 and
Protein of unknown function; flow model biofilm repressed
Protein with Mob2p-dependent hyphal regulation
Ortholog of C. dubliniensis CD36 : Cd36_86660, Candida tenuis NRRL Y-1498 : cten_CGOB_00028, Cand
Putative mitochondrial protein with a predicted role in respiratory growth; fluconazole-induced; ketoconazole
Protein of unknown function; regulated by Sef1p-, Sfu1p-, and Hap43p
Putative enoyl-CoA hydratase; Spider biofilm induced
Protein with a predicted mitochondrial ATPase expression domain; possibly an essential gene, disruptants
Ortholog(s) have protein transmembrane transporter activity, protein-transporting ATPase activity, structura
Ortholog(s) have role in rRNA processing and preribosome, large subunit precursor localization
Ortholog(s) have NEDD8 transferase activity, cullin family protein binding, protein-macromolecule adaptor a
Ortholog(s) have ubiquitin protein ligase activity
Essential component of transcription factor TFIID complex, involved in transcription regulation
Has domain(s) with predicted ATP binding, helicase activity, nucleic acid binding activity
Putative xylose and arabinose reductase; flow model biofilm induced; Spider biofilm repressed
Protein of unknown function; Hap43-induced gene
Putative phosphomutase-like protein; protein present in exponential and stationary growth phase yeast; Ha
Predicted ORF in retrotransposon Tca17 with similarity to parts of the Gag-Pol region of retrotransposons;
Protein of unknown function; Spider biofilm induced
Ortholog(s) have role in SRP-dependent cotranslational protein targeting to membrane and signal recogniti
Ortholog(s) have palmitoyltransferase activity, role in protein palmitoylation, vacuole fusion, non-autophagic
Ortholog of C. dubliniensis CD36 : Cd36_86960, C. parapsilosis CDC317 : CPAR2_808800, C. auris B8441
Ortholog(s) have enzyme activator activity
Protein of unknown function; Sef1, Sfu1, and Hap43 regulated; rat catheter and Spider biofilm induced
Ortholog(s) have mRNA binding activity, role in 3'-UTR-mediated mRNA destabilization, mitochondrion orga
S. cerevisiae ortholog Nud1 is a spindle pole body outer plaque component; it acts through the mitotic exit
Protein with a predicted role in cotranslational protein targeting to membrane; induced during chlamydospo
Ortholog(s) have cargo receptor activity and role in ascospore formation, axial cellular bud site selection, er
Protein of unknown function; flow model biofilm induced
Putative geranylgeranyltransferase regulatory component
Aminophospholipid translocase (flippase); maintains membrane lipid asymmetry in post-Golgi secretory ves
Ortholog of Candida albicans WO-1 : CAWG_03032
protein with ENTH Epsin domain, N-terminal; Spider biofilm repressed
Has domain(s) with predicted intracellular anatomical structure localization
Predcted glucose 1-dehydrogenase (NADP+); rat catheter biofilm repressed
Ortholog(s) have Golgi apparatus localization
Protein of unknown function; Spider biofilm induced
Protein with a predicted RING-type zinc finger; possibly an essential gene, disruptants not obtained by UAU
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Ortholog(s) have tRNA (cytosine-2'-O-)-methyltransferase activity, tRNA (guanosine-2'-O-)-methyltransfera
Ortholog(s) have eukaryotic 43S preinitiation complex, eukaryotic translation initiation factor 3 complex loca
Ortholog(s) have acid phosphatase activity and role in dephosphorylation, intracellular sterol transport
Has domain(s) with predicted endodeoxyribonuclease activity, producing 5'-phosphomonoesters activity
Ortholog(s) have RNA polymerase II CTD heptapeptide repeat phosphatase activity, protein serine/threonin
Putative plasma membrane protein; predicted role in cell wall integrity; regulated by Nrg1, Tup1; induced du
Ortholog(s) have ubiquitin-protein transferase activity and role in generation of catalytic spliceosome for firs
Ortholog(s) have phosphopentomutase activity and role in guanosine catabolic process, inosine catabolic p
Protein of unknown function; mutants are viable; induced in a cyr1, ras1, or efg1 homozygous null
Protein required for mitochondrial ribosome small subunit biogenesis; role in maturation of SSU-rRNA; Spic

Ortholog(s) have thiamine phosphate phosphatase activity and role in phosphate ion transport
Ortholog of C. dubliniensis CD36 : Cd36_87460, C. parapsilosis CDC317 : CPAR2_808260, C. auris B8441
Protein of unknown function; repressed by alpha pheromone in SpiderM medium; Spider biofilm induced
Ortholog of S. cerevisiae : YCR016W, C. glabrata CBS138 : CAGL0L07832g, C. dubliniensis CD36 : Cd36_
Ortholog(s) have DNA binding, DNA secondary structure binding activity
Protein of unknown function; Spider biofilm induced
Protein similar to S. cerevisiae Rad4p; down-regulation associated with azole resistance
P-Loop domain-containing protein of unknown function; transposon mutation affects filamentous growth; Sp
Putative nucleosome assembly protein; homozygous transposon insertion causes decreased colony wrinkli
Has domain(s) with predicted sequence-specific DNA binding activity
Putative serine hydrolase; Spider biofilm repressed
Ortholog of S. cerevisiae : SGM1, C. glabrata CBS138 : CAGL0M00462g, C. dubliniensis CD36 : Cd36_876
Predicted alpha/beta hydrolase; Spider biofilm induced
Ortholog(s) have microtubule binding, microtubule plus-end binding activity
Putative 35S rRNA processing protein; Hap43-induced; repressed by prostaglandins; Spider biofilm induced
Protein of unknown function; Spider biofilm repressed
Ortholog of Candida albicans WO-1 : CAWG_03090
Protein similar to Pichia anomala YDL054c and S. cerevisiae Ydl054cp; transmembrane regions predicted;
Protein of unknown function; Spider biofilm repressed
Predicted protein of unknown function; overlaps orf19.6185
Putative pseudouridine-5'-phosphate glycosidase; overlaps orf19.6186 and orf19.6187; Spider biofilm repre
possible pseudouridine monophosphate glycosidase; overlaps orf19.6185 and orf19.618; has intron; Spider
Chalcone related protein family; flow model biofilm induced
Putative vacuolar H+-ATPase subunit; required for proper vacuolar ATPase assembly and vacuolar functio
Ortholog(s) have double-stranded DNA binding activity, role in DNA damage checkpoint signaling, double-s
Ortholog of C. dubliniensis CD36 : Cd36_40110, C. parapsilosis CDC317 : CPAR2_402300, C. auris B8441
Putative protein of unknown function; Hap43p-repressed gene
Ortholog(s) have role in protein transport to vacuole involved in ubiquitin-dependent protein catabolic proce
Protein of unknown function; Hap43-repressed; Spider biofilm induced
F-box domain-containing protein; flow model biofilm induced
Ortholog of S. cerevisiae Dif1; which regulates nuclear localization of Rnr2 and Rnr4; colony morphology-re
Ortholog(s) have role in ascospore-type prospore membrane formation, spore membrane bending pathway
Ortholog of S. cerevisiae : YPL034W, C. dubliniensis CD36 : Cd36_40280, C. parapsilosis CDC317 : CPAF
Ortholog of C. dubliniensis CD36 : Cd36_40300, C. parapsilosis CDC317 : CPAR2_402190, C. auris B8441
Ortholog of Candida lusitaniae ATCC 42720 : CLUG_00275 and Candida albicans WO-1 : CAWG_03759
Ortholog(s) have histone demethylase activity (H3-K4 specific), histone demethylase activity (H3-dimethyl-K
Has domain(s) with predicted 2 iron, 2 sulfur cluster binding, iron ion binding, oxidoreductase activity, oxido
Ortholog(s) have ubiquitin protein ligase activity and role in protein import into peroxisome matrix, protein po
Ortholog(s) have proton-transporting ATP synthase activity, rotational mechanism, structural molecule activ
Ortholog(s) have D-arabinose 1-dehydrogenase [NAD(P)+] activity and role in dehydro-D-arabinono-1,4-lac
Ortholog(s) have chromatin binding activity
Protein with B-cell receptor-associated protein 31-like domain; membrane-localized protein
Ortholog(s) have enzyme inhibitor activity and role in actin cortical patch assembly, negative regulation of ca
Protein involved in proteolytic control of sumoylated substrates; interacts with SUMO; member of the SWI/S
Has domain(s) with predicted zinc ion binding activity
Has domain(s) with predicted role in peptidyl-diphthamide biosynthetic process from peptidyl-histidine and c
Ortholog(s) have ubiquitin-ubiquitin ligase activity and role in free ubiquitin chain polymerization, protein poly
Has domain(s) with predicted hydrolase activity
Subunit of ER-mitochondrion tether ERMES complex, required for evasion of host immune response
Ortholog(s) have phosphatase activity, phosphoprotein phosphatase activity, thiosulfate sulfurtransferase ac
Protein with a predicted role in clathrin cage assembly; Hap43-repressed; Spider biofilm repressed
Has domain(s) with predicted oxidoreductase activity and role in metabolic process
Putative adhesin-like protein
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Ortholog(s) have nicotinamide riboside transmembrane transporter activity, nucleobase transmembrane tra
Ortholog(s) have role in peptidyl-diphthamide biosynthetic process from peptidyl-histidine
Has domain(s) with predicted hydrolase activity and role in metabolic process
Has domain(s) with predicted ATP binding activity
Ortholog of C. dubliniensis CD36 : Cd36_40780, Candida tenuis NRRL Y-1498 : CANTEDRAFT_116553, L
Ortholog(s) have RNA binding, ribonuclease MRP activity, ribonuclease P activity
Protein of unknown function; Spider biofilm induced
Has domain(s) with predicted translation initiation factor activity and role in translational initiation
Ortholog(s) have role in protein localization to plasma membrane, protein targeting to vacuole, receptor-me
Ortholog(s) have SUMO transferase activity, role in DNA repair and Smc5-Smc6 complex localization

Ortholog(s) have N(6)-L-threonylcarbamoyladenine synthase activity and role in mitochondrial tRNA threony
Ortholog(s) have magnesium ion transmembrane transporter activity, role in magnesium ion export from mi
Ortholog of C. dubliniensis CD36 : Cd36_40890, C. parapsilosis CDC317 : CPAR2_401100, C. auris B8441
Putative secreted acid sphingomyelin phosphodiesterase; possible Kex2p substrate
Protein of unknown function; induced in cyr1 or ras1 mutant; induced by fluconazole, by alpha pheromone i
Ortholog(s) have ATP binding, ATP:3'-cytidine-cytidine-tRNA adenylyltransferase activity, CTP:3'-cytidine-tF
Protein with similarity to mutator-like element (MULE) transposase
Possible similarity to mutator-like element (MULE) transposase; flow model biofilm induced; expression reg
Ortholog(s) have ATPase, tRNA binding activity, role in protein urmylation, regulation of transcription by RN
Putative phospholipase of patatin family; similar to S. cerevisiae Tgl3p; predicted Kex2p substrate
NRAMP metal ion transporter domain-containing protein; induced by nitric oxide independent of Yhb1; flow
Ortholog of S. cerevisiae : ESL1, C. glabrata CBS138 : CAGL0H06611g, C. dubliniensis CD36 : Cd36_410
Possile protease; mutation confers hypersensitivity to toxic ergosterol analog
Predicted triglyceride lipase; Spider biofilm induced
Putative protein of unknown function, transcript is upregulated in clinical isolates from HIV+ patients with ora
Protein with homology to mitochondrial intermembrane space proteins; regulated by Sef1p-, Sfu1p-, and Ha
Protein with a glycoside hydrolase domain; mutants are viable
Protein of unknown function; hyphal-induced expression, regulated by Cyr1, Ras1, Efg1; Spider biofilm indu
Protein of unknown function; Spider biofilm induced
Ortholog(s) have RNA binding activity, role in mRNA splicing, via spliceosome and U2 snRNP, U2-type pre
RING finger and CHY zinc finger domain-containing protein; mutant are viable
Ortholog(s) have phosphoprotein phosphatase activity
Ortholog of C. dubliniensis CD36 : Cd36_41300, C. parapsilosis CDC317 : CPAR2_400390, C. auris B8441
Protein similar to GPI-linked cell-wall proteins; induced in low iron; Spider biofilm induced; regulated in Spid
Ortholog of C. dubliniensis CD36 : Cd36_41430, Candida tropicalis NEW ASSEMBLY : CTRG1_00187, Ca
Protein of unknown function; Hap43-induced gene
Protein present in exponential and stationary growth phase yeast cultures
Ortholog(s) have role in SCF-dependent proteasomal ubiquitin-dependent protein catabolic process, cellula
Protein required for thiolation of uridine at wobble position of Gln, Lys, and Glu tRNAs; has a role in urmylat
Ortholog(s) have carbonyl reductase (NADPH) activity, oxidoreductase activity, serine 3-dehydrogenase ac
Ortholog(s) have ubiquitin-ubiquitin ligase activity, role in ATP export, mitochondrion inheritance, protein mo
Putative cleavage and polyadenylation factor; heterozygous null mutant exhibits hypersensitivity to parnafur
Ortholog(s) have structural constituent of nuclear pore activity
Ortholog(s) have role in TOR signaling, positive regulation of transcription by RNA polymerase I and cytoso
Protein of unknown function; Spider biofilm repressed
Ortholog(s) have role in cellular response to DNA damage stimulus, protein ubiquitination, telomere mainte
Ortholog(s) have P-body localization
Predicted peptide alpha-N-acetyltransferase; flow model biofilm induced
Ortholog(s) have histone deacetylase activity
Adapter protein for pexophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; Spider biofilm induce
Protein with a dienelactone hydrolase domain; Hap43-repressed gene
Ortholog(s) have ribose phosphate diphosphokinase activity, role in 5-phosphoribose 1-diphosphate biosyn
Predicted metallocarboxypeptidase; role in proteolysis; rat catheter biofilm repressed
Putative dienelactone hydrolase; protein abundance is affected by URA3 expression in the CAI-4 strain bac
Possible Golgi membrane protein; Hap43-repressed; hypha induced; flow model biofilm induced; Spider bic
Putative RNA polymerase III transcription initiation factor complex (TFIIIC) subunit; possibly an essential ge
Protein of unknown function; possible mitochondrial protein; Spider biofilm induced
Putative F-actin-capping protein subunit beta; possibly an essential gene, disruptants not obtained by UAU1
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_41860, C. parapsilosis CDC317 : CPAR2_400440, C. auris B8441
Protein with a predicted role in mitochondrial respiratory chain complex II assembly; rat catheter biofilm indu
Ortholog(s) have polyamine oxidase activity and role in pantothenate biosynthetic process, spermine catabo
Protein with a mitochondrial carrier protein domain; possibly an essential gene, disruptants not obtained by
Ortholog(s) have role in U1 snRNA 3'-end processing, U4 snRNA 3'-end processing and U5 snRNA 3'-end
Catalytic subunit of glycosylphosphatidylinositol-alpha 1,4 mannosyltransferase I, involved in GPI anchor bio
Protein of unknown function; Hap43-repressed gene
Ortholog(s) have GTPase activating protein binding, cAMP-dependent protein kinase inhibitor activity
Ortholog of S. cerevisiae : YPL109C, C. glabrata CBS138 : CAGL0J07018g, C. dubliniensis CD36 : Cd36_
Ortholog(s) have lysophospholipase activity, role in lipid homeostasis and lipid droplet localization
CoA-transferase family protein; rat catheter biofilm repressed
Ortholog of C. dubliniensis CD36 : Cd36_42090, Debaryomyces hansenii CBS767 : DEHA2C14872g, Pichi
Ortholog of C. dubliniensis CD36 : Cd36_42100, Debaryomyces hansenii CBS767 : DEHA2C14850g, Pichi
Catechol 1,2-dioxygenase (1,2-CTD), involved in degradation of aromatic compounds; Spider biofilm induce
Protein similar to S. cerevisiae Rot1p, which has roles in cytoskeletal dynamics and cell wall biosynthesis; p

Protein of unknown function; repressed by prostaglandins; Hap43-induced, Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_42220, C. parapsilosis CDC317 : CPAR2_500340, Debaryomyce
Putative protease B inhibitor; hyphal-induced expression; Cyr1p- and Ras1p-repressed
Protein not essential for viability; orf19.10279 possibly transcriptionally regulated upon hyphal formation
Putative glycosylphosphatidylinositol (GPI) anchor assembly protein; transposon insertion causes decrease
Putative mRNA cleavage and polyadenylation factor; heterozygous null mutant exhibits hypersensitivity to p
Has domain(s) with predicted role in cell redox homeostasis
Ortholog(s) have HDEL sequence binding activity, role in endoplasmic reticulum to Golgi vesicle-mediated t
Subunit of the 20S core particle of the proteasome
Predicted membrane transporter; member of the monocarboxylate porter (MCP) family, major facilitator su
BTB/POZ domain protein; induced by Mnl1 under weak acid stress; flow model biofilm induced; Spider biofi
Ortholog(s) have DNA-binding transcription repressor activity, RNA polymerase II-specific, histone demethy
Ortholog of C. parapsilosis CDC317 : CPAR2_400095, C. dubliniensis CD36 : Cd36_42560, Candida tenui
Putative endonuclease involved in DNA repair
Ortholog(s) have histone binding activity, role in DNA replication-dependent nucleosome assembly and CA
Carbohydrate kinase domain-containing protein; Spider biofilm induced
Protein with a glucose/ribitol dehydrogenase family domain; mutants are viable
Putative subunit of phosphatidylinositol 3-kinase complexes I and II; transcription is activated in the presen
Ortholog of Debaryomyces hansenii CBS767 : DEHA2E16016g, Pichia stipitis Pignal : PICST_38487, Cand
Has domain(s) with predicted zinc ion binding activity
Ortholog(s) have DNA clamp loader activity, role in DNA damage checkpoint signaling, nucleotide-excision
Putative plasma membrane protein; Plc1-regulated; Spider biofilm induced
Protein of unknown function; flow model, rat catheter and Spider biofilm induced; Hap43-repressed
Ortholog(s) have ATP binding, magnesium ion binding activity and role in eukaryotic translation initiation fa
Cytosolic chaperonin Cct ring complex subunit; role in the assembly of actin and tubulins; Spider biofilm re
Ortholog(s) have D-loop DNA binding, Y-form DNA binding, double-stranded DNA binding, four-way junctio
Similar to S. cerevisiae Elp2, an Elongator complex subunit required for modification of wobble nucleosides
Ortholog(s) have enzyme activator activity and role in chromosome segregation
Ortholog(s) have guanyl-nucleotide exchange factor activity and role in mature ribosome assembly
Specificity factor required for ubiquitination and sorting of specific cargo proteins at the multivesicular body;
Protein of unknown function; Ras1 and Cyr1 repressed; rat catheter and Spider biofilm induced
Ortholog(s) have EMC complex localization
Ortholog(s) have ubiquitin protein ligase activity, ubiquitin-protein transferase activity
Planktonic growth-induced gene
Putative mitochondrial GTPase; required for mitochondrial morphology and genome maintenance; Spider b
Ortholog(s) have DNA-directed 5'-3' RNA polymerase activity, RNA polymerase I activity, RNA polymerase
Ortholog(s) have carboxypeptidase activity, role in nitrogen compound metabolic process, proteolysis involv
Protein of unknown function; flow model biofilm repressed
Ortholog(s) have TBP-class protein binding, transcription coregulator activity and role in RNA polymerase II
Ortholog(s) have phosphatidylcholine flippase activity, phosphatidylethanolamine flippase activity, phosphat
Putative GPI transamidase component; possibly an essential gene, disruptants not obtained by UAU1 meth
Predicted hexameric RecA-like ATPase Elp456 Elongator subcomplex subunit; required for modification of
Ortholog(s) have mRNA binding activity, role in mRNA splicing, via spliceosome, spliceosomal complex ass
Protein of unknown function; Hap43p-repressed gene
Ortholog(s) have SUMO transferase activity, role in DNA repair and Smc5-Smc6 complex localization
Protein with a predicted FAD-dependent pyridine nucleotide reductase domains; putative oxidoreductase; P
Ortholog(s) have 3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity and mitochondrion localization
ORF in retrotransposon Tca4; similar to Pol region of retrotransposons encoding reverse transcriptase, pro
Ortholog(s) have mRNA 3'-UTR binding activity and role in biological process involved in interspecies intera
Ortholog of C. dubliniensis CD36 : Cd36_62310 and Candida tropicalis NEW ASSEMBLY : CTRG1_CGOB
Protein of unknown function
Ortholog of C. dubliniensis CD36 : Cd36_43090, C. parapsilosis CDC317 : CPAR2_403340, C. auris B844
Protein with homology to NADH dehydrogenase; regulated by Sef1p-, Sfu1p-, and Hap43p
Has domain(s) with predicted flavin adenine dinucleotide binding, oxidoreductase activity
Ortholog of C. parapsilosis CDC317 : CPAR2_403360, Debaryomyces hansenii CBS767 : DEHA2D00814g
Protein of unknown function; Hap43-repressed gene
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Putative protein of unknown function; transcript upregulated in clinical isolates from HIV+ patients with oral
Ortholog of C. dubliniensis CD36 : Cd36_43270 and Candida albicans WO-1 : CAWG_03460
Ortholog of Candida albicans WO-1 : CAWG_03459
Protein of unknown function; regulated by Tsa1, Tsa1B in minimal media at 37 degrees C
Ortholog of Candida albicans WO-1 : CAWG_03455
Phosphorylated protein of unknown function; Hap43p-repressed gene
Ortholog of C. dubliniensis CD36 : Cd36_43350, C. parapsilosis CDC317 : CPAR2_403560, Debaryomyce

Protein of unknown function; planktonic growth-induced gene
Ortholog(s) have role in nucleotide-excision repair
Has domain(s) with predicted role in RNA catabolic process and ribonuclease H2 complex localization
Predicted membrane transporter, member of the drug:proton antiporter (14 spanner) (DHA2) family, major
Predicted membrane protein; rat catheter biofilm induced
Has domain(s) with predicted 2-oxoglutarate-dependent dioxygenase activity
Ortholog(s) have tRNA (guanine-N1-)-methyltransferase activity, role in mitochondrial tRNA methylation, tR
Ortholog(s) have role in U4 snRNA 3'-end processing, exonucleolytic trimming to generate mature 3'-end o
Ortholog(s) have translation release factor activity, role in mitochondrial translation, mitochondrial translatio
Ortholog of C. dubliniensis CD36 : Cd36_43500, Candida tropicalis NEW ASSEMBLY : CTRG1_00335, Sp
Ortholog(s) have protein-macromolecule adaptor activity and role in proteasome regulatory particle assemb
Putative mitochondrial membrane protein; homozygous transposon insertion causes decreased colony wrin
Ortholog(s) have phosphatidylinositol-3-phosphate binding activity and role in autophagy of mitochondrion,
Predicted tRNA (guanine) methyltransferase activity; Spider biofilm induced
Ortholog(s) have phospholipid binding, single-stranded DNA binding, structural constituent of nuclear pore
Ortholog of C. dubliniensis CD36 : Cd36_43600, C. parapsilosis CDC317 : CPAR2_403780, Candida tenuis
Ortholog of C. dubliniensis CD36 : Cd36_43610, C. parapsilosis CDC317 : CPAR2_403770, C. auris B8441
Ortholog(s) have clathrin binding activity, role in clathrin-dependent endocytosis, histone H2B ubiquitination
Ortholog(s) have 7S RNA binding activity, role in SRP-dependent cotranslational protein targeting to memb
Protein of unknown function
Protein of unknown function; ORF added to Assembly 21 based on comparative genome analysis; protein
Predicted ORF in the Major Repeat Sequence on chromosome 4; member of a family encoded by FGR6-re
Ortholog of C. dubliniensis CD36 : Cd36_43850, C. parapsilosis CDC317 : CPAR2_402060, Pichia stipitis
Protein of unknown function; induced by Rgt1
Ortholog of C. dubliniensis CD36 : Cd36_43820 and Candida albicans WO-1 : CAWG_03393
Calnexin; integral membrane ER chaperone involved in folding and quality control of glycoproteins; caspofu
Protein of unknown function
Ortholog(s) have phosphatidylinositol-3-phosphate binding, phosphatidylinositol-5-phosphate binding activit
Ortholog(s) have role in mitochondrial cytochrome c oxidase assembly and integral component of mitochon
Protein with a predicted endonuclease/exonuclease/phosphatase family domain and a carbon catabolite re
Ortholog of C. dubliniensis CD36 : Cd36_43710, C. parapsilosis CDC317 : CPAR2_402940, C. auris B8441
Ortholog(s) have role in phospholipid biosynthetic process, phospholipid metabolic process, postreplication
Ortholog of C. dubliniensis CD36 : Cd36_43870, C. parapsilosis CDC317 : CPAR2_402120, Candida tropic
Protein of unknown function; repressed by Sfu1; Hap43-induced gene
Putative transporter; fungal-specific; Spider biofilm induced
Ortholog of S. cerevisiae Skg6; localizes to the cell cortex, cell bud neck, cell bud tip, incipient cellular bud
Predicted membrane transporter, member of the oxalate:formate antiporter (OFA) family, major facilitator s
Ortholog(s) have ureidoglycolate lyase activity
Ortholog(s) have protein-macromolecule adaptor activity and role in vesicle-mediated transport
Ortholog of C. dubliniensis CD36 : Cd36_43970, C. parapsilosis CDC317 : CPAR2_401720, C. auris B8441
Protein of unknown function; transcript is upregulated in an RHE model of oral candidiasis; Hap43-represse
Ortholog of C. dubliniensis CD36 : Cd36_44020, C. parapsilosis CDC317 : CPAR2_302330, C. auris B8441
Putative cytochrome P450; Hap43-repressed gene
Protein of unknown function; Spider biofilm induced
Ribosomal 60S subunit protein L22B; Spider biofilm repressed
Protein of unknown function; Spider biofilm induced
Ortholog(s) have protein transmembrane transporter activity and role in filamentous growth, posttranslationa
Serine/threonine protein kinase, acts as an upstream activating factor for the SNF1 complex that regulates
Ortholog(s) have protein-lysine N-methyltransferase activity and role in peptidyl-lysine trimethylation
Putative DNA-binding transcription factor; decreased transcription is observed upon fluphenazine treatment
Ortholog(s) have enzyme activator activity, telomerase inhibitor activity, role in box C/D RNA 3'-end process
Putative metalloendopeptidase of mitochondrial inner membrane, involved in TOR-mediated signaling
Predicted transmembrane protein with a role in cell wall polymer composition; Plc1-regulated; Spider biofilm
Ortholog of C. dubliniensis CD36 : Cd36_44290, C. parapsilosis CDC317 : CPAR2_500740, C. auris B8441
Protein with DNA binding domain, an endonuclease domain; adjacent to CEN4, the centromere region of C
Protein of unknown function; transcript detected on high-resolution tiling arrays
Has domain(s) with predicted nucleic acid binding, zinc ion binding activity
Ortholog(s) have thiol-dependent deubiquitinase activity and role in protein deubiquitination
Ortholog of C. dubliniensis CD36 : Cd36_44340, C. parapsilosis CDC317 : CPAR2_302240, Candida tenuis
Ortholog(s) have methylenetetrahydrofolate dehydrogenase (NAD+) activity, role in folic acid-containing co
Ortholog(s) have role in negative regulation of gluconeogenesis, proteasome-mediated ubiquitin-dependent
Protein of unknown function; filament induced
Ortholog(s) have role in ER-dependent peroxisome organization, endoplasmic reticulum inheritance, endop
Ortholog(s) have tRNA (guanine-N7-)-methyltransferase activity, role in tRNA (guanine-N7)-methylation an

Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Protein of unknown function; mRNA binds She3; regulated by Nrg1; upregulated in a cyr1 or ras1 mutant
Ortholog(s) have RNA binding, chromatin binding, mRNA binding activity
Ortholog(s) have chromatin DNA binding activity
DnaJ chaperone domain protein; role in pre-mRNA splicing; Spider biofilm induced
Protein of unknown function; rat catheter biofilm induced
Ortholog(s) have role in cristae formation, membrane organization and MICOS complex, mitochondrial crist
Predicted membrane transporter; member of the peptide-acetyl-coA transporter (PAT) family, major facilitat
Protein of unknown function; Hap43-repressed; Spider biofilm induced
Protein likely to be essential for growth, based on an insertional mutagenesis strategy
Protein with a predicted role in ribosome biogenesis; mutation confers hypersensitivity to 5-fluorocytosine (5
Ortholog(s) have protein tag activity
Ortholog(s) have zinc ion transmembrane transporter activity, role in zinc ion transport and endoplasmic ret
Has domain(s) with predicted role in protein transport, vacuolar transport
Ortholog(s) have RNA binding, structural constituent of nuclear pore activity
Ortholog of C. dubliniensis CD36 : Cd36_44860, Candida tropicalis NEW ASSEMBLY : CTRG1_04054, Ca
Ortholog(s) have CDP-diacylglycerol-inositol 3-phosphatidyltransferase activity, role in phosphatidylinositol
Ortholog(s) have ubiquitin protein ligase activity, role in anaphase-promoting complex-dependent catabolic
Hap43-induced gene; mutation confers hypersensitivity to 5-fluorocytosine (5-FC), 5-fluorouracil (5-FU), an
Putative ubiquitin-protein ligase; role in protein ubiquitination; Spider biofilm induced
Subunit of Elongator complex; required for modification of wobble nucleosides in tRNA in S. cerevisiae; Ha
Ortholog of S. cerevisiae : MRX12, C. glabrata CBS138 : CAGL0J11110g, C. dubliniensis CD36 : Cd36_44
Putative protein with a predicted role in 60S ribosomal subunit biogenesis; Hap43p-induced gene; ortholog
Ortholog(s) have ubiquitin protein ligase activity
Ortholog(s) have phosphatidylinositol-3,5-bisphosphate binding, phosphatidylinositol-3-phosphate binding,
Ortholog(s) have mRNA 5'-UTR binding, pre-mRNA intronic binding, translation regulator activity and role i
Ortholog(s) have role in protein targeting to ER, signal peptide processing and signal peptidase complex loc
Putative glyoxylate reductase; acts on glyoxylate and hydroxypyruvate substrates; Spider biofilm repressed
D-arabinose 5-phosphate isomerase; has GutQ domain which is associated with phosphosugar binding; oth
Protein of unknown function; Spider biofilm induced
Secreted protein; exogenously expressed protein is a substrate for Kex2 processing in vitro; fluconazole-reg
Ortholog of S. cerevisiae : YPR117W, C. glabrata CBS138 : CAGL0D04510g, C. dubliniensis CD36 : Cd36_
Putative eisosome component role in proper eisosome assembly; upregulated in cyr1 null mutant
Ortholog of C. dubliniensis CD36 : Cd36_45230, C. parapsilosis CDC317 : CPAR2_500450, C. auris B8441
Putative RNA polymerase II subunit B44; heterozygous null mutant exhibits resistance to parnafungin in the
Ortholog(s) have 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxam
Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA,
Adhesin-like protein; regulated by Tsa1, Tsa1B in minimal media at 37 deg; clade-associated gene express
Ortholog(s) have ubiquitin protein ligase activity, role in histone catabolic process, histone ubiquitination, reg
Ortholog(s) have role in cytoplasm to vacuole transport by the Cvt pathway, early endosome to Golgi transp
Protein of unknown function; transcript detected on high-resolution tiling arrays
Ortholog of S. cerevisiae : CAJ1, C. glabrata CBS138 : CAGL0J02750g, C. dubliniensis CD36 : Cd36_4538
Ortholog(s) have cysteine desulfurase activity, role in iron-sulfur cluster assembly and L-cysteine desulfuras
Protein of unknown function; transcript detected on high-resolution tiling arrays; rat catheter biofilm induced
Protein of unknown function; may play a role in regulation of cell size; rat catheter biofilm repressed
Ortholog(s) have tubulin binding activity and role in cytoplasm protein quality control by the ubiquitin-proteas
Has domain(s) with predicted DNA binding, zinc ion binding activity, role in transcription, DNA-templated an
Protein with a selenoprotein domain and a thioredoxin-like fold domain; similar to S. cerevisiae Vhs3p, whic
Protein of unknown function; Rgt1, Hap43-repressed; flow model biofilm induced; Spider biofilm induced
Protein of unknown function; Hap43-repressed gene
Ortholog(s) have nucleoside-triphosphatase activity, nucleoside-triphosphate diphosphatase activity and rol
Ortholog(s) have DNA-directed DNA polymerase activity, deoxycytidyl transferase activity and role in cellula
Ortholog of C. dubliniensis CD36 : Cd36_45590, C. parapsilosis CDC317 : CPAR2_501450, C. auris B8441
Has domain(s) with predicted role in gamma-tubulin complex localization
Predicted component of the core factor rDNA transcription factor complex; required for transcription of 35S
Ortholog(s) have tubulin binding activity and role in microtubule cytoskeleton organization, mitochondrial fiss
Predicted membrane transporter, member of the drug:proton antiporter (14 spanner) (DHA2) family, MFS s
Ortholog(s) have double-stranded DNA binding activity, role in homologous chromosome pairing at meiosis
Ortholog(s) have alpha-tubulin binding activity, role in protein folding, tubulin complex assembly and cytopla
Ortholog(s) have role in ribosome biogenesis and cytosol localization
Ortholog of C. parapsilosis CDC317 : CPAR2_401885, C. auris B8441 : B9J08_000906, Pichia stipitis Pign
Putative GTPase; heterozygous null mutant exhibits resistance to parnafungin in the C. albicans fitness test
Ortholog of C. dubliniensis CD36 : Cd36_45740, C. parapsilosis CDC317 : CPAR2_401900, Candida tenuis
Ortholog(s) have ATPase, GTPase activity, adenosine-diphosphatase activity, cytidine-diphosphatase activi

Ortholog of C. dubliniensis CD36 : Cd36_45760, C. parapsilosis CDC317 : CPAR2_401920, C. auris B8441
Predicted oxidoreductase; rat catheter biofilm induced
Ortholog(s) have chromatin DNA binding activity
Ortholog of C. dubliniensis CD36 : Cd36_45850, C. parapsilosis CDC317 : CPAR2_500750, Pichia stipitis F
Ortholog(s) have borate efflux transmembrane transporter activity, role in borate transport, protein targeting
Protein of unknown function; regulation correlates with clinical development of fluconazole resistance; trans
Ortholog of C. dubliniensis CD36 : Cd36_45910, C. parapsilosis CDC317 : CPAR2_501110, C. auris B8441
Ortholog(s) have role in cellular response to oxidative stress, protein quality control for misfolded or incomp
Has domain(s) with predicted carbohydrate:proton symporter activity, pyrimidine nucleotide-sugar transmen
Ortholog(s) have role in ATP-dependent chromatin remodeling, chromatin remodeling, histone exchange ar
Ortholog(s) have role in cellular protein-containing complex assembly, early endosome to Golgi transport ar
Ortholog in S. cerevisiae is localizedto the bud, mating projection tip, and associates with ribosomes; Spide
Protein involved in cell cycle regulation; ortholog of S. pombe SPAC1071.09c DNAJ domain protein; Hap43
Protein of unknown function; rat catheter and Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_46110, Candida tropicalis NEW ASSEMBLY : CTRG1_03792, Ca
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Ortholog(s) have cargo adaptor activity, phosphatidylinositol-3-phosphate binding activity
Has domain(s) with predicted DNA binding, nucleic acid binding activity
Ortholog of C. dubliniensis CD36 : Cd36_46140, C. parapsilosis CDC317 : CPAR2_501210, C. auris B8441
Ortholog(s) have role in endoplasmic reticulum to Golgi vesicle-mediated transport and endoplasmic reticul
Ortholog(s) have role in cellular response to DNA damage stimulus, proteasome assembly, ubiquitin-depen
Putative NADP-dependent oxidoreductase; Hap43-repressed; induced by benomyl treatment; oxidative stre
Ortholog(s) have transcription coactivator activity and role in carbon catabolite regulation of transcription fro
Ortholog(s) have protein-containing complex binding, protein-macromolecule adaptor activity
Predicted endoplasmic reticulum zinc transporter; induced by nitric oxide
Ortholog of S. cerevisiae Gpn3 a GTPase with a role in biogenesis of RNA pol II and polIII; possibly an esse
Putative chromatin remodelling complex protein; heterozygous null mutant displays sensitivity to virgineone
Ortholog(s) have SNARE binding, syntaxin binding activity
Has domain(s) with predicted sequence-specific DNA binding activity
Ortholog(s) have mRNA binding, metalloaminopeptidase activity and role in negative regulation of gene exp
Ortholog(s) have cytidine deaminase activity, role in cytidine catabolic process, deoxycytidine catabolic proc
Component of the 19S regulatory particle lid of the proteasome
PDR-subfamily ABC transporter (half-size); similar to WHITE subfamily proteins; repressed by fluphenazine
Protein of unknown function; rat catheter and Spider biofilm induced
Predicted pseudouridine synthase; Spider biofilm induced
Protein of unknown function; Spider biofilm induced
Possible mannosyltransferase; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_46470, C. parapsilosis CDC317 : CPAR2_500900, Debaryomyces
Putative DNA repair methyltransferase; induced by nitric oxide independent of Yhb1; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_46490, Pichia stipitis Pignal : PICST_33598, Candida tropicalis NE
Putative cytochrome P450 protein; possibly an essential gene, disruptants not obtained by UAU1 method
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III and RNA po
Protein with t-SNARE domains and a microtubule associated domain; Hap43-induced gene; repressed by a
Predicted RNA-dependent ATPase RNA helicase; Hap43-induced gene
Protein of unknown function; repressed during core stress response
Predicted mitochondrial intermembrane space protein; predicted role in phospholipid metabolism; rat cathe
bZIP transcription factor; possibly transcriptionally regulated upon hyphal formation; Hap43; F-12/CO2 early
Ortholog of C. dubliniensis CD36 : Cd36_26300, Candida tenuis NRRL Y-1498 : cten_CGOB_00015, Deba
Ortholog of C. dubliniensis CD36 : Cd36_54140, Candida tropicalis NEW ASSEMBLY : CTRG1_CGOB_00
Putative lipid phosphatase of the endoplasmic reticulum; role in DNA repair, actin cytoskeleton organization
Ortholog(s) have acetyltransferase activity, histone acetyltransferase activity, role in chromatin silencing at t
Ortholog(s) have double-stranded DNA binding, kinetochore binding activity
Ortholog(s) have role in vesicle-mediated transport and integral component of Golgi membrane localization
Protein of unknown function
Putative mitochondrial ribosomal protein of the large subunit; transcript is upregulated in clinical isolates fro
Subunit of the GPI (glycosylphosphatidylinositol):protein transamidase complex; removes the GPI-anchor si
Predicted ORF from Assembly 19; removed from Assembly 20; restored based on transcription data
Ortholog(s) have ubiquitin protein ligase activity, role in anaphase-promoting complex-dependent catabolic
Epsilon-COP subunit of the coatomer; regulates retrograde Golgi-to-ER protein traffic; Spider biofilm repres
Predicted ORF from Assembly 19; removed from Assembly 20; subsequently reinstated in Assembly 21 ba
Protein of unknown function; Spider biofilm induced
Ortholog of Candida tropicalis NEW ASSEMBLY : CTRG1_CGOB_00063
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Putative integral membrane protein of unknown function; clade-associated gene expression; Spider biofilm

Ortholog(s) have nuclear localization sequence binding, protein-containing complex binding activity and role
Ortholog of C. dubliniensis CD36 : Cd36_50190, C. parapsilosis CDC317 : CPAR2_302680, C. auris B8441
Protein with predicted hydrolase domains; similar to a universal stress protein family protein; possibly essen
Ortholog(s) have 5'-flap endonuclease activity, role in DNA-dependent DNA replication and Slx1-Slx4 comp
Protein with a predicted role in microtubule-related processes; Spider biofilm induced
Ortholog(s) have ribose phosphate diphosphokinase activity and role in 5-phosphoribose 1-diphosphate bio
Major mitochondrial nuclease; has RNAse and DNA endo- and exonucleolytic activities; roles in mitochondr
Protein with a fungal RNA polymerase I subunit RPA14 domain; proposed to play a role in the recruitment c
Has domain(s) with predicted structural constituent of ribosome activity, role in translation and ribosome loc
Ortholog(s) have role in fermentation, protein maturation
Probable securin that interacts with and regulates cohesin protease (separase) Esp1p to ensure chromatid
Putative DnaJ-like chaperone; Hap43-repressed gene
Has domain(s) with predicted DNA binding activity
Protein of unknown function; transcript repressed upon yeast-hyphal switch; fluconazole-induced; Hap43-re
Ortholog of C. dubliniensis CD36 : Cd36_50420, C. parapsilosis CDC317 : CPAR2_304100, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_50520, C. parapsilosis CDC317 : CPAR2_304000, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_50530, C. parapsilosis CDC317 : CPAR2_303990, Candida tenuis
Predicted ORF from Assembly 19; removed from Assembly 20; subsequently reinstated in Assembly 21 an
Ortholog(s) have ubiquitin conjugating enzyme activity, ubiquitin protein ligase activity, ubiquitin-protein tran
Putative aminophospholipid translocase (flippase); merged with orf19.2226 in Assembly 21; possibly an ess
Ortholog of Candida albicans WO-1 : CAWG_04452
Protein of unknown function; rat catheter biofilm repressed
Ortholog of C. dubliniensis CD36 : Cd36_50610, C. parapsilosis CDC317 : CPAR2_303690, C. auris B8441
Ortholog(s) have role in DNA recombination, positive regulation of transcription by RNA polymerase II, regu
Predicted protein tyrosine phosphatase; rat catheter biofilm induced
Ortholog(s) have GTPase activator activity and role in activation of GTPase activity, endocytosis, exocytosis
Protein of unknown function; mutants are viable; Spider biofilm induced
Putative RNA-binding protein; transcript is upregulated in an RHE model of oral candidiasis
Indoleamine 2,3-dioxygenase (IDO); rate-limiting enzyme of tryptophan catabolism via kynurenine; enzyme
Has domain(s) with predicted heme binding, peroxidase activity and role in response to oxidative stress
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Ortholog(s) have transcription export complex localization
Ortholog(s) have role in aerobic respiration and mitochondrial intermembrane space localization
Ortholog(s) have role in mRNA splicing, via spliceosome and U4/U6 x U5 tri-snRNP complex, U5 snRNP lo
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity and role in gene silencing, his
Putative vacuole biogenesis protein
Predicted non-catalytic subunit of N-terminal acetyltransferase; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_51280, C. parapsilosis CDC317 : CPAR2_501840, Candida tenuis
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Protein of unknown function; repressed by fluphenazine treatment; induced by benomyl treatment and in an
Planktonic growth-induced gene
Ortholog of S. cerevisiae : OTU2, C. dubliniensis CD36 : Cd36_51210, C. parapsilosis CDC317 : CPAR2_3
Ortholog(s) have role in reciprocal meiotic recombination and mitochondrial matrix, mitochondrion localizati
Ortholog(s) have palmitoyltransferase activity, role in protein palmitoylation, protein targeting to membrane
Predicted protein of unknown function; merged with orf19.1952 in Assembly 21
Ortholog(s) have ADP-ribosyl-[dinitrogen reductase] hydrolase activity, phosphatase activity
Ortholog of C. dubliniensis CD36 : Cd36_51110, C. parapsilosis CDC317 : CPAR2_302560, C. auris B8441
Similar to an aldose 1-epimerase-related protein; antigenic during murine systemic infection; protein presen
Ortholog of C. dubliniensis CD36 : Cd36_51070, C. parapsilosis CDC317 : CPAR2_302610, Candida tropic
Ortholog(s) have 2-octoprenyl-3-methyl-6-methoxy-1,4-benzoquinone hydroxylase activity, role in ubiquinon
Ortholog(s) have mRNA 3'-UTR binding activity, role in regulation of mRNA stability, regulation of phosphat
Ortholog of S.pombe SPCC825.05c; a predicted splicing coactivator; transcription repressed in azole-resist
Ortholog(s) have role in ER-dependent peroxisome organization, peroxisome organization and endoplasmic
Ortholog(s) have EMC complex localization
Protein of unknown function; UPF0057 protein family member; localizes to the plasma membrane; Spider b
Protein wth a predicted role in transcription from RNA polymerase II promoters; Spider biofilm induced
Ortholog(s) have palmitoyltransferase activity, role in protein palmitoylation and plasma membrane localizat
Putative transporter; decreased transcription is observed upon fluphenazine treatment
Predicted protein kinase; clade-associated gene expression
Ortholog of C. dubliniensis CD36 : Cd36_50820, C. parapsilosis CDC317 : CPAR2_501670, C. auris B8441
Protein component of the small (40S) ribosomal subunit; Spider biofilm repressed
Predicted protein of unknown function; overlaps orf19.4149.1
Putative glutaredoxin; induced by nitric oxide; Spider biofilm induced
Ortholog(s) have NEDD8 activating enzyme activity and role in protein neddylation

Ortholog(s) have pseudouridine synthase activity, role in mRNA pseudouridine synthesis, tRNA pseudourid
Ortholog of C. dubliniensis CD36 : Cd36_51610, C. parapsilosis CDC317 : CPAR2_303630, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_51590, C. parapsilosis CDC317 : CPAR2_303610, C. auris B8441
Ortholog(s) have acetyltransferase activator activity, peptide alpha-N-acetyltransferase activity, ribosome bi
Has domain(s) with predicted role in vesicle-mediated transport
Protein with a role in insertion of tail-anchored proteins into the ER membrane; required for efficient mating,
Protein of unknown function; involved in secretion of proteins that lack classical secretory signal sequences
Ortholog(s) have phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity, role in phosphatidylinositol
Ortholog(s) have RNA binding activity, role in mRNA 5'-splice site recognition, mRNA splicing, via spliceoso
Ortholog(s) have 2,5-diamino-6-ribitylamino-4(3H)-pyrimidinone 5'-phosphate deaminase activity, pseudour
Putative ortholog of human electron transfer flavoprotein dehydrogenase (ETF-dH); alkaline repressed; rep
Has domain(s) with predicted calcium ion binding activity
Ortholog of C. dubliniensis CD36 : Cd36_51840, Candida tropicalis NEW ASSEMBLY : CTRG1_05315, Ca
Ortholog(s) have role in RNA polymerase I assembly, RNA polymerase II core complex assembly, RNA pol
Ortholog(s) have role in establishment of mitotic sister chromatid cohesion, protein import into nucleus
Heme A:farnesyltransferase; catalyzes the 1st step in conversion of protoheme to the heme A prosthetic gr
Ortholog(s) have role in cell morphogenesis, cleistothecium development, conidium formation, positive regu
Ortholog of C. dubliniensis CD36 : Cd36_51910, C. parapsilosis CDC317 : CPAR2_101650, C. auris B8441
Ortholog(s) have ATPase activator activity, RNA binding activity
Putative heat shock protein; decreased expression in hyphae; transcription is increased in populations of ce
Predicted pyridoxal 5'-phosphate synthase; regulated by Gcn4; repressed by amino acid starvation (3-AT tr
Ortholog(s) have oxoglutarate dehydrogenase (succinyl-transferring) activity, structural constituent of riboso
Ortholog of C. dubliniensis CD36 : Cd36_52020, C. parapsilosis CDC317 : CPAR2_100400, C. auris B8441
Protein with a role in insertion of tail-anchored proteins into the ER membrane; Spider biofilm repressed
Putative polyphosphate phosphatase; role in hydrolysis of diphosphorylated inositol polyphosphates and dia
20S proteasome subunit (beta7); protein present in exponential and stationary growth phase yeast cultures
Protein of unknown function; Hap43-induced gene; Ctr86 ortholog in S. cerveisiae is essential; Spider biofil
Planktonic growth-induced gene
Ortholog(s) have role in GPI anchor biosynthetic process, cellular manganese ion homeostasis and endopla
Protein of unknown function; transcript detected on high-resolution tiling arrays
Ortholog(s) have endonuclease activity, ubiquitin binding activity and role in mRNA cleavage, nuclear-trans
Ortholog of Candida albicans WO-1 : CAWG_04619
Protein with a predicted pleckstrin domain; Hap43-repressed gene
Protein with similarity to S. cerevisiae Ykr070w; Tn mutation affects filamentation; Hog1-repressed; colony
Protein of unknown function; rat catheter and Spider biofilm repressed
Ortholog of S. cerevisiae YLR118C (alias Apt1); acyl-protein thioesterase responsible for depalmitoylation c
Ortholog of C. dubliniensis CD36 : Cd36_52200, C. parapsilosis CDC317 : CPAR2_502480, C. auris B8441
Ortholog(s) have protein serine/threonine kinase activity
Ortholog(s) have role in negative regulation of gluconeogenesis, proteasome-mediated ubiquitin-dependent
Puttaive pre-mRNA polyadenylation factor; heterozygous null mutant exhibits hypersensitivity to parnafungi
Ortholog(s) have mRNA binding activity and role in cellular protein-containing complex localization, establis
Has domain(s) with predicted nucleotide binding activity
Protein of unknown function; induced during chlamydospore formation in both C. albicans and C. dublinien
Has domain(s) with predicted ATP binding, protein kinase activity and role in protein phosphorylation
Predicted ORF from Assembly 19; removed from Assembly 20; subsequently reinstated in Assembly 21 ba
Putative mitochondrial membrane protein; ortholog of S. cerevisiae Sls1; coordinates expression of mitocho
Ortholog(s) have chromatin binding, methylated histone binding activity and role in negative regulation of tra
Protein of unknown function; Spider biofilm induced; rat catheter biofilm repressed
Ortholog(s) have role in cytoplasmic translational initiation
Protein of unknown function; flow model biofilm induced; Spider biofilm induced
Putative oxidoreductase; Hap43-repressed gene; clade-associated gene expression
Ortholog(s) have role in protein maturation by iron-sulfur cluster transfer, tRNA wobble uridine modification
Ortholog(s) have oxidoreductase activity, role in cytochrome c-heme linkage, mitochondrial membrane orga
Ortholog(s) have DNA binding, nucleosome binding, transcription corepressor activity
Ortholog(s) have role in chromatin silencing at telomere, rDNA heterochromatin assembly, regulation of tra
Ortholog of C. dubliniensis CD36 : Cd36_52590, C. parapsilosis CDC317 : CPAR2_100565, Debaryomyces
Ortholog(s) have RNA binding activity, role in mRNA splicing, via spliceosome and U4/U6 x U5 tri-snRNP c
Ortholog(s) have methylthioribulose 1-phosphate dehydratase activity and role in L-methionine salvage fron
Ortholog(s) have role in ESCRT III complex assembly, late endosome to vacuole transport, late endosome
Ortholog(s) have TBP-class protein binding, transcription coregulator activity
Trimethyllysine dioxygenase, the first enzyme in the carnitine biosynthesis pathway; hypha-induced express
Ortholog(s) have phosphatidylinositol-3-phosphate binding activity
Has domain(s) with predicted NADH dehydrogenase (ubiquinone) activity, role in mitochondrial respiratory
Ortholog of C. dubliniensis CD36 : Cd36_52760, C. parapsilosis CDC317 : CPAR2_303150, C. auris B8441

Ortholog(s) have role in mRNA splicing, via spliceosome, maturation of 5S rRNA and U4/U6 x U5 tri-snRNF
Ortholog of C. dubliniensis CD36 : Cd36_52790, Candida tropicalis NEW ASSEMBLY : CTRG1_05968, Ca
Ortholog of C. dubliniensis CD36 : Cd36_52800, C. parapsilosis CDC317 : CPAR2_303110, C. auris B8441
Predicted membrane transporter; monocarboxylate porter (MCP) family, major facilitator superfamily (MFS)
Has domain(s) with predicted RNA 7-methylguanosine cap binding, mRNA binding activity
Ortholog(s) have poly(U) RNA binding, splicing factor binding activity and U1 snRNP, U2 snRNP, U4/U6 x U
Ortholog(s) have role in attachment of GPI anchor to protein and GPI-anchor transamidase complex localiz
Ortholog(s) have protein-membrane adaptor activity and role in COPII vesicle coating, macroautophagy, pro
Putative serine/threonine protein kinase; Hog1p-induced
Protein of unknown function; transcript repressed by elevated CO2; Spider biofilm induced
Protein of unknown function
Protein with a transient receptor potential (TRP) ion channel domain; mutants are viable; rat catheter and S
Mitochondrial ribosomal protein of the small subunit; Spider biofilm repressed
Protein of unknown function; rat catheter biofilm induced
Ortholog(s) have myosin II heavy chain binding activity, role in mitotic actomyosin contractile ring disasseml
Lsm (Like Sm) protein; predicted role in involved in mRNA decay; Spider biofilm repressed
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit localiz
Protein of unknown function; Spider biofilm induced
Protein of unknown function
Has domain(s) with predicted role in GPI anchor biosynthetic process
Predicted membrane transporter, member of the L-amino acid transporter-3 (LAT3) family, major facilitator
Spermidine transporter; induced in strains from HIV patients with oral candidiasis; alkaline repressed; amph
Stationary phase enriched protein; predicted ORF from Assembly 19; removed from Assembly 20; subsequ
Protein of unknown function; mRNA binds to She3; Hap43-repressed; rat catheter and flow model biofilm in
Predicted ORF from Assembly 19; removed from Assembly 20; subsequently reinstated in Assembly 21 ba
Putative coenzyme Q (ubiquinone) binding protein; transcript is upregulated in clinical isolates from HIV+ pa
Ortholog(s) have structural constituent of nuclear pore activity
Predicted histone deacetylase activity; Spider biofilm induced
Ortholog(s) have ubiquitin binding, ubiquitin-protein transferase activator activity and role in establishment o
Protein of unknown function; from Assembly 19; removed from Assembly 20; restored based on comparativ
Has domain(s) with predicted diphthine synthase activity, methyltransferase activity and role in metabolic pr
Protein of unknown function; Hap43-repressed gene
Has domain(s) with predicted metal ion binding activity
Protein of unknown function; Spider biofilm induced
Ortholog(s) have diphthine synthase activity and role in peptidyl-diphthamide biosynthetic process from pep
Protein of unknown function; flow model biofilm induced; Spider biofilm induced
Protein of unknown function; induced by alpha pheromone in SpiderM medium; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_53470, Candida tenuis NRRL Y-1498 : CANTEDRAFT_93324, Ca
Protein similar to Candida boidinii formate dehydrogenase; virulence-group-correlated expression; Hap43-re
Protein of unknown function; planktonic growth-induced gene
Cytochrome c oxidase subunit; membrane-localized protein; rat catheter biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_53540, Debaryomyces hansenii CBS767 : DEHA2G07854g, Pichi
Ortholog(s) have chromatin binding, molecular adaptor activity and role in RNA polymerase II preinitiation c
Thiamine pyrophosphokinase, phosphorylates thiamine to produce the coenzyme thiamine pyrophosphate (
Ortholog of C. dubliniensis CD36 : Cd36_53580, C. parapsilosis CDC317 : CPAR2_303030, Debaryomyces
Protein of unknown function; Spider biofilm induced
Protein with Mob2p-dependent hyphal regulation; fluconazole-induced
Protein of unknown function
Ortholog of C. dubliniensis CD36 : Cd36_53630, C. parapsilosis CDC317 : CPAR2_302980, Pichia stipitis P
Putative rRNA processing protein; Spider biofilm induced
Ortholog of S. cerevisiae Sia1; involved in activation of the Pma1 plasma membrane H+-ATPase by glucose
Putative multidrug resistance protein; upregulated by Efg1p
Similar to Rab GTPase activators; Hap43p-induced gene
Putative plasma membrane protein; in S. cerevisiae it is localized to the cell bud and mating projection mem
Alpha/beta-HydrolasE superfamily protein; membrane-localized
Protein of unknown function; Spider biofilm induced
Predicted protein of unknown function; Plc1-regulated
Protein of unknown function; flow model biofilm induced; Spider biofilm induced
Plasma membrane-localized protein of unknown function; Hap43p-repressed gene
Putative splicing factor required for the first step of pre-mRNA splicing; Spider biofilm induced
Putative inositol oxygenase; mutation confers hypersensitivity to toxic ergosterol analog; Spider biofilm indu
Protein of unknown function; decreased transcription is observed upon fluphenazine treatment or in an azol
Ortholog(s) have SNAP receptor activity, role in endocytosis, vesicle fusion and SNARE complex, endosom
Ortholog(s) have role in mitochondrial fusion and integral component of mitochondrial outer membrane loca

Putative benzene desulfurase; induced by nitric oxide independent of Yhb1p
Has domain(s) with predicted RNA binding, ribonuclease T2 activity
Has domain(s) with predicted translation initiation factor activity, role in translational initiation and cytoplasm
Putative metallodipeptidase; protein present in exponential and stationary growth phase yeast; Hog1-induce
Ortholog of C. dubliniensis CD36 : Cd36_53980, C. parapsilosis CDC317 : CPAR2_100980, C. auris B8441
RNI-like superfamily domain-containing protein; early-stage flow model biofilm induced; Spider biofilm induc
Putative adhesin-like protein
Ortholog(s) have protein disulfide isomerase activity, protein-disulfide reductase (glutathione) activity, protei
Ortholog of S. cerevisiae : FSH3, C. glabrata CBS138 : CAGL0L11044g, C. dubliniensis CD36 : Cd36_540
Possible pyrimidine 5' nucleotidase; protein present in exponential and stationary growth phase yeast cultur
Ortholog of Candida albicans WO-1 : CAWG_04810
Putative protein of unknown function, transcription is activated in the presence of elevated CO2
Putative transcription factor with zinc finger DNA-binding motif
Ortholog(s) have role in cellular response to heat, cellular response to oxidative stress, negative regulation
Protein of unknown function
Predicted RNA binding protein; stationary phase enriched; induced in core caspofungin response; induced I
Has domain(s) with predicted nucleic acid binding, nucleotide binding activity
Putative mitochondrial ribosomal protein of the small subunit; mutation confers hypersensitivity to 5-fluorocy
Ortholog of C. dubliniensis CD36 : Cd36_54170, C. parapsilosis CDC317 : CPAR2_100960, C. auris B8441
Ortholog(s) have EMC complex localization
Protein involved in utilization of L-sorbose as carbon source
Predicted COP9 signalosome complex subunit 12; flow model biofilm induced
Ortholog(s) have role in mitochondrial cytochrome c oxidase assembly, protein insertion into mitochondrial i
Ortholog(s) have RNA polymerase II complex binding, protein-containing complex binding, rDNA binding, si
Ortholog(s) have ATPase, chromatin binding, histone binding activity
Ortholog of C. parapsilosis CDC317 : CPAR2_101170, C. auris B8441 : B9J08_004296, Candida tenuis NF
Ortholog(s) have glutaminyl-tRNA synthase (glutamine-hydrolyzing) activity and role in endoplasmic reticulu
Ortholog(s) have GTP cyclohydrolase I activity, role in folic acid-containing compound biosynthetic process
Ortholog of S. cerevisiae : FMP10, C. glabrata CBS138 : CAGL0F09163g, C. dubliniensis CD36 : Cd36_54
Ortholog(s) have role in double-strand break repair via homologous recombination, meiosis I and Smc5-Sm
Putative ribosome biogenesis factor; possibly essential, disruptants not obtained by UAU1 method; rat cath
Protein of unknown function; early-stage flow model biofilm induced
Ortholog(s) have role in endoplasmic reticulum to Golgi vesicle-mediated transport, retrograde transport, er
Ortholog of S. cerevisiae HUA1, which is a cytoplasmic zinc finger domain protein with similarity to Type I J
Ortholog(s) have structural constituent of cytoskeleton activity, role in establishment of mitotic spindle orient
Protein with a role in translation; flow model biofilm repressed
Protein required for maturation of 18S rRNA; rat catheter biofilm repressed
Ortholog(s) have role in cytoplasmic translation, regulation of translation and cytoplasmic stress granule loc
Maltase; induced during growth on sucrose; induced by alpha pheromone in SpiderM medium; early-stage f
Protein with a predicted transcription factor BTF3 domain; flow model biofilm induced
Protein of unknown function; induced in core caspofungin response; induced in ssr1 mutant; induced by nitr
Putative adhesin-like protein; induced by Mnl1 under weak acid stress; rat catheter and Spider biofilm induc
Ortholog(s) have DNA-directed 5'-3' RNA polymerase activity, RNA polymerase III activity and role in tRNA
Ortholog(s) have acylglycerol lipase activity, role in cellular lipid metabolic process and cytoplasm, nucleus l
BLOC-1 complex subunit involved in endosomal maturation; Predicted ORF from Assembly 19; removed fro
Dolichyl-diphosphooligosaccharide-protein glycotransferase; predicted role in protein N-linked glycosylation
Putative mannosyltransferase; similar to S. cerevisiae Gpi10p; has HKEXRF motif
Ortholog(s) have Atg8 ligase activity, protein-macromolecule adaptor activity
Ortholog of S. cerevisiae : YMR160W, C. glabrata CBS138 : CAGL0M09493g, C. dubliniensis CD36 : Cd36
Protein involved in mitochondrial function; mutants are sensitive to chitosan and SDS
Putative dephospho-CoA kinase; protein likely to be essential for growth, based on an insertional mutagene
Has domain(s) with predicted 2-dehydropantoate 2-reductase activity, NADP binding, oxidoreductase activit
Ortholog(s) have protein-lysine N-methyltransferase activity, role in peptidyl-lysine methylation, peptidyl-lysi
Similar to S. pombe mug180, a predicted esterase/lipase; highly induced during chlamydospore formation ir
Putative protein of unknown function; Hap43p-repressed gene; S. cerevisiae ortholog YHR045W localizes t
Planktonic growth-induced gene
Putative ubiquinol-cytochrome-c reductase; amphotericin B induced; repressed by nitric oxide; protein level
Ortholog of C. dubliniensis CD36 : Cd36_54840, C. parapsilosis CDC317 : CPAR2_100270, C. auris B8441
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Regulatory subunit of protein phosphatase PP4; required for recovery from filamentation induced by DNA d
Ortholog of C. dubliniensis CD36 : Cd36_54870, C. parapsilosis CDC317 : CPAR2_100250, Debaryomyces
Ortholog(s) have unfolded protein binding activity, role in ribosomal large subunit assembly, ribosomal large
Ortholog(s) have DNA primase activity, single-stranded DNA binding activity and role in DNA replication, DN
Ortholog(s) have steryl-beta-glucosidase activity, role in ergosteryl 3-beta-D-glucoside catabolic process an

Protein with a predicted pleckstrin homology domain; induced by alpha pheromone in SpiderM medium
Putative transcription factor containing a Zn(2)-Cys(6) binuclear cluster
Protein similar to S. cerevisiae Ybr075wp; transposon mutation affects filamentous growth; clade-associate
Protein of unknown function; opaque-specific transcript; fluconazole-repressed; induced in cyr1 mutant and
Putative protein of the mitochondrial intermembrane space; predicted role in acetate utilization and glucone
Ortholog of C. dubliniensis CD36 : Cd36_60130, C. parapsilosis CDC317 : CPAR2_603380, C. auris B8441
Ortholog of S. cerevisiae : MRX7, C. glabrata CBS138 : CAGL0K04785g, C. dubliniensis CD36 : Cd36_198
Ortholog(s) have mRNA binding, thiol-dependent deubiquitinase activity
Protein of unknown function; Hap43p-repressed gene
Ortholog of S. cerevisiae Rtt106; histone chaperone that regulates chromatin structure in transcribed and si
Subunit of mitochondrial respiratory chain complex I; induced in high iron; possibly subject to Kex2 process
Putative 2-aminoadipate transaminase; rat catheter and Spider biofilm repressed
Has domain(s) with predicted catalytic activity and membrane localization
Ortholog(s) have SNAP receptor activity, phosphatidylinositol-3-phosphate binding activity
Ortholog of S. cerevisiae : YNL115C, C. glabrata CBS138 : CAGL0L03938g, C. dubliniensis CD36 : Cd36_
Ortholog(s) have ubiquitin protein ligase activity, ubiquitin-protein transferase activity
Has domain(s) with predicted role in attachment of GPI anchor to protein and GPI-anchor transamidase co
Protein of unknown function; regulated by yeast-hypha switch; induced by Mnl1 in weak acid stress; 5' UTR
Ortholog(s) have ubiquitin-protein transferase activity and role in negative regulation of protein autoubiquitin
Ortholog(s) have metalloendopeptidase activity, role in cellular iron ion homeostasis, protein processing inv
Predicted mitochondrial intermembrane space protein of unknown function; possibly an essential gene, disr
Protein of unknown function; Spider biofilm induced
Ortholog(s) have serine-tRNA ligase activity, role in mitochondrial seryl-tRNA aminoacylation, spore germin
Ortholog of C. dubliniensis CD36 : Cd36_60350, C. parapsilosis CDC317 : CPAR2_603550, C. auris B8441
Phosphorylated protein of unknown function; transcript is upregulated clinical isolates from HIV positive pati
Ortholog(s) have phospholipase A2 activity, role in cardiolipin acyl-chain remodeling, cardiolipin metabolic p
Ortholog(s) have NEDD8 activating enzyme activity and role in protein neddylation
Predicted ORF from Assembly 19; removed from Assembly 20; restored based on comparative genome an
Ortholog(s) have splicing factor binding activity, role in mRNA splicing, via spliceosome and U1 snRNP, U2
Ortholog(s) have crossover junction endodeoxyribonuclease activity, endodeoxyribonuclease activity, enzym
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Ortholog(s) have structural constituent of nuclear pore activity, role in nuclear pore organization, spindle pol
Ortholog of C. dubliniensis CD36 : Cd36_60540, C. parapsilosis CDC317 : CPAR2_602830, Candida tenuis
Putative TFIIH complex subunit; possibly an essential gene, disruptants not obtained by UAU1 method
Ortholog(s) have Arp2/3 complex binding activity, role in actin filament debranching, negative regulation of
Ortholog of C. dubliniensis CD36 : Cd36_60590, C. parapsilosis CDC317 : CPAR2_602880, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_60600, C. parapsilosis CDC317 : CPAR2_602890, C. auris B8441
Putative CTD phosphatase; role in dephosphorylation of RNA polymerase II C-terminal domain, transcriptio
Ortholog(s) have integral component of endoplasmic reticulum membrane localization
Ortholog of C. dubliniensis CD36 : Cd36_60640, C. parapsilosis CDC317 : CPAR2_602930, C. auris B8441
Ortholog(s) have adenyl-nucleotide exchange factor activity, role in cytoplasm protein quality control by the
Ortholog(s) have crossover junction endodeoxyribonuclease activity, endodeoxyribonuclease activity
Protein of unknown function; Cyr1-repressed; rat catheter and Spider biofilm induced
Protein of unknown function; Hap43-repressed gene
Putative glutathione peroxidase; induced by peroxide, exposure to neutrophils and macrophage blood fracti
Ortholog of C. dubliniensis CD36 : Cd36_60900, C. parapsilosis CDC317 : CPAR2_603130, C. auris B8441
Protein of unknown function; flow model biofilm induced; Hap43-repressed
Protein that stimulates actin assembly; interacts with polarisome components Bni1p and Bud6p; Hap43-rep
Putative mitochondrial intermembrane space protein; colony morphology-related gene regulation by Ssn6; r
Protein of unknown function; Spider biofilm induced
Ortholog of S. cerevisiae : PRM5, C. dubliniensis CD36 : Cd36_60980, C. parapsilosis CDC317 : CPAR2_6
Alpha/beta hydrolase and lipase domain protein; Hap43-repressed; Spider and flow model biofilm induced
Protein required for expression of mitochondrial ATP synthase and cytochrome c oxidase (respiratory chain
Protein of unknown function; induced by alpha pheromone in SpiderM medium
DEAH-box ATP-dependent RNA helicase, required for 18S rRNA synthesis; rat catheter biofilm induced
Probable mitochondrial tyrosyl-tRNA synthetase, based on conservation in other fungi
Ortholog of C. dubliniensis CD36 : Cd36_61190, C. parapsilosis CDC317 : CPAR2_603230, C. auris B8441
Ortholog of Candida tropicalis NEW ASSEMBLY : CTRG1_CGOB_00181, Candida tropicalis MYA-3404 : C
Ortholog(s) have protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity
Has domain(s) with predicted protein C-terminal S-isoprenylcysteine carboxyl O-methyltransferase activity,
Ortholog of C. dubliniensis CD36 : Cd36_61330, C. parapsilosis CDC317 : CPAR2_602800, C. auris B8441
Ortholog of S. cerevisiae : YPR063C, C. glabrata CBS138 : CAGL0D01540g, C. dubliniensis CD36 : Cd36_
Ortholog(s) have role in histone deacetylation, negative regulation of chromatin silencing at telomere, negat
Putative transferase involved in phospholipid biosynthesis; induced by alpha pheromone in SpiderM mediu

Ortholog of C. dubliniensis CD36 : Cd36_61450, C. parapsilosis CDC317 : CPAR2_602710, Candida tenuis
Putative mitochondrial phosphatidylglycerophosphatase (PGP phosphatase); essential for cardiolipin biosyr
Ortholog(s) have ubiquitin protein ligase activity and role in histone catabolic process, histone ubiquitination
Protein of unknown function; ketoconazole-repressed
Ortholog(s) have mannosyltransferase activity, role in GPI anchor biosynthetic process, protein processing,
Ortholog(s) have role in protein import into nucleus and nucleus localization
Predicted membrane transporter, member of the drug:proton antiporter (14 spanner) (DHA2) family, major
Putative oxidoreductase; Hap43-repressed gene
Protein of unknown function; Cyr1-repressed; rat catheter and Spider biofilm induced
Ortholog(s) have chaperone binding activity, role in protein folding in endoplasmic reticulum, response to ur
Has domain(s) with predicted serine-type endopeptidase activity and role in proteolysis
Protein with a Rho GDP-dissociation inhibitor domain; macrophage-induced gene
Ortholog of Candida albicans WO-1 : CAWG_05215
Predicted membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) family, major
Protein similar to S. cerevisiae small proteolipid associated with plasma membrane ATPase Pma1p; null m
Ortholog(s) have 3'-5' exonuclease activity, DNA-directed DNA polymerase activity, role in mitochondrial DN
Plasma membrane-associated protein; physically interacts with TAP-tagged Nop1p
Protein of unknown function; flow model biofilm induced
RING/FYVE/PHD zinc finger protein; Spider biofilm induced
Guanidinobutyrase (Gbase), enzyme involved in metabolism of guanidinobutyrate
Ortholog of S. cerevisiae : BUD17, C. glabrata CBS138 : CAGL0M10725g, C. dubliniensis CD36 : Cd36_61
Predicted chloride transporter; member of conserved Mcm1 regulon; Spider biofilm repressed
Protein of unknown function; transcription repressed by fluphenazine treatment
Ortholog(s) have histone binding activity, role in chromatin remodeling, histone exchange and Swr1 comple
Predicted MFS membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) family; ir
Predicted membrane protein; induced by alpha pheromone in SpiderM medium
Putative DEAD-box helicase; Hap43-induced; Spider biofilm induced
Putative transcription factor with zinc finger DNA-binding motif; heterozygous null mutant exhibits hypersens
Ortholog of C. parapsilosis CDC317 : CPAR2_602135, Candida tenuis NRRL Y-1498 : cten_CGOB_00042
Protein of unknown function; regulated by Nrg1
Ortholog of C. dubliniensis CD36 : Cd36_62090, C. parapsilosis CDC317 : CPAR2_602150, C. auris B8441
Mitochondrial ribosomal protein of the small subunit; S. cerevisiae ortholog is essential for viability; Spider b
Protein of unknown function; Hap43-repressed gene; rat catheter and Spider biofilm induced
Putative protein of unknown function; stationary phase enriched protein
S. cerevisiae ortholog Pxl1 localizes to sites of polarized growth and is required for selection and/or mainter
Secreted potein; Hap43-repressed; fluconazole-induced; regulated by Tsa1, Tsa1B under H2O2 stress con
Ortholog of C. dubliniensis CD36 : Cd36_62270, C. parapsilosis CDC317 : CPAR2_602240, C. auris B8441
Has domain(s) with predicted role in signal transduction and intracellular anatomical structure localization
Putative mitochondrial inner membrane magnesium transporter; possibly an essential gene, disruptants not
Protein with a predicted serine/threonine kinase and tyrosine kinase domain; possibly an essential gene, dis
Ortholog(s) have role in late endosome to vacuole transport via multivesicular body sorting pathway and Vp
Putative serine/threonine/tyrosine (dual-specificity) kinase; disruptants not obtained by UAU1 method
Protein of unknown function; mRNA binds She3; transcript regulated upon yeast-hypha switch; induced in c
Protein of unknown function; oxidative stress-induced via Cap1; induced by alpha pheromone in SpiderM m
Putative GTPase; role in 60S ribosomal subunit biogenesis; Spider biofilm induced
Predicted methyltransferase; downregulated by fluphenazine treatment or in an azole-resistant strain that o
S. cerevisiae ortholog Stb1 has a role in regulation of MBF-specific transcription at Start; induced in a cyr1
Putative flavodoxin; similar to S. cerevisiae Tyw1, an iron-sulfur protein required for synthesis of wybutosine
Protein with a predicted anaphase-promoting complex APC subunit 1 CDC26 domain; Hap43-repressed ge
Ortholog(s) have enzyme activator activity, histone acetyltransferase activity, structural molecule activity
Described as a Gag-related protein; hyphal induced; downregulation correlates with clinical development of
Putative pseudouridine synthase; predicted role in snRNA pseudouridine synthesis, tRNA pseudouridine sy
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Putative mitochondrial ATP-dependent RNA helicase of the DEAD-box family, transcription is activated in th
Ortholog(s) have NAD+ diphosphatase activity, role in NADH metabolic process and peroxisome localizatio
Putative phosphatidyl glycerol phospholipase C; Plc1-regulated; flow model biofilm induced; Spider biofilm i
Ortholog(s) have role in chromatin silencing at telomere, negative regulation of transcription from RNA poly
Ortholog of S. pombe SPCC550.08, an N-acetyltransferase; transcript induced during growth in the mouse
Ortholog(s) have mRNA binding, ribosome binding activity and role in mitochondrial respiratory chain compl
Ortholog(s) have role in SRP-dependent cotranslational protein targeting to membrane and signal recogniti
Similar to alcohol dehydrogenases; induced by benomyl treatment, nitric oxide; induced in core stress respo
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_62760, C. parapsilosis CDC317 : CPAR2_601700, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_62780, C. parapsilosis CDC317 : CPAR2_601690, C. auris B8441

Ortholog of C. dubliniensis CD36 : Cd36_62790, C. parapsilosis CDC317 : CPAR2_601680, C. auris B8441
Putative oxidoreductase; protein levels affected by URA3 expression in CAI-4 strain background; Efg1, Efh
Protein with a predicted role in 5.8S rRNA processing; flow model biofilm induced
Protein of unknown function; Spider biofilm induced
Ortholog(s) have guanyl-nucleotide exchange factor activity, ubiquitin binding activity
Protein with a predicted role in mitotic spindle elongation, vesicle-mediated transport; flow model biofilm ind
Predicted membrane transporter, member of the anion:cation symporter (ACS) family, major facilitator supe
Has domain(s) with predicted carbon-nitrogen ligase activity, with glutamine as amido-N-donor, hydrolase a
Ortholog(s) have SNAP receptor activity, role in retrograde vesicle-mediated transport, Golgi to endoplasmi
Protein with similarity to S. pombe Nrd1p; transcription induced upon induction of hyphal growth; regulated
Has domain(s) with predicted zinc ion binding activity and role in intracellular protein transport, vesicle-medi
Protein of unknown function; Hap43-repressed gene
Ortholog of C. dubliniensis CD36 : Cd36_63380 and Candida albicans WO-1 : CAWG_05071
Putative transcriptional regulator of ribonucleotide reductase genes; Spider biofilm induced
Ortholog(s) have methionine-R-sulfoxide reductase activity and role in cellular response to oxidative stress
Ortholog of C. dubliniensis CD36 : Cd36_63300, Candida tropicalis NEW ASSEMBLY : CTRG1_05769, Ca
Ortholog(s) have RNA-DNA hybrid ribonuclease activity and role in RNA catabolic process
Ortholog(s) have role in protein lipoylation and mitochondrion localization
Ortholog(s) have role in establishment of mitotic sister chromatid cohesion, maintenance of rDNA, mitotic s
Protein of unknown function; Spider biofilm repressed
Protein of unknown function; expression downregulated in an ssr1 null mutant
Ortholog of S. cerevisiae : MCY1, C. glabrata CBS138 : CAGL0F08789g, C. dubliniensis CD36 : Cd36_630
Putative peripheral peroxisomal membrane peroxin; required for regulating peroxisome size and maintenan
Putative pantothenate kinase; ortholog of S. cerevisiae Cab1; transposon mutation affects filamentous grow
Ortholog of C. dubliniensis CD36 : Cd36_63050 and Candida albicans WO-1 : CAWG_05094
Protein with a predicted double-strand break repair domain; Hap43-repressed gene
Ortholog(s) have phosphatidylinositol-3,5-bisphosphate 5-phosphatase activity, role in phosphatidylinositol
Protein of unknown function; transcript is upregulated in clinical isolates from HIV+ patients with oral candid
Protein of unknown function; transcript detected on high-resolution tiling arrays
Ortholog of C. dubliniensis CD36 : Cd36_63980, Candida tenuis NRRL Y-1498 : CANTEDRAFT_115187, C
Ortholog of S. cerevisiae : ASA1, C. glabrata CBS138 : CAGL0K07920g, C. dubliniensis CD36 : Cd36_639
Has domain(s) with predicted proton-transporting ATP synthase activity, rotational mechanism, proton-trans
Ortholog(s) have extracellular region localization
Ortholog(s) have protein-macromolecule adaptor activity, ubiquitin protein ligase binding activity and role in
Ortholog of C. dubliniensis CD36 : Cd36_63860, C. parapsilosis CDC317 : CPAR2_601140, C. auris B8441
RNA polymerase III subunit; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_63840, C. parapsilosis CDC317 : CPAR2_601510, Debaryomyces
Predicted 3-methylbutanol:NAD(P) oxidoreductase and methylglyoxal reductase (NADPH-dependent); role
Putative ribonuclease H1; possibly an essential gene, disruptants not obtained by UAU1 method; flow mode
Ortholog of C. dubliniensis CD36 : Cd36_63740, C. parapsilosis CDC317 : CPAR2_503850, Pichia stipitis P
Ortholog(s) have methylated histone binding, transcription factor binding activity
Ortholog(s) have SNARE binding, unfolded protein binding activity
Protein of unknown function; induced by alpha pheromone in SpiderM medium; Spider biofilm induced
Stationary phase enriched protein; Gcn4-regulated; induced by amino acid starvation (3-AT), benomyl or in
Putative protein of unknown function; mutation confers hypersensitivity to amphotericin B; overlaps orf19.56
Ortholog of C. dubliniensis CD36 : Cd36_63640, C. auris B8441 : B9J08_001441, Pichia stipitis Pignal : PIC
Protein of unknown function; Plc1-regulated; induced by Mnl1 under weak acid stress; flow model biofilm in
S. cerevisiae ortholog Hek2/Khd1 is a putative RNA binding protein involved in the asymmetric localization
Mitochondrial dicarboxylate transporter; possibly an essential gene, disruptants not obtained by UAU1 meth
Ortholog(s) have role in DNA replication initiation, chromosome segregation, establishment of mitotic sister
Has domain(s) with predicted catalytic activity and role in metabolic process
Ortholog(s) have rRNA binding activity, role in RNA splicing, mitochondrial RNA processing, mitochondrial
Nucleoporin component of central core of the nuclear pore complex; mRNA binds She3
Putative phosphatidylinositol transfer protein; possibly an essential gene, disruptants not obtained by UAU1
Has domain(s) with predicted zinc ion binding activity and role in intracellular protein transport, vesicle-medi
Predicted ORF from Assembly 19; removed from Assembly 20; subsequently reinstated in Assembly 21 an
Predicted membrane transporter, member of the monocarboxylate porter (MCP) family, major facilitator sup
Ortholog(s) have DNA binding activity, role in rDNA heterochromatin assembly, termination of RNA polymer
Protein involved in oxidative stress response and autophagy; mutants have fragmented mitochondria and a
Ortholog of C. dubliniensis CD36 : Cd36_64130, C. parapsilosis CDC317 : CPAR2_601230, C. auris B8441
Putative cytochrome P450; Spider biofilm induced
Putative phenylacrylic acid decarboxylase; clade-associated gene expression
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Ortholog of C. dubliniensis CD36 : Cd36_64250, Candida tenuis NRRL Y-1498 : cten_CGOB_00218, Deba

Ortholog(s) have ubiquitin-protein transferase activity, role in SCF-dependent proteasomal ubiquitin-depend
Putative membrane protein with a predicted role in zinc ion homeostasis; Hap43-induced; fluconazole-induc
Ortholog(s) have cyclin-dependent protein serine/threonine kinase regulator activity
Ortholog(s) have FAD diphosphatase activity and role in flavin-containing compound metabolic process
Has domain(s) with predicted oxidoreductase activity and role in metabolic process
Ortholog(s) have U2 snRNA binding activity, role in RNA folding, U2-type prespliceosome assembly and U2
Ortholog(s) have role in chromatin remodeling, histone exchange and Swr1 complex, cytosol, nucleus local
Putative dipeptidyl-peptidase III; protein detected by mass spec in exponential and stationary phase culture
Predicted ORF overlapping the Major Repeat Sequence on chromosome 6; member of a family encoded b
Ortholog of Spathaspora passalidarum NRRL Y-27907 : SPAPADRAFT_149713
Ortholog(s) have ribosomal large subunit binding, ubiquitin-protein transferase activity
Ortholog of C. dubliniensis CD36 : Cd36_64550, Candida tropicalis NEW ASSEMBLY : CTRG1_02747, Ca
Ortholog(s) have metalloaminopeptidase activity and role in protein initiator methionine removal involved in
Ortholog(s) have FFAT motif binding, phosphatidylinositol binding activity
Ortholog(s) have L-arginine transmembrane transporter activity, L-aspartate transmembrane transporter ac
Ortholog(s) have microtubule binding activity and role in mitotic spindle assembly checkpoint signaling, prot
Ortholog of C. dubliniensis CD36 : Cd36_64990, C. parapsilosis CDC317 : CPAR2_600170, Candida tenuis
Protein of unknown function; Hap43-repressed gene
Putative metalloprotease; associates with ribosomes and is involved in ribosome biogenesis; Spider biofilm
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_64900, C. parapsilosis CDC317 : CPAR2_600390, Pichia stipitis
Protein with an Alba DNA/RNA-binding protein domain; Spider biofilm induced
Ortholog(s) have cytochrome-c oxidase activity, role in mitochondrial cytochrome c oxidase assembly and r
Putative protein of unknown function; macrophage-induced gene
Ortholog(s) have proteasome binding, ubiquitin-protein transferase activity and role in ubiquitin-dependent
Ortholog(s) have role in protein deubiquitination, regulation of ER to Golgi vesicle-mediated transport, regul
Ortholog of C. dubliniensis CD36 : Cd36_64620, C. parapsilosis CDC317 : CPAR2_601130, Candida tropic
Ortholog of C. dubliniensis CD36 : Cd36_64660, C. parapsilosis CDC317 : CPAR2_601110, Candida tenuis
Dolichol-P-Man dependent alpha(1-3) mannosyltransferase; role in the synthesis of dolichol-linked oligosac
Has domain(s) with predicted ion channel activity, voltage-gated chloride channel activity, role in chloride tra
Predicted ORF from Assembly 19; removed from Assembly 20; restored based on comparative genome an
Predicted alcohol dehydrogenase; Spider biofilm induced
Protein of unknown function; GlcNAc-induced protein; Spider biofilm induced; rat catheter biofilm repressed
Ortholog of S. cerevisiae Spo71; a meiosis-specific protein required for spore wall formation during sporulat
Has domain(s) with predicted GTP binding activity
Ortholog(s) have ubiquitin protein ligase activity, ubiquitin-protein transferase activity
Ortholog of C. dubliniensis CD36 : Cd36_65220, C. parapsilosis CDC317 : CPAR2_213740, C. auris B8441
Has domain(s) with predicted ATP binding, ligase activity, forming carbon-nitrogen bonds activity, role in tR
Ortholog(s) have tRNA (guanosine-2'-O-)-methyltransferase activity, role in endocytic recycling, tRNA meth
Putative sulfate permease; S. cerevisiae ortholog YPR003C localizes to the endoplasmic reticulum; regulat
Putative ortholog of mammalian electron transfer flavoprotein complex subunit ETF-alpha; Spider biofilm re
Has domain(s) with predicted peptidase activity and role in proteolysis
Protein of unknown function; Spider biofilm repressed
Protein of unknown function; Spider biofilm repressed
Protein of unknown function; Spider biofilm repressed
Ortholog(s) have adenylate kinase activity, nucleoside triphosphate adenylate kinase activity, role in nucleot
Protein of unknown function; transcript induced in RHE model of oral candidiasis; Spider biofilm repressed
Putative mitochondrial outer membrane protein membrane fission effector; possibly an essential gene, disru
Ortholog(s) have tRNA-specific adenosine-37 deaminase activity and role in tRNA modification
Ortholog of S. cerevisiae : YGL242C, C. glabrata CBS138 : CAGL0H07755g, C. dubliniensis CD36 : Cd36_
D-ribulose-5-phosphate 3-epimerase; stationary phase enriched protein
Ortholog(s) have role in ribosomal large subunit biogenesis and cytoplasm, nucleus localization
Adhesin-like cell wall protein; similar to mucins and to a Litomosoides microfilarial sheath protein; N-termina
Predicted exonuclease; Spider biofilm induced
Ortholog(s) have telomeric DNA binding activity and role in protein localization to chromosome, telomere m
Has domain(s) with predicted exonuclease activity and intracellular anatomical structure localization
Putative vacuolar transporter of large neutral amino acids; possibly transcriptionally regulated upon hyphal f
Putative protein of unknown function; Hap43-repressed; repressed by nitric oxide; Spider biofilm induced
Putative cytoplasmic RNA-binding protein; heterozygous null mutant exhibits hypersensitivity to parnafungin
Ortholog of S. cerevisiae : YLR001C, C. dubliniensis CD36 : Cd36_70470, C. parapsilosis CDC317 : CPAR
Ortholog(s) have fluoride transmembrane transporter activity, role in cellular detoxification of fluoride, fluoric
Putative NAD dependent epimerase/dehydratase family protein; Spider biofilm repressed
Protein of unknown function; induced by nitric oxide; Spider biofilm repressed
Ortholog(s) have N(6)-L-threonylcarbamoyladenine synthase activity, single-stranded telomeric DNA bindin

Ortholog(s) have role in NLS-bearing protein import into nucleus, protein import into nucleus and cytoplasm
Protein of unknown function; induced in core stress response; induced by cadmium stress via Hog1; oxidati
S-adenosylmethionine transporter of the mitochondrial inner membrane; mitochondrial carrier family; predic
Ortholog(s) have role in axial cellular bud site selection, cytogamy, positive regulation of GTPase activity an
Ortholog of S. cerevisiae : YCL012C, C. dubliniensis CD36 : Cd36_65270, C. parapsilosis CDC317 : CPAR
Putative ferric reductase; induced by Mac1 under copper starvation; Plc1-regulated; Rim101-repressed
Ortholog(s) have methylated histone binding activity
Ortholog of S. cerevisiae : YCL002C, C. dubliniensis CD36 : Cd36_70180, C. parapsilosis CDC317 : CPAR
Putative AdoMet-dependent proline methyltransferase; Hap43-induced; required for normal flow model biofi
Ortholog of Candida guilliermondii ATCC 6260 : PGUG_03499, Candida lusitaniae ATCC 42720 : CLUG_0
Ortholog(s) have RNA polymerase II C-terminal domain phosphoserine binding, RNA polymerase II comple
Ortholog(s) have ATPase activity
Ortholog of C. dubliniensis CD36 : Cd36_70070, C. parapsilosis CDC317 : CPAR2_301080, C. auris B8441
Ortholog(s) have endoribonuclease activity, role in nuclear mRNA surveillance of mRNP export, transcriptio
Ortholog of S. cerevisiae : RMD8, C. glabrata CBS138 : CAGL0C01969g, C. dubliniensis CD36 : Cd36_700
Putative protein of unknown function; transcript is upregulated in clinical isolates from HIV+ patients with ora
Putative polyphosphatidylinositol phosphatase; possibly an essential gene, disruptants not obtained by UAU
Maf-like protein; rat catheter biofilm induced
Ortholog of S. cerevisiae : YLR050C, C. glabrata CBS138 : CAGL0F01991g, C. parapsilosis CDC317 : CPA
Protein of unknown function; induced by benomyl or in an azole-resistant strain overexpressing MDR1; indu
Putative pre-tRNA processing protein; heterozygous null mutant exhibits hypersensitivity to parnafungin and
Ortholog(s) have phosphatidylinositol-3-phosphate binding activity, role in plasma membrane tubulation, pro
Ortholog(s) have protein phosphatase binding activity
Putative eIF4E-associated protein;, accelerates mRNA degradation by promoting decapping; Spider biofilm
Putative dual specificity protein phosphatase, similar to S. cerevisiae Pps1p
Ortholog of C. dubliniensis CD36 : Cd36_70790, C. parapsilosis CDC317 : CPAR2_301530, C. auris B8441
Putative guanine deaminase; mutation confers hypersensitivity to toxic ergosterol analog; Spider biofilm ind
Protein of unknown function; Spider biofilm induced
Ortholog of S. cerevisiae Ioc4, a protein that influences gene expression through chromatin remodeling; oxi
Ortholog of C. dubliniensis CD36 : Cd36_70850, C. auris B8441 : B9J08_003277, Candida tenuis NRRL Y-
Carboxypeptidase involved in maturation of candidalysin Ece1p
Putative protein of unknown function; transcription is positively regulated by Tbf1p; overlaps orf19.7015
Ortholog of C. dubliniensis CD36 : Cd36_70940, C. parapsilosis CDC317 : CPAR2_300280, Debaryomyces
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA,
Ortholog(s) have ubiquitin ligase complex localization
Has domain(s) with predicted catalytic activity and role in cellular metabolic process
Ortholog of C. dubliniensis CD36 : Cd36_70990 and Candida albicans WO-1 : CAWG_05464
Ortholog(s) have role in reciprocal meiotic recombination
Predicted ORF overlapping the Major Repeat Sequence on chromosome 7; member of a family encoded by
Protein of unknown function
Protein similar to S. pombe SPBC1709.16c a predicted aromatic ring-opening dioxygenase; induced by ber
Ortholog of C. dubliniensis CD36 : Cd36_71020, C. parapsilosis CDC317 : CPAR2_300360, C. auris B8441
Putative oxidoreductase; mutation confers hypersensitivity to toxic ergosterol analog; rat catheter and Spide
Ortholog(s) have lipid transfer activity, phosphatidylcholine binding, phosphatidylethanolamine binding, phos
Ortholog(s) have RNA 7-methylguanosine cap binding, exoribonuclease activator activity, hydrolase activity
Predicted RNA polymerase III subunit C37; Spider biofilm induced
Has domain(s) with predicted LPPG:FO 2-phospho-L-lactate transferase activity
Ortholog(s) have DNA binding activity, role in regulation of DNA damage checkpoint and cytoplasm, nuclea
Dihydrofolate synthetase involved in folic acid biosynthesis
Putative ethanolamine kinase
Ortholog(s) have unfolded protein binding activity, role in mitochondrial proton-transporting ATP synthase c
Putative heat shock protein with a zinc finger motif; required for protein import into mitochondria in S. cerevi
Mitochondrial protein required for expression of respiratory chain complex III (coenzyme Q:cytochrome c ox
Ortholog of C. dubliniensis CD36 : Cd36_71210, C. parapsilosis CDC317 : CPAR2_702710, C. auris B8441
Protein of unknown function; induced during chlamydospore formation in both C. albicans and C. dubliniens
Ortholog(s) have RNA polymerase I general transcription initiation factor activity and role in chromatin orga
Protein of unknown function; transcript induced by benomyl or in azole-resistant strain overexpressing MDR
Ortholog(s) have role in protein maturation by [4Fe-4S] cluster transfer and mitochondrial matrix localization
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Ortholog(s) have palmitoyltransferase activity, role in protein palmitoylation and endoplasmic reticulum loca
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_71340, C. parapsilosis CDC317 : CPAR2_301350, C. auris B8441
Predicted membrane transporter; vesicular neurotransmitter (VNT) family, major facilitator superfamily (MF

Predicted transmembrane transporter; induced during chlamydospore formation in both C. albicans and C.
Mitochondrial protein required for expression of respiratory chain complex IV (cytochrome c oxidase)
Conserved mitochondrial inner membrane insertase; mediates insertion of mitochondrial- and nuclear-enco
Ortholog(s) have role in mitochondrial cytochrome c oxidase assembly, negative regulation of mitochondria
RNA polymerase III transcription initiation factor complex (TFIIIC) subunit; growth phase regulated protein;
Ortholog(s) have GTPase activator activity and cytosol localization
Protein with a predicted fatty acid amide hydrolase I domain; induced by Mnl1 under weak acid stress
Protein of unknown function; rat catheter, flow model and Spider biofilm induced
Ortholog(s) have zinc ion binding activity, role in protein import into mitochondrial intermembrane space and
Regulator of calcineurin; regulated by calcineurin-Crz1 pathway; feedback regulator of calcineurin-depende
Membrane-localized protein of unknown function; possibly secreted; fluconazole-induced
Flavin-linked sulfhydryl oxidase; predicted localization to endoplasmic reticulum lumen; involved in disulfide
Ortholog(s) have SNAP receptor activity, role in Golgi vesicle transport, vesicle fusion and Golgi medial cist
Mitochondrial outer membrane protein, component of vacuole and mitochondria patches (vCLAMPs); involv
Ortholog(s) have role in chromosome segregation and kinetochore, nuclear MIS12/MIND complex, spindle
Ortholog(s) have FAD transmembrane transporter activity, role in FAD transport and mitochondrion localiza
Similar to bacterial DnaJ; transcript upregulated in low iron; flow model biofilm induced; Spider biofilm induc
Ortholog of C. dubliniensis CD36 : Cd36_71740, C. parapsilosis CDC317 : CPAR2_703440, C. auris B8441
Pheromone-regulated protein (Prm10) of S. cerevisiae; colony morphology-related gene regulation by Ssn6
Ortholog(s) have nuclear periphery localization
S. cerevisiae ortholog Inp1 is a peripheral membrane protein of peroxisomes involved in peroxisomal inheri
Putative allantoate permease; Gcn4-regulated; Spider biofilm induced
Putative allantoate permease; fungal-specific (no human or murine homolog)
Predicted aldehyde dehydrogenase [NAD(P)+]; Spider biofilm induced
Ortholog(s) have glutathione disulfide oxidoreductase activity and cytosol localization
Ortholog(s) have GTPase activator activity, role in positive regulation of GTPase activity, positive regulation
Putative curved DNA-binding protein orthologous to S. pombe Cdb4; stationary phase enriched protein; rat
Ortholog(s) have role in histone deacetylation, negative regulation of antisense RNA transcription and positi
Ortholog(s) have structural constituent of ribosome activity, role in mitochondrial translation and mitochondr
Short-chain dehydrogenase/reductase; upregulation correlates with clinical development of fluconazole resi
Ortholog of C. dubliniensis CD36 : Cd36_71960, Pichia stipitis Pignal : psti_CGOB_00136, Candida tropica
Predicted DNA-directed RNA polymerase; role in transcription; Spider biofilm induced
Ortholog(s) have role in nucleocytoplasmic transport, protein import into nucleus and cytoplasm, nucleus lo
Ortholog of C. dubliniensis CD36 : Cd36_72020 and Candida albicans WO-1 : CAWG_05570
Predicted protein serine/threonine kinase and/or protein tyrosine kinase; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_72050, C. parapsilosis CDC317 : CPAR2_301140, Candida tenuis
Ortholog of C. parapsilosis CDC317 : CPAR2_808350, C. dubliniensis CD36 : Cd36_72060, Candida meta
Ortholog of C. parapsilosis CDC317 : CPAR2_808370, C. dubliniensis CD36 : Cd36_72070, Candida meta
Protein of unknown function; induced by nitric oxide independent of Yhb1p; regulated by Sef1, Sfu1, and Ha
Ortholog(s) have role in UDP-glucose transmembrane transport
Ortholog(s) have tRNA (guanine-N7-)-methyltransferase activity, role in tRNA (guanine-N7)-methylation and
Putative protein with a predicted role in exocytic transport from the Golgi; filament induced
Protein of unknown function; flow model biofilm induced
Protein with chitin synthesis regulation, resistance to Congo red domain; membrane-localized protein; Spide
Predicted ORF in retrotransposon Tca11 with similarity to the Gag-Pol region of retrotransposons, which en
Ortholog of C. dubliniensis CD36 : Cd36_83910, Candida tropicalis NEW ASSEMBLY : CTRG1_05087, Ca
Protein of unknown function; induced upon adherence to polystyrene; oxidative stress-induced via Cap1
Putative ortholog of S. cerevisiae Npa3p; possibly essential for growth (however, depletion mutant is viable)
Ortholog(s) have EMC complex localization
Ortholog(s) have unfolded protein binding activity and role in mitochondrial cytochrome c oxidase assembly
Ortholog(s) have U6 snRNA binding activity and role in P-body assembly, mRNA splicing, via spliceosome
Ortholog of C. dubliniensis CD36 : Cd36_72260, C. parapsilosis CDC317 : CPAR2_702840, Candida tenuis
Ortholog of S. cerevisiae : YBL086C, C. glabrata CBS138 : CAGL0C01815g, C. dubliniensis CD36 : Cd36_
Ortholog of C. dubliniensis CD36 : Cd36_72280, C. parapsilosis CDC317 : CPAR2_703040, C. auris B8441
Protein of unknown function, transcript is upregulated in clinical isolates from HIV+ patients with oral candid
Ortholog of C. dubliniensis CD36 : Cd36_72300, C. parapsilosis CDC317 : CPAR2_703060, C. auris B8441
Pol protein of retrotransposon Tca2; separated by a stop codon from Gag protein orf19.2371; likely translat
Putative Gag protein of retrotransposon Tca2; separated by a stop codon from Pol protein orf19.2372; likel
Protein of unknown function; mutants are viable; ortholog of S. cervisiae Art10, a protein of unknown functio
Protein of unknown function that may function in RNA processing; filament induced
Ortholog(s) have role in mitotic intra-S DNA damage checkpoint signaling, positive regulation of macroauto
Diacylglycerol cholinephosphotransferase and ethanolaminephosphotransferase, catalyzes the final step in
Putative Ran guanyl-nucleotide exchange factor; probable signal transducer; Spider biofilm repressed
Ortholog of Candida albicans WO-1 : CAWG_05627

Ortholog(s) have ubiquitin protein ligase activity, ubiquitin-protein transferase activity and role in ubiquitin-de
Has domain(s) with predicted carbon-nitrogen ligase activity, with glutamine as amido-N-donor, hydrolase a
Ortholog(s) have unfolded protein binding activity, role in maturation of SSU-rRNA, ribosomal small subunit
Ortholog of S. cerevisiae : YNR029C, C. glabrata CBS138 : CAGL0M10747g, C. dubliniensis CD36 : Cd36_
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Regulatory subunit of PP2A-like protein phosphatase Sit4p, involved in cell wall maintenance, regulation of
Protein with similarity to a human gene associated with colon cancer and to orf19.5158; regulated by Gcn4,
Protein with a protein tyrosine phosphatase-like protein domain; putative membrane-spanning regions; rat c
Protein similar to S. cerevisiae Phs1p, which is required for growth; has six putative membrane-spanning re
Ortholog of Candida albicans WO-1 : CAWG_05647
Protein of unknown function; rat catheter and Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_72800, Candida tropicalis NEW ASSEMBLY : CTRG1_05211, Ca
Putative pyridoxamine 5'-phosphate oxidase; planktonic growth and early-stage flow model biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_72870, C. parapsilosis CDC317 : CPAR2_704140, Candida tropic
Protein of unknown function; transcript detected on high-resolution tiling arrays; Spider biofilm induced
Ortholog of S. cerevisiae Gid7, a GID complex protein; involved in proteasome-dependent catabolite inactiv
Ortholog of C. dubliniensis CD36 : Cd36_72910, C. parapsilosis CDC317 : CPAR2_704100, C. auris B8441
Putative adhesin-like protein
Protein of unknown function; induced by ketoconazole; Spider, F-12/CO2 and flow model biofilm induced
Protein of unknown function; fluconazole-induced; Spider biofilm induced
Putative aldose reductase; protein level decreases in stationary phase cultures; Spider biofilm repressed
Protein of unknown function; possible COPI-coated vesicle, Golgi apparatus, ribosome localization; rat cath
Ortholog(s) have role in mitochondrial respiratory chain complex assembly and mitochondrial intermembrar
Ortholog of S. cerevisiae Mtr4, an ATP-dependent 3'-5' RNA helicase of the DEAD-box family; Hap43-induc
Protein of unknown function; repressed by alpha pheromone in SpiderM medium
Ortholog of Candida albicans WO-1 : CAWG_05678
Protein of unknown function; Hap43-repressed gene
Putative guanyl nucleotide exchange factor with Sec7 domain; required for normal filamentous growth; regu
Predicted vacuolar protein with a calcineurin-like phosphoesterase domain; repressed by alpha pheromone
Protein of unknown function; rat catheter biofilm repressed
Protein of unknown function; expression decreases by benomyl treatment or in an azole-resistant strain ove
Protein of unknown function; Hap43-repressed gene
Putative ember of the multi-drug and toxin extrusion (MATE) family of the multidrug/oligosaccharidyl-lipid/po
Has domain(s) with predicted metal ion binding activity
Ortholog of C. dubliniensis CD36 : Cd36_73320, C. parapsilosis CDC317 : CPAR2_703860, C. auris B8441
Ortholog(s) have asparagine-tRNA ligase activity, role in asparaginyl-tRNA aminoacylation, mitochondrial a
Ortholog(s) have histidinol-phosphatase activity and role in histidine biosynthetic process
Protein with similarity to amino acid-tRNA ligase; stationary phase enriched protein; GlcNAc-induced protei
Ortholog of C. dubliniensis CD36 : Cd36_73260 and Candida albicans WO-1 : CAWG_05699
Ortholog of Candida albicans WO-1 : CAWG_05700
Ortholog of C. dubliniensis CD36 : Cd36_73400, C. parapsilosis CDC317 : CPAR2_703180, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_73420, C. auris B8441 : B9J08_004732, Debaryomyces hansenii
Has domain(s) with predicted catalytic activity, nitronate monooxygenase activity
Ortholog(s) have role in protein retention in ER lumen, retrograde vesicle-mediated transport, Golgi to endo
Ortholog of C. dubliniensis CD36 : Cd36_73480, Pichia stipitis Pignal : PICST_30727, Candida tropicalis N
Ortholog(s) have role in posttranslational protein targeting to endoplasmic reticulum membrane and TRC co
CCR4-NOT complex component; involved in controlling mRNA initiation, elongation and degradation; rat ca
Putative intranuclear transport and DNA replication mediator; heterozygous null mutant exhibits resistance t
Putative vacuolar protease; upregulated in the presence of human neutrophils; Spider biofilm induced
Protein required for virulence in reconstituted human epithelium (RHE) model of ex vivo infection; decrease
Specificity factor required for ubiquitination; role in protein targeting to vacuole; involved in ubiquitin-depend
Ortholog of C. dubliniensis CD36 : Cd36_73640, C. parapsilosis CDC317 : CPAR2_702340, C. auris B8441
Ortholog(s) have EMC complex localization
Ortholog(s) have RNA binding activity and role in tRNA modification
Ortholog of C. dubliniensis CD36 : Cd36_73670, C. parapsilosis CDC317 : CPAR2_702370, C. auris B8441
Protein involved in intracellular sequestering of iron ion and mitochondrial iron-sulfur cluster assembly; repr
Ortholog of C. dubliniensis CD36 : Cd36_73730, C. parapsilosis CDC317 : CPAR2_702310, Candida tropic
Putative adhesin-like protein
Predicted mitochondrial cardiolipin-specific phospholipase; upregulated in an azole-resistant strain that over
Membrane-associated protein kinase localized in trans-Golgi network; interacts with Arl1p and Sys3p
Ortholog of C. dubliniensis CD36 : Cd36_73790, C. parapsilosis CDC317 : CPAR2_702880, C. auris B8441
Ortholog(s) have unfolded protein binding activity
Putative protein of unknown function; Hap43p-repressed gene; ortholog of S. cerevisiae YMR185W
Protein of allantoate permease family; fungal-specific (no human or murine homolog); Hap43p-repressed g

Protein with a tubulin binding cofactor C domain; flow model biofilm induced
Putative exportin, member of the Exportin-T family; flow model biofilm repressed
Protein similar to Aspergillus CYSK O-acetylserine sulfhydrylase, suggesting that C. albicans uses an O-ac
Putative GTPase inhibitor; predicted role in endocytosis, protein targeting to vacuole; rat catheter biofilm re
Ortholog(s) have GTP binding, GTPase activity, ribosome binding activity
Putative catechol o-methyltransferase; stationary phase enriched protein; transcription upregulated in clinic
Ortholog(s) have role in mRNA splicing, via spliceosome
Butyrobetaine dioxygenase, the fourth enzyme of the carnitine biosynthesis pathway
Protein of unknown function; Hap43-repressed gene
Putative protein of unknown function, transcript is upregulated in an RHE model of oral candidiasis
Component of the chromatin assembly factor I (CAF-1); involved in regulation of white-opaque switching fre
ABC family protein, predicted not to be a transporter; Hap43, caspofungin repressed; rat catheter and Spid
Heterotrimeric G protein alpha subunit; positive role in mating pheromone response; opaque-enriched trans
Monomeric CDK-activating kinase; functional homolog of S. cerevisiae Cak1p; phosphorylates cyclin-free h
Putative translation elongation factor eEF1 gamma; protein level decreased in stationary phase cultures; S
Putative translation elongation factor; downregulated upon phagocytosis by murine macrophages; Hap43-i
Basic amino acid permease; complements lysine transport mutation; 10 predicted transmembrane regions,
Basic amino acid permease; arginine metabolism; regulated by Nrg1/Tup1; caspofungin, flucytosine induce
Predicted amino acid transmembrane transporter; transcript regulated by white-opaque switch; Hap43-repr
AP-1 bZIP transcription factor; apoptotic, oxidative stress response/resistance, multidrug resistance; nucle
Predicted bZip transcription factor; possibly an essential gene, disruptants not obtained by UAU1 method
Arginase; arginine catabolism; transcript regulated by Nrg1, Mig1, Tup1; colony morphology-related regulat
Ornithine aminotransferase; arginine metabolism; alkaline induced; mutant sensitivite to toxic ergosterol an
Putative transcription factor with Ku70/Ku80 beta-barrel DNA-binding motif; involved in telomerase regulatio
RAM cell wall integrity signaling network protein; cell separation, azole sensitivity; needed for hyphal growth
Transcription factor involved in regulation of cell wall homeostasis, adherence, stress response; mutants ha
Catalase; resistance to oxidative stress, neutrophils, peroxide; role in virulence; regulated by iron, ciclopirox
Major carnitine acetyl transferase; intracellular acetyl-CoA transport; localized in peroxisomes and mitocho
Zn(II)2Cys6 transcription factor; similar to S. cerevisiae Cat8 but mutant phenotype suggests different targe
Transcription factor; binds ribosomal protein gene promoters and rDNA locus with Tbf1; regulates sulfur sta
Ser/Thr kinase of cell wall integrity pathway; mutants show abnormal morphology and aggregation; Mob2p
Corticosteroid binding protein; transcription induced at late log-phase or upon adherence to polystyrene; no
Putative cytochrome B5 reductase; plasma membrane-localized
Manganese transporter; required for normal filamentous growth; mRNA binds She3, localized to hyphal tips
Copper-transporting P-type ATPase of Golgi; required for wild-type iron assimilation (indirect effect via Fet3
Putative Holliday junction resolving enzyme; similar to S. cerevisiae Cce1p
Voltage-gated Ca2+ channel of the high affinity calcium uptake system; roles in thigmotropism, establishme
G1 cyclin; required for hyphal growth maintenance (not initiation); cell-cycle regulated transcription (G1/S);
Cytochrome-c peroxidase N terminus; Rim101, alkaline pH repressed; induced in low iron or by macrophag
Component of the Ccr4-Pop2 mRNA deadenylase; transposon mutation affects filamentous growth
Copper chaperone involved in activation and protection of superoxide dismutase Sod1p
Chaperonin of the cytosolic TCP1 ring complex; protein present in exponential and stationary-phase yeast
Putative cytosolic chaperonin Cct ring complex subunit; mutation confers hypersensitivity to cytochalasin D
T-complex protein 1, epsilon subunit; protein present in exponential and stationary growth phase yeast cult
Putative cytosolic chaperonin Cct ring complex subunit; mutation confers hypersensitivity to cytochalasin D;
Cytosolic chaperonin Cct ring complex; protein is present in exponential and stationary growth phase yeast
Chaperonin-containing T-complex subunit; role in hyphal morphogenesis, particularly starvation-induced; es
Putative mannoprotein of cell wall with role in response to stress; increased mRNA abundance observed in
Putative chitin deacetylase; transcription is positively regulated by Tbf1p
Septin, required for wild-type cell, hyphal, or chlamydospore morphology; role in virulence and kidney tissue
Septin; cell and hyphal morphology, agar-invasive growth, full virulence and kidney tissue invasion in mous
Septin; essential for viability; forms ring at sites of cell division and also forms filaments in mature chlamyd
Essential protein with similarity to S. cerevisiae Cdc13p, involved in telomere maintenance
Protein involved in exit from mitosis and morphogenesis; ortholog of S. cerevisiae Cdc14p, which is a dual-
Putative protein serine/threonine kinase, essential for mitotic exit and cytokinesis; localized to the spindle p
Pyruvate kinase at yeast cell surface; Gcn4/Hog1/GlcNAc regulated; Hap43/polystyrene adherence induce
Activator of anaphase-promoting complex/cyclosome; induced under Cdc5 depletion; member of conserve
Putative thymidylate synthase; flucytosine induced; rat catheter biofilm repressed; Spider biofilm repressed
Similar to anaphase-promoting complex component; possibly transcriptionally regulated by Tac1p
GDP-GTP exchange factor for Cdc42p; phosphorylated; required for maintenance of hyphal growth; misex
Putative ubiquitin-protein ligase; periodic mRNA expression, peak at cell-cycle S/G2 phase
Cyclin-dependent protein kinase; interacts with regulatory subunit Cyb1; determination of cell morphology d
Septin; essential for viability; functional homolog of S. cerevisiae Cdc3p; down-regulation associated with a
Putative ubiquitin-protein ligase; transcript regulated by Nrg1 and Tup1, and by Gcn2 and Gcn4; rat cathete

Chaperone for Crk1p; interacts with Crk1p kinase domain and with Sti1p; putative phosphorylation site at S
Protein similar to S. cerevisiae Cdc39p, which is part of the CCR4-NOT transcription regulatory complex; tr
F-box subunit of SCF(CDC4) ubiquitin ligase; functional homolog of S. cerevisiae Cdc4; mutation/depletion
Rho-type GTPase; required for budding and maintenance of hyphal growth; GGTase I geranylgeranylated;
Beta subunit of heterodimeric protein geranylgeranyltransferase type I; GGTase I enzyme binds zinc, is Mg
Putative DNA replication initiation factor; transcriptionally regulated by interaction with macrophage
Putative hexameric MCM complex subunit; predicted role in control of cell division; periodic mRNA express
Phosphorylated protein described as having role in control of cell division; RNA abundance regulated by tyr
Putative microsomal ATPase; plasma membrane-localized; regulated by Gcn2 and Gcn4; induced by amino
Polo-like kinase; member of conserved Mcm1 regulon; depletion causes defects in spindle elongation and
Predicted non-catalytic subunit of phospholipid flippase; involved in endocytosis, hyphal development, drug
Cullin, a scaffold subunit of the SCF ubiquitin-ligase complexes; depletion leads to increased filamentous gr
Putative pre-replication complex helicase subunit; transcript regulated by Nrg1 and Mig1; periodic mRNA ex
Ortholog(s) have protein phosphatase regulator activity, protein serine/threonine phosphatase activity
Putative ATP-binding protein with a predicted role in DNA replication; member of conserved Mcm1p regulon
Cytosolic leucyl tRNA synthetase; conserved amino acid and ATP binding class I signature, tRNA binding,
Functional homolog of S. cerevisiae Cdc68, a transcription elongation factor; essential; possible drug target
Catalytic subunit of Dbf4p-regulated serine/threonine protein kinase; negative regulator of hyphal developm
Putative transcription elongation factor; cdc73 kap114 double transposon mutation affects filamentous grow
Putative cysteine dioxygenases; role in conversion of cysteine to sulfite; transcript regulated upon white-opa
Protein involved in regulation of mitosis; similar to S. cerevisiae Cdh1, which is an APC/C component; trans
Putative RNAse III, ortholog of S. cerevisiae RNT1; merged with orf19.3772 in Assembly 21
Multidrug transporter of ABC superfamily; transports phospholipids in an in-to-out direction; induced by beta
Putative transporter of PDR subfamily of ABC family; Gcn4-regulated; induced by Rim101 at pH 8; Spider b
Multidrug transporter, ATP-binding cassette (ABC) superfamily; transports phospholipids, in-to-out direction
Transporter of the Pdr/Cdr family of the ATP-binding cassette superfamily; transports phospholipids out-to-i
Putative ABC transporter superfamily; fluconazole, Sfu1, Hog1, core stress response induced; caspofungin
Protein similar to S. cerevisiae Cds1p; transposon mutation affects filamentous growth
Putative mRNA splicing factor; ortholog is essential in S. cerevisiae; Spider biofilm induced
Translation elongation factor 3; antigenic in humans; predicted C-term nucleotide-binding active site; protei
ERK-family protein kinase; required for wild-type yeast-hypha switch, mating efficiency, virulence in mice; C
MAP kinase required for wild-type efficiency of mating; component of the signal transduction pathway that r
Protein similar to S. cerevisiae Cem1p, an acyl carrier protein involved in fatty acid biosynthesis; likely to be
mRNA 5'-triphosphatase; large subunit of mRNA capping enzyme; positively regulates Ceg1 activity; functio
Ortholog(s) have tRNA binding activity, role in tRNA export from nucleus and cytoplasm, nuclear pore locali
Protein similar to ferric reductase Fre10p; possible functional homolog of S. cerevisiae Fre1p (reports differ
Superoxide-generating NADPH oxidase, produces extracellular burst of reactive oxygen species at growing
Oxidoreductase; iron utilization; Sfu1/Sef1/Hap43/Nrg1/Tup1/Rim101 regulated; alkaline/low iron/fluphenaz
C-terminus similar to ferric reductases; induced in low iron; Sfu1-repressed; ciclopirox olamine induced; col
Ferric reductase; induced in low iron; ciclopirox olamine, flucytosine induced; amphotericin B, Sfu1 represse
Negative regulator of yeast-form growth; HSP70 family member; induced by growth cessation at yeast-hyph
mRNA 5' guanylyltransferase; small subunit of mRNA capping enzyme; binds an RNA Pol II C-terminal dom
Similar to catabolic ser/thr dehydratases; repressed by Rim101; induced in low iron; regulated on white-opa
Clathrin heavy chain; subunit of the major coat protein; role in intracellular protein transport and endocytosis
Histidine kinase; 2-component signaling, cell wall synthesis; hyphal growth defect; avirulent in mouse, not ra
Protein described as having role in chromosome segregation; RNA abundance regulated by tyrosol and cel
Putative phosphatidylserine synthase; ortholog of S. cerevisiae CHO1; transposon mutation affects filament
Phosphatidyl-ethanolamine N-methyltransferase; fungal-specific (no human or murine homolog); amphoteri
Predicted DEAD-box ATP-dependent RNA helicase; functional homolog of S. cerevisiae Rok1; Hap43-indu
Chitin synthase; essential; for primary septum synthesis in yeast and hyphae; 1 of several chitin synthases;
Chitin synthase; nonessential; required for wild-type chitin deposition in hyphae; transcript regulated during
Major chitin synthase of yeast and hyphae; synthesizes short-chitin fibrils; Chs4-activated; transcript induce
Activator of Chs3p chitin synthase; required for wild-type wall chitin content, but not for hyphal growth; muta
Putative chitin biosynthesis protein; fungal-specific; repressed upon yeast-to-hypha switch; rat catheter biofi
Protein with tetratricopeptide repeats (TPRs); ortholog of S. cerevisiae Chs6, which has role in localizing ch
Protein required for wild-type chitin synthase III activity; similar to (but not functional homolog of) S. cerevisi
Chitin synthase required for synthesis of long-chitin fibrils; nonessential; 8 or 9 membrane spanning regions
Chitinase; putative N-terminal catalytic domain; has secretory signal sequence; lacks S/T region and N-glyc
GPI-linked chitinase; required for normal filamentous growth; repressed in core caspofungin response; fluc
Major chitinase; secreted; functional homolog of S. cerevisiae Cts1p; 4 N-glycosylation motifs; possible O-m
Chitinase; similar to S. cerevisiae sporulation-specific Cts2p; functionally complements A. gossypii cts2 mut
Putative proteasome-interacting protein; rat catheter biofilm induced
Possible oxidoreductase; transcript induced by cadmium but not other heavy metals, heat shock, yeast-hyp
Cirt family transposase; transcript repressed in an azole-resistant strain that overexpresses CDR1 and CDF

Putative role in regulation of biogenesis of the cell wall; upregulated in biofilm; Gcn4p-regulated
Citrate synthase; induced by phagocytosis; induced in high iron; Hog1-repressed; Efg1-regulated under yea
Putative alpha subunit (catalytic subunit) of protein kinase CK2; Cka1p and Cka2p have a common target w
Catalytic alpha-subunit of protein kinase CK2; interaction with calcineurin pathway affects fluconazole sensi
Regulatory subunit of protein kinase CK2 (casein kinase II), beta subunit; null mutants are hypersensitive to
Regulatory subunit of protein kinase CK2 (casein kinase II), beta' subunit; null mutants are hypersensitive t
Ortholog(s) have cyclin-dependent protein serine/threonine kinase activator activity, histone binding, protein
Ste20p family Ser/Thr kinase required for wild-type filamentous growth, organ colonization and virulence in
B-type mitotic cyclin (cyclin-dependent protein kinase regulatory subunit); essential; required for wild-type m
B-type mitotic cyclin; nonessential; negative regulator of pseudohyphal growth; dispensible for mitotic exit, c
Clathrin light chain; subunit of the major coat protein involved in intracellular protein transport and endocyto
Putative cyclin-like protein; transcription is regulated upon yeast-hyphal switch
G1 cyclin; depletion abolishes budding and causes hyphal growth defects; farnesol regulated, functional in S
Calmodulin; calmodulin inhibitors cause a defect in hyphal growth; transcript not regulated by yeast-hyphal t
Putative calcium/calmodulin-dependent protein kinase II; expression regulated upon white-opaque switching
Putative calmodulin-dependent protein kinase; involved in cell wall integrity and oxidative stress response
Catalytic subunit of calcineurin (Ca[2+]-calmodulin-regulated S/T protein phosphatase); required for wild-typ
Regulatory subunit of calcineurin B (Ca[2+]-calmodulin-regulated S/T protein phosphatase); required for wil
Na+/H+ antiporter; required for wild-type growth, cell morphology, and virulence in a mouse model of syster
Putative co-chaperone; Hap43p-induced gene; mutation confers hypersensitivity to radicicol
CNT family H(+)/nucleoside symporter; transports adenosine, uridine, inosine, guanosine, tubercidin; variar
Putative cofilin; macrophage-induced protein; protein present in exponential and stationary-phase yeast cell
Ortholog(s) have role in autophagy of peroxisome, cytoplasm to vacuole transport by the Cvt pathway, esta
Secreted protein; ciclopirox olamine induced; regulated by Ssn6; induced by nitric oxide independent of Yhb
Protein with a predicted role in coenzyme Q biosynthesis; transcriptionally induced by interaction with macro
Protein with a putative role in coenzyme Q biosynthesis; transcriptionally induced by interaction with macrop
Putative methyltransferase of ubiquinone biosynthesis; regulated by Gcn4; repressed by amino acid starvat
Ortholog(s) have oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecu
Cytochrome oxidase assembly protein; transcript regulated by Nrg1; protein repressed during the mating pr
Cytochrome c oxidase; flucytosine induced; repressed by nitric oxide
Cytochrome oxidase assembly protein; transcript regulated by Nrg1 and Tup1; alkaline repressed; Hap43-r
Putative copper metallochaperone; Hap43p-repressed gene; rat catheter biofilm induced; Spider biofilm ind
Putative cytochrome c oxidase assembly protein; Plc1-regulated; rat catheter biofilm induced
Putative cytochrome c oxidase subunit IV; Mig1-regulated; macrophage/pseudohyphal-induced gene; macro
Cytochrome oxidase subunit V; putative upstream CCAAT box regulatory element; macrophage/pseudohyp
Putative cytochrome c oxidase; flucytosine induced
Putative cytochrome c oxidase; flucytosine induced; repressed by nitric oxide
Putative cytochrome c oxidase; flucytosine induced; caspofungin repressed
Putative subunit VIIa of cytochrome c oxidase; flucytosine induced
Putative carbamoyl-phosphate synthase subunit; alkaline repressed; rat catheter, Spider and flow model bio
Putative arginine-specific carbamoylphosphate synthetase; protein enriched in stationary phase yeast cultur
Transcription factor; for mating, filamentation on solid media, pheromone-stimulated biofilms; in pathway wi
Myc-bHLH transcription factor; promotes hyphal growth; directly regulates Tec1 to induce hypha-specific ge
VH1 family MAPK phosphatase; regulates Cst20-Hst7-Cek1-Cph1 filamentation pathway; negatively regula
Putative peptidyl-prolyl cis-trans isomerase; macrophage-induced protein; protein levels decrease in station
Putative peptidyl-prolyl cis-trans isomerase; macrophage/pseudohyphal-repressed; heavy metal (cadmium)
Carboxypeptidase Y; transcript regulated at yeast-hypha transition or macrophage response; induced huma
Protein similarity to mutator-like element (MULE) transposase
Putative adhesin-like protein; transcription detected in high-resolution tiling array experiments
DNA helicase involved in rDNA replication; Spider biofilm repressed
Protein of unknown function; stationary phase enriched protein; induced upon yeast-hypha transition; benor
Ortholog of C. dubliniensis CD36 : Cd36_25130, C. parapsilosis CDC317 : CPAR2_800100, C. auris B8441
Protein with a pyridoxal phosphate-dependent transferase domain; Hap43-repressed; mutation confers hyp
Ortholog of C. dubliniensis CD36 : Cd36_25180, C. parapsilosis CDC317 : CPAR2_800030, C. auris B8441
Has domain(s) with predicted electron transfer activity, heme binding, iron ion binding, monooxygenase acti
Ortholog(s) have structural constituent of nuclear pore activity and role in nuclear pore organization, regulat
Ortholog of C. dubliniensis CD36 : Cd36_25310, Pichia stipitis Pignal : PICST_30877, Candida tropicalis NE
Ortholog(s) have ATPase, DNA binding, nucleosome binding activity, role in chromatin remodeling and Isw
Ortholog of S. cerevisiae Rts3; a component of the protein phosphatase type 2A complex; Plc1-regulated; i
Protein of unknown function; Hap43-induced gene; upregulated in a cyr1 null mutant; Spider biofilm induced
Ortholog of C. parapsilosis CDC317 : CPAR2_800380, Candida tenuis NRRL Y-1498 : CANTEDRAFT_114
Putative nicotinic acid mononucleotide adenylyltransferase, involved in NAD salvage pathway; Spider biofilm
Ortholog(s) have ubiquitin-protein transferase activity, role in ubiquitin-dependent protein catabolic process
Protein with NADPH oxidoreductase containing flavin mononucleotide (FMN) domain; induced by nitric oxid

Predicted membrane transporter; fucose:proton symporter family member, MFS superfamily; flow model bi
Ortholog(s) have 2 iron, 2 sulfur cluster binding, iron-sulfur cluster binding activity
Component of the SSU processome; predicted role in pre-18S rRNA processing; Spider biofilm induced
Has domain(s) with predicted RNA binding, RNA-directed DNA polymerase activity and role in RNA-depend
Putative mitochondrial ribosomal protein of the large subunit; Hap43p-repressed gene; ortholog of S. cerevi
Ortholog of C. dubliniensis CD36 : Cd36_25640, C. parapsilosis CDC317 : CPAR2_803740, Candida tropic
Ortholog(s) have di-trans,poly-cis-decaprenylcistransferase activity, trans-hexaprenyltranstransferase activi
Ortholog(s) have role in endocytosis and actin cortical patch localization
Transcriptional activator of genes involved in biotin metabolism; required for survival and proliferation in ma
Putative subtilisin-family protease; mutation confers hypersensitivity to toxic ergosterol analog
Ortholog(s) have role in ascospore wall assembly and ascospore wall, nuclear envelope localization
Putative 2'-O-methyltransferase with a predicted role in tRNA modification; transcription is activated in the p
Ortholog(s) have alpha-1,4-glucosidase activity, role in N-glycan processing, polysaccharide biosynthetic pr
Ortholog of C. dubliniensis CD36 : Cd36_25800, C. auris B8441 : B9J08_002156, Candida tenuis NRRL Y-
Ortholog(s) have 3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity, role in aerobic respiration, fatt
Ortholog of Candida albicans WO-1 : CAWG_01431
Ortholog(s) have histone demethylase activity (H3-K36 specific), methylated histone binding activity and rol
Ortholog of C. dubliniensis CD36 : Cd36_25870, C. parapsilosis CDC317 : CPAR2_804000, C. auris B8441
Ortholog(s) have actin monomer binding, polysome binding, protein kinase inhibitor activity, ribosome bindi
Ortholog(s) have chaperone binding activity, role in box C/D snoRNP assembly, protein folding and R2TP c
Ortholog of Candida albicans WO-1 : CAWG_01442
Ortholog(s) have palmitoyltransferase activity and role in cortical actin cytoskeleton organization, establishm
Ortholog of C. dubliniensis CD36 : Cd36_25930, C. parapsilosis CDC317 : CPAR2_800910, C. auris B8441
Ortholog of C. parapsilosis CDC317 : CPAR2_800920, C. auris B8441 : B9J08_003484, Candida tenuis NF
Protein of unknown function; Spider biofilm repressed
Putative phosphopantothenoylcysteine decarboxylase, binds to protein phosphatase Ppz1p and regulates it
Ortholog(s) have peptidase activity, role in protein targeting to ER, signal peptide processing and endoplasr
Ortholog of C. dubliniensis CD36 : Cd36_26020, Candida tropicalis NEW ASSEMBLY : CTRG1_00984, Ca
Ortholog(s) have RNA binding activity, role in mRNA splicing, via spliceosome and U1 snRNP, U2-type pres
Ortholog of C. dubliniensis CD36 : Cd36_26070, C. parapsilosis CDC317 : CPAR2_803220, C. auris B8441
Putative ortholog of S. cerevisiae Laa1p; likely to be essential for growth, based on an insertional mutagene
Ortholog of C. dubliniensis CD36 : Cd36_26090, C. parapsilosis CDC317 : CPAR2_801510, C. auris B8441
Ortholog(s) have role in mitochondrial respiratory chain complex assembly and cytoplasm, mitochondrion lo
Putative TFIID and SAGA complex subunit; possibly an essential gene, disruptants not obtained by UAU1 r
Ortholog(s) have role in positive regulation of TORC1 signaling and Seh1-associated complex, extrinsic cor
Ortholog(s) have proteasome regulatory particle binding, ubiquitin protein ligase activity
Putative F-actin capping protein subunit alpha; possibly an essential gene, disruptants not obtained by UAU
Putative transporter; mutation confers hypersensitivity to toxic ergosterol analog; fungal-specific (no human
Protein of unknown function; transcript detected on high-resolution tiling arrays
Putative endosomal transmembrane protein; Hap43p-induced; mutation confers hypersensitivity to amphote
Ortholog(s) have sterol binding activity, role in intracellular sterol transport, sterol transport and extracellular
Putative 12kDa subunit of mitochondrial NADH-ubiquinone oxidoreductase; gene has intron
Predicted vacuolar protein; rat catheter biofilm repressed; flow model biofilm repressed
Predicted membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) family, major
Ortholog(s) have ATPase activator activity, soluble NSF attachment protein activity and role in SNARE com
Ortholog(s) have role in chromosome segregation and kinetochore, nuclear MIS12/MIND complex localizati
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Ortholog of C. dubliniensis CD36 : Cd36_26390, Debaryomyces hansenii CBS767 : DEHA2C05302g, Pichi
Putative protein of unknown function; Hap43-induced; required for normal biofilm growth; F-12/CO2 early bi
Putative RNA polymerase III transcription factor (TFIIIB) subunit; flucytosine repressed
Ortholog of S. cerevisiae Gpa15; involved in the synthesis of glycosylphosphatidylinositol (GPI) anchors; sh
Protein of unknown function; Spider biofilm repressed
Protein with a predicted role in protein translocation from the endoplasmic reticulum
Protein of unknown function; transcript detected on high-resolution tiling arrays
Protein of unknown function; transcript detected on high-resolution tiling arrays
Ortholog(s) have 3'-5'-exodeoxyribonuclease activity, endonuclease activity and role in apoptotic DNA fragn
Ortholog of C. dubliniensis CD36 : Cd36_26520, C. parapsilosis CDC317 : CPAR2_802860, C. auris B8441
Ortholog(s) have aminoacyl-tRNA hydrolase activity and role in negative regulation of proteasomal ubiquitin
Has domain(s) with predicted RNA binding, ribonuclease activity
Protein similar to S. cerevisiae Pmr1p; amphotericin B induced; previously merged with orf19.2553; unmerg
Plasma membrane potassium transporter; amphotericin B induced; previously merged with orf19.2552 in A
Has domain(s) with predicted zinc ion binding activity and nucleus localization
Ortholog(s) have U6 snRNA binding, snRNA binding activity, role in spliceosomal complex assembly, splice
Putative nucleolar protein; implicated in ribosome biogenesis; rat catheter biofilm repressed

Predicted intermediate filament protein; required for nuclear and mitochondrial transmission to daughter bu
Ortholog(s) have AP-1 adaptor complex binding activity, role in clathrin-coated vesicle cargo loading and ex
Putative S-adenosylmethionine-dependent methyltransferase; Hap43p-induced gene
Msh4 ortholog of S. cerevisiae; involved in meiotic recombination and is required for normal levels of crossi
Protein with a predicted epimerase/dehydratase domain; Hap43-repressed gene
Ortholog(s) have ribosomal large subunit binding, tRNA binding activity and role in peptide biosynthetic proc
Putative dethiobiotin synthetase; transcript upregulated in clinical isolates from HIV+ patients with oral cand
Putative adenosylmethionine-8-amino-7-oxononanoate transaminase involved in biotin biosynthesis; transc
Ortholog(s) have RNA polymerase I activity and role in nucleolar large rRNA transcription by RNA polymera
S. pombe ortholog SPAC2C4.06c is a predicted tRNA (cytosine-5-)-methyltransferase; Spider biofilm induc
Protein of unknown function; Spider biofilm induced
Putative tRNA binding protein; intron-containing gene; Spider biofilm induced
C2H2 zinc finger transcription factor; expression reduced in ssr1 null mutant; flow model biofilm induced
Putative serine/threonine protein kinase; possibly an essential gene, disruptants not obtained by UAU1 met
Ortholog of C. dubliniensis CD36 : Cd36_27230, C. parapsilosis CDC317 : CPAR2_801320, C. auris B8441
Protein of unknown function; Spider biofilm induced; upregulated in a cyr1 null mutant
Protein with a Vps9 vacuolar protein sorting protein domain; Hap43-repressed; repressed by ciclopirox olan
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Protein similar to S. cerevisiae Kre27p, which has a role in resistance to killer toxin; predicted Kex2p substr
Ortholog(s) have protein phosphatase 1 binding, protein phosphatase regulator activity and role in chromos
Ortholog of C. dubliniensis CD36 : Cd36_65640 and Candida albicans WO-1 : CAWG_01583
Ortholog(s) have small ribosomal subunit rRNA binding activity
Predicted protein of rapamycin resistance; Spider biofilm induced
Protein of unknown function; Spider biofilm induced
Ortholog(s) have role in positive regulation of endo-1,4-beta-xylanase activity and SCF ubiquitin ligase com
Ortholog of C. dubliniensis CD36 : Cd36_27430, C. parapsilosis CDC317 : CPAR2_802450, C. auris B8441
C2H2 transcription factor; induced by Mnl1 under weak acid stress
Ortholog(s) have role in U4 snRNA 3'-end processing, exonucleolytic trimming to generate mature 3'-end o
Ortholog(s) have triglyceride lipase activity, role in triglyceride catabolic process and peroxisomal matrix loc
Ortholog(s) have ATPase, acting on RNA, second spliceosomal transesterification activity and role in RNA
Mitochondrial protein required for expression of mitochondrial respiratory chain complex I (NADH:ubiquinon
Ortholog(s) have structural constituent of nuclear pore activity and role in NLS-bearing protein import into nu
Protein of unknown function; Hap43-repressed gene; repressed by nitric oxide
Essential component of the conserved oligomeric Golgi complex; role in fusion of transport vesicles to Golg
Ortholog of C. dubliniensis CD36 : Cd36_27680, C. parapsilosis CDC317 : CPAR2_801140, C. auris B8441
Ortholog(s) have microtubule binding, molecular adaptor activity
Ortholog(s) have alpha-tubulin binding, microtubule binding activity, role in cytoplasmic microtubule organiz
Ortholog(s) have role in protein transport
Ortholog(s) have SUMO activating enzyme activity, role in mitotic chromosome condensation, protein sumo
Protein with similarity to carbonic anhydrases
Protein of unknown function; mutation confers hypersensitivity to amphotericin B; flow model biofilm induce
Protein of unknown function; Hap43-repressed; induced in core caspofungin response; regulated by yeast-h
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III and RNA po
Predicted regulatory subunit of the Atg1 signaling complex; required for vesicle formation during autophagy
Protein of unknown function; induced by nitric oxide independent of Yhb1p
Putative ornithine transport protein; localized to the mitochondrial membrane
Ortholog(s) have structural constituent of ribosome activity, role in mitochondrial translation, mitochondrial t
Protein of unknown function; rat catheter biofilm induced
Ortholog(s) have DNA helicase activity, DNA translocase activity
Ortholog of C. dubliniensis CD36 : Cd36_28090, C. parapsilosis CDC317 : CPAR2_802560, C. auris B8441
Predicted HD domain metal dependent phosphohydrolase; Spider biofilm repressed
Endonuclease involved in regulation of translation; stimulates translation of protein O-mannosyltransferase
Ortholog of C. dubliniensis CD36 : Cd36_28190, C. parapsilosis CDC317 : CPAR2_802530, Candida tenuis
Ortholog(s) have role in mitochondrial translation and mitochondrion localization
Ortholog of S. cerevisiae Mpm1; a mitochondrial intermembrane space protein of unknown function; Hap43
Ortholog(s) have role in late endosome to vacuole transport via multivesicular body sorting pathway and Vp
Ortholog(s) have tRNA methyltransferase activity and role in tRNA methylation, wybutosine biosynthetic pro
Ortholog(s) have GTP binding, GTPase activity
Ortholog(s) have RNA binding, ribonuclease MRP activity, ribonuclease P activity, tRNA binding activity
Ortholog(s) have Atg8-specific protease activity
Ortholog(s) have role in mRNA splicing, via spliceosome, maturation of SSU-rRNA, positive regulation of A
Putative transcription factor with zinc finger DNA-binding motif; similar to bacterial DnaJ; induced in low iron
Protein of unknown function; Hap43-repressed; transcript increased in azole-resistant strain overexpressing
Putative aminotransferase; Hap43-repressed; homozygous Tn insertion decreases colony wrinkling in filam

Predicted membrane transporter, involved in biotin import; member of the anion:cation symporter (ACS) far
Ortholog(s) have aldehyde dehydrogenase (NAD+) activity, role in response to furfural and intracellular ana
Putative transcription factor with zinc finger DNA-binding motif
Ortholog of C. dubliniensis CD36 : Cd36_28460, Debaryomyces hansenii CBS767 : DEHA2B00704g, Pichi
Putative protein of unknown function; Hap43p-repressed gene; S. cerevisiae ortholog YKR023W localizes t
Ortholog(s) have DNA replication origin binding, single-stranded DNA binding activity
Putative tRNA-Pro synthetase; genes encoding ribosomal subunits, translation factors, and tRNA synthetas
Ortholog(s) have role in endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S
Protein similar to isoleucyl-tRNA synthetase; isoleucyl-tRNA synthetase is the target of drugs including the
Protein of unknown function; possibly an essential gene, disruptants not obtained by UAU1 method
Ortholog(s) have role in vacuolar proton-transporting V-type ATPase complex assembly and integral compo
Ortholog(s) have DNA 5'-adenosine monophosphate hydrolase activity, DNA-3'-diphospho-5'-guanosine dip
Protein with a histone fold domain; similar to TAFII47 proteins from S. cerevisiae, Danio rerio, Drosophila m
Protein of unknown function; repressed by alpha pheromone in SpiderM medium; transcript induced by Mnl
Ortholog of C. dubliniensis CD36 : Cd36_28730, Candida tropicalis NEW ASSEMBLY : CTRG1_00749, Ca
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Putative actin cytoskeleton component; protein present in exponential and stationary growth phase yeast cu
Mitochondrial inner membrane protein; mammalian mitofilin domain; Spider biofilm repressed
Protein of unknown function; rat catheter biofilm induced
Has domain(s) with predicted role in anaphase-promoting complex-dependent catabolic process, regulation
Putative MFS transporter; predicted ORF in Assembly 20; removed from Assembly 21; restored based on c
Ortholog(s) have DNA 5'-adenosine monophosphate hydrolase activity, DNA-3'-diphospho-5'-guanosine dip
Ortholog(s) have role in retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum and COPI ve
Ortholog(s) have role in mitochondrial genome maintenance and integral component of mitochondrial inner
Ortholog(s) have role in protein targeting to mitochondrion and mitochondrial outer membrane, peroxisomal
Has domain(s) with predicted RNA methyltransferase activity and role in RNA processing
Ortholog of C. dubliniensis CD36 : Cd36_28870, Candida tropicalis NEW ASSEMBLY : CTRG1_00731, Ca
Has domain(s) with predicted hydrolase activity and role in cellular process
Ortholog of S. cerevisiae Spp41; protein involved in negative regulation of expression of spliceosome comp
Protein of unknown function; induced by nitric oxide; oxidative stress-induced via Cap1; fungal-specific (no
Predicted transmembrane transporter; rat catheter and Spider biofilm induced
Protein similar to S. cerevisiae Fmn1p, which is riboflavin kinase; predicted Kex2p substrate; Hap43p-repre
Ortholog(s) have N-terminal protein N-methyltransferase activity, S-adenosylmethionine-dependent methylt
Protein of unknown function; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_29080, C. parapsilosis CDC317 : CPAR2_202490, Candida tenuis
Putative protein similar to S. cerevisiae Mgr3p, a subunit of the i-AAA protease supercomplex that degrades
Putative protein of unknown function; Hap43p-repressed gene; S. cerevisiae ortholog YDL157C localizes to
Non-essential component of the SAGA complex, involved in transcription regulation
Ortholog(s) have role in lipid homeostasis, nuclear envelope organization and endoplasmic reticulum, integr
Putative rRNA processing protein; rat catheter biofilm induced
Ortholog(s) have role in mitochondrial translation and mitochondrion localization
Protein required for fusion of cvt-vesicles and autophagosomes with the vacuole; plays a role in autophagy,
Protein of unknown function; rat catheter and Spider biofilm induced
Ortholog(s) have role in mitotic spindle pole body duplication, proteasome-mediated ubiquitin-dependent pr
Endoplasmic reticulum (ER) protein-translocation complex subunit
Putative RNA-binding protein; role in assembly of box H/ACA snoRNPs and thus pre-rRNA processing; Spi
Ortholog(s) have ATPase, acting on DNA, dinucleotide insertion or deletion binding, guanine/thymine mispa
Putative mitochondrial ribosomal component of the small subunit; possibly an essential gene, disruptants n
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity and role in translational readt
Ortholog(s) have tRNA (adenine-N1-)-methyltransferase activity, role in tRNA methylation and nucleus, tRN
Ortholog(s) have rRNA (cytosine-C5-)-methyltransferase activity
Ortholog(s) have 3'-5' DNA helicase activity
Protein of unknown function; Spider biofilm induced
Ortholog(s) have ribosylnicotinamide kinase activity and role in NAD biosynthesis via nicotinamide riboside
Ortholog of S. cerevisiae Kre33; essential; S. cerevisiae ortholog is essential and is required for biogenesis
Protein with a DNA-binding domain, similar to S. cerevisiae meiosis-specific transcription factor Ndt80p; reg
Has domain(s) with predicted nucleic acid binding, zinc ion binding activity
S. cerevisiae ortholog Rft1p has role in glycolipid translocation, protein N-linked glycosylation and localizes
Ortholog(s) have tRNA (cytosine-5-)-methyltransferase activity, tRNA binding activity
Ortholog(s) have RNA polymerase I cis-regulatory region sequence-specific DNA binding, RNA polymerase
Ortholog of C. dubliniensis CD36 : Cd36_29660, C. parapsilosis CDC317 : CPAR2_205200, C. auris B8441
Has domain(s) with predicted ubiquitin-protein transferase activity, zinc ion binding activity
Protein of unknown function; flow model biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_29750, C. parapsilosis CDC317 : CPAR2_205260, C. auris B8441

Protein of unknown function
Protein with a UV radiation resistance protein/autophagy-related protein 14 domain; Hap43p-induced gene;
Ortholog(s) have chromatin binding, molecular adaptor activity, ubiquitin binding activity and role in chromat
Ortholog of C. dubliniensis CD36 : Cd36_29810, C. parapsilosis CDC317 : CPAR2_206030, C. auris B8441
Has domain(s) with predicted palmitoyl-(protein) hydrolase activity and role in cellular protein modification p
Has domain(s) with predicted 2-oxoglutarate-dependent dioxygenase activity
Ortholog(s) have 5'-3' exonuclease activity, 5'-flap endonuclease activity, double-stranded DNA 5'-3' exodec
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
Ortholog of C. dubliniensis CD36 : Cd36_29980, C. parapsilosis CDC317 : CPAR2_204170, C. auris B8441
Ortholog of a S. cerevisiae Atg22; a vacuolar integral membrane protein required for efflux of amino acids c
Predicted membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) family, major
Protein involved in microtubule morphogenesis; required for protection from excess free beta-tubulin; possi
Protein of unknown function; transcript detected on high-resolution tiling arrays
Ortholog(s) have U2-type spliceosomal complex localization
Putative ATPase and nucleosome spacing factor; heterozygous null mutant displays sensitivity to virgineon
Has domain(s) with predicted membrane localization
Protein of unknown function; Hap43-induced; rat catheter and Spider biofilm induced
Predicted membrane transporter, member of the L-amino acid transporter-3 (LAT3) family, major facilitator
Ortholog of C. dubliniensis CD36 : Cd36_30140, C. parapsilosis CDC317 : CPAR2_204040, C. auris B8441
Protein of unknown function; Hap43-induced; rat catheter and Spider biofilm induced
Has domain(s) with predicted myosin binding activity
Ortholog of Candida albicans WO-1 : CAWG_01818
Ortholog of C. dubliniensis CD36 : Cd36_30250, C. auris B8441 : B9J08_001969, Candida tenuis NRRL Y-
Trimethylaminobutyraldehyde dehydrogenase, the third enzyme of the carnitine biosynthesis pathway
Hydroxytrimethyllysine aldolase, the second enzyme in the carnitine biosynthesis pathway; rat catheter biofi
Ortholog(s) have glycine transmembrane transporter activity, role in glycine import into mitochondrion, hem
Ortholog of C. dubliniensis CD36 : Cd36_30340, C. parapsilosis CDC317 : CPAR2_203900, Candida tenuis
Ortholog of C. dubliniensis CD36 : Cd36_30370, Candida tropicalis NEW ASSEMBLY : CTRG1_00536, Ca
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Predicted protein only found in C. albicans and C. dubliniensis; highly induced during chlamydospore devel
Ortholog(s) have crossover junction endodeoxyribonuclease activity, role in DNA repair, cellular response t
Ortholog of C. dubliniensis CD36 : Cd36_30530, C. parapsilosis CDC317 : CPAR2_203340, C. auris B8441
BIR-containing protein, inhibitor of apoptosis; regulates caspase-like activity under apoptotic stresses
Regulatory subunit of PP2A-like protein phosphatase Sit4p, involved in cell wall maintenance, regulation of
Ortholog(s) have role in protein folding and endoplasmic reticulum localization
Integral membrane protein of the ER; role in the synthesis of beta-1,6-glucan in the cell wall; S. cerevisiae c
Ortholog(s) have structural constituent of ribosome activity and mitochondrial large ribosomal subunit locali
S. cerevisiae ortholog YDR370C/DXO1 has decapping and 5′-3′ exoRNase activity; decrea
Protein similar to S. cerevisiae Cis3p, which has a role cell-wall-related processes; predicted Kex2p substra
Protein of unknown function; regulated by Ssn6
Protein of unknown function; Hap43-repressed; Spider biofilm repressed
Ortholog(s) have role in Golgi to vacuole transport, endosomal transport, vesicle-mediated transport and AP
Protein of unknown function; Spider biofilm repressed
Ortholog of C. dubliniensis CD36 : Cd36_30690, C. parapsilosis CDC317 : CPAR2_204140, Debaryomyces
Putative 3-hydroxyanthranilic acid dioxygenase, involved in NAD biosynthesis; Hap43p-repressed gene
Protein of unknown function; Hap43-repressed; Spider biofilm repressed
Ortholog(s) have role in positive regulation of cellular response to hypoxia, regulation of protein glycosylatio
Ortholog(s) have dicarboxylic acid transmembrane transporter activity, role in mitochondrial transport and m
Protein of unknown function; rat catheter biofilm repressed
RING-type zinc finger protein; upregulated during oral infection; mutants have reduced ability to damage ora
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III and RNA po
Putative TFIIH and nucleotide excision repair factor 3 complex subunit; possibly an essential gene, disrupta
Ortholog(s) have role in meiotic DNA recombinase assembly, reciprocal meiotic recombination and conden
Ortholog of C. dubliniensis CD36 : Cd36_30990, C. parapsilosis CDC317 : CPAR2_204660, C. auris B8441
Protein of unknown function; 2 predicted transmembrane domains; transcript detected on high-resolution til
Ortholog(s) have role in endoplasmic reticulum to Golgi vesicle-mediated transport and COPII-coated ER to
Ortholog of Candida albicans WO-1 : CAWG_01892
Ortholog of S. cerevisiae Mdm36; mitochondrial distribution and morphology protein; Hap43-repressed gen
Predicted glycosyl hydrolase; hypoxia induced; flow model biofilm induced
Protein of unknown function; rat catheter biofilm repressed
Ortholog of C. dubliniensis CD36 : Cd36_31170, C. parapsilosis CDC317 : CPAR2_205340, C. auris B8441
Ortholog of S. cerevisiae : LCL2, C. glabrata CBS138 : CAGL0M11572g, C. dubliniensis CD36 : Cd36_312
Protein of unknown function; rat catheter biofilm repressed
Protein of unknown function; possibly transcriptionally regulated upon hyphal formation

Predicted homeodomain-containing protein; possible transcription factor; possibly transcriptionally regulate
NAP1 family histone chaperone
Ortholog(s) have GTPase activator activity, role in activation of GTPase activity and endosome, trans-Golgi
Ortholog(s) have RNA polymerase II complex binding activity and role in chromatin-mediated maintenance
Ortholog of C. parapsilosis CDC317 : CPAR2_205150, C. auris B8441 : B9J08_000660, Debaryomyces ha
Ortholog(s) have ATPase-coupled transmembrane transporter activity, protein transmembrane transporter
Ortholog(s) have Lys63-specific deubiquitinase activity, thiol-dependent deubiquitinase activity
Ortholog of C. dubliniensis CD36 : Cd36_31420, C. parapsilosis CDC317 : CPAR2_205100, C. auris B8441
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Has domain(s) with predicted carbohydrate binding, catalytic activity and role in carbohydrate metabolic pro
Ortholog of S. cerevisiae Sat4; amphotericin B induced; clade-associated gene expression; Spider biofilm i
Protein of unknown function; rat catheter and Spider biofilm induced
Putative microsomal beta-keto-reductase; transcript upregulated by treatment with ciclopirox olamine; induc
Putative intracellular transport protein; heterozygous null mutant displays sensitivity to rapamycin; expressio
Ortholog of C. dubliniensis CD36 : Cd36_31580, C. parapsilosis CDC317 : CPAR2_205000, Debaryomyce
Protein of unknown function; regulated by Tsa1, Tsa1B in minimal media at 37 degrees C; shows colony m
Protein of unknown function; oral infection induced; mutants have reduced capacity to damage oral epitheli
Predicted cation transmembrane transporter; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_73360 and Candida albicans WO-1 : CAWG_01936
Protein of unknown function; flow model biofilm induced
Predicted protein of unknown funtion; overlaps orf19.3879.1, which is a region annotated as blocked readin
Ortholog of C. dubliniensis CD36 : Cd36_31790, C. parapsilosis CDC317 : CPAR2_204900, C. auris B8441
Has domain(s) with predicted N-acetyltransferase activity; highly induced during chlamydospore formation i
Ortholog of C. dubliniensis CD36 : Cd36_31820, C. parapsilosis CDC317 : CPAR2_205050, Debaryomyce
Ortholog of S. cerevisiae : YML108W, C. glabrata CBS138 : CAGL0J06666g, C. dubliniensis CD36 : Cd36_
Predicted ORF overlapping the Major Repeat Sequence on chromosome R; member of a family encoded b
Ortholog of C. dubliniensis CD36 : Cd36_31880, C. parapsilosis CDC317 : CPAR2_702220, C. auris B8441
Ortholog(s) have polynucleotide 5'-hydroxyl-kinase activity
Ortholog(s) have ubiquitin protein ligase activity, ubiquitin-protein transferase activity
Protein of unknown function; Hap43-induced; regulated by Nrg1, Tup1; repressed by alpha pheromone in S
Protein of unknown function; Hap43-induced; rat catheter and Spider biofilm induced
Ortholog(s) have GTPase activity
Ortholog(s) have role in hydrogen peroxide-mediated programmed cell death
Protein of unknown function; induced by nitric oxide; predicted ORF from Assembly 19; removed from Asse
Putative protein involved in apoptosis; Spider biofilm induced
Protein of unknown function; Spider biofilm induced
Protein of unknown function; Spider biofilm induced; rat catheter biofilm repressed
Ortholog of S. cerevisiae : YSC83, C. glabrata CBS138 : CAGL0A02134g, C. dubliniensis CD36 : Cd36_32
Integral ER membrane protein; predicted role in maintenance of ER zinc homeostasis; Spider biofilm induc
Protein of unknown function; flow model, rat catheter, Spider biofilm induced
Ortholog(s) have DNA helicase activity, role in regulation of translational termination and cytoplasmic stress
Ortholog(s) have 2',3'-cyclic-nucleotide 3'-phosphodiesterase activity and role in cyclic nucleotide metabolic
Ortholog(s) have gamma-tubulin binding activity
Putative L-azetidine-2-carboxylic acid acetyltransferase; mutants are viable
Ortholog(s) have histone deacetylase activity
Predicted membrane transporter, member of the anion:cation symporter (ACS) family, major facilitator supe
Ortholog(s) have mitochondrion localization
Ortholog(s) have U3 snoRNA binding, rRNA binding activity and role in maturation of SSU-rRNA from tricist
Ortholog of S. cerevisiae : KSH1, C. dubliniensis CD36 : Cd36_32390, C. parapsilosis CDC317 : CPAR2_2
Protein similar to ferric reductase Fre10p
Protein of unknown function; Hap43-induced gene
Ortholog of C. dubliniensis CD36 : Cd36_32460, C. parapsilosis CDC317 : CPAR2_205480, C. auris B8441
Ortholog(s) have ATP binding, DNA replication origin binding activity
Predicted component of U5 snRNP; Spider biofilm induced
Putative protein of unknown function; Hap43-induced; repressed by Rim101; Spider biofilm induced
Has domain(s) with predicted DNA binding activity and role in DNA integration
Ortholog(s) have thiosulfate sulfurtransferase activity
Putative 90S preribosome component; Hap43p-induced gene; possibly an essential gene, disruptants not o
Ortholog of S. cerevisae/S. pombe Tif6; constituent of 66S pre-ribosomal particles; Spider biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_32690, C. parapsilosis CDC317 : CPAR2_204290, Candida tenui
Ortholog of C. dubliniensis CD36 : Cd36_32700, C. parapsilosis CDC317 : CPAR2_204280, C. auris B8441
Protein of unknown function; transcript regulated by Mig1 and Tup1; rat catheter biofilm induced
Has domain(s) with predicted role in transmembrane transport and integral component of membrane localiz
Possible dehydrogenase; flow model biofilm induced; rat catheter biofilm induced; Spider biofilm induced

Ortholog(s) have GTPase activator activity and role in establishment or maintenance of actin cytoskeleton p
Ortholog of C. dubliniensis CD36 : Cd36_32830, C. parapsilosis CDC317 : CPAR2_205930, C. auris B8441
Homolog of nuclear distribution factor NudE, NUDEL; regulates dynein targeting to microtubule plus ends; f
Putative histone chaperone; role in chromatin remodeling; rat catheter and Spider biofilm repressed
Predicted long-chain-alcohol oxidase; Spider biofilm induced
Ortholog(s) have double-stranded DNA binding activity, role in reciprocal meiotic recombination and conder
Protein similar to ferric reductase Fre10p; possibly an essential gene, disruptants not obtained by UAU1 me
Has domain(s) with predicted ATP binding, nucleic acid binding activity
Ortholog of S. cerevisiae Mrpl4, a mitochondrial ribosomal protein of the large subunit; repressed by nitric o
Ortholog of C. dubliniensis CD36 : Cd36_32970, C. parapsilosis CDC317 : CPAR2_701710, C. auris B8441
Ortholog(s) have role in ER-dependent peroxisome organization, retrograde vesicle-mediated transport, Go
Ortholog of C. dubliniensis CD36 : Cd36_33000, C. parapsilosis CDC317 : CPAR2_701740, C. auris B8441
Protein of unknown function; Spider biofilm repressed
Putative guanine nucleotide dissociation stimulator; transcription is positively regulated by Tbf1p
S. pombe ortholog SPAC5D6.04 is a predicted auxin family transmembrane transporter; ketoconazole and
Ortholog of C. dubliniensis CD36 : Cd36_33120 and Candida albicans WO-1 : CAWG_02046
Ortholog(s) have U1 snRNP, U2 snRNP, U2-type prespliceosome, U4/U6 x U5 tri-snRNP complex, U5 snR
Protein of unknown function; downregulated by fluphenazine treatment or in an azole-resistant strain that ov
Adaptor protein required for specific mRNA transport; protein similar but not orthologous to S. cerevisiae Sh
Ortholog(s) have ATPase, acting on DNA, DNA binding, chromatin binding activity
Ortholog(s) have ATPase activator activity, role in positive regulation of ATPase activity, vacuolar transport
Ortholog(s) have signal recognition particle binding activity, role in protein targeting to ER and integral comp
Has domain(s) with predicted iron ion binding, iron-sulfur cluster binding activity and role in iron-sulfur cluste
Ortholog of C. dubliniensis CD36 : Cd36_33320, C. parapsilosis CDC317 : CPAR2_701970, C. auris B8441
Ortholog of C. dubliniensis CD36 : Cd36_33330, C. parapsilosis CDC317 : CPAR2_701980, C. auris B8441
Has aminoglycoside phosphotransferase and protein kinase domains; rat catheter and flow model biofilm in
Ortholog of C. dubliniensis CD36 : Cd36_00150, Lodderomyces elongisporus NRLL YB-4239 : LELG_0126
Ortholog(s) have role in maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA,
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Has domain(s) with predicted oxidoreductase activity
Protein with monooxygenase domains; flow model biofilm induced
Protein of unknown function; induced by Mnl1 under weak acid stress; flow model biofilm induced; Spider b
Protein of unknown function; flow model biofilm induced; Spider biofilm induced; induced by Mnl1 under wea
Ortholog of C. dubliniensis CD36 : Cd36_33530, C. parapsilosis CDC317 : CPAR2_201980, C. auris B8441
Ortholog of S. cerevisiae : AIM32, C. glabrata CBS138 : CAGL0L01529g, C. dubliniensis CD36 : Cd36_335
Protein involved in transcription-coupled nucleotide excision repair of UV-induced DNA lesions; Spider biofil
Protein of unknown function; Hap43-induced; Spider biofilm induced
Has domain(s) with predicted FAD binding, oxidoreductase activity and role in metabolic process
Protein with an aspartate aminotransferase domain; Gcn4-regulated
Ortholog of S. cerevisiae YNL092W and S. pombe SPBC1778.07; a putative N2227-like methyltransferase;
Putative thiamine biosynthesis enzyme; decreased expression in an ssr1 null mutant; protein present in exp
Has domain(s) with predicted RNA binding activity
Ortholog of C. dubliniensis CD36 : Cd36_33750, C. parapsilosis CDC317 : CPAR2_205650, C. auris B8441
Ortholog(s) have unfolded protein binding activity, role in mitochondrial proton-transporting ATP synthase co
Ortholog(s) have protein C-terminal leucine carboxyl O-methyltransferase activity and role in C-terminal pro
Ortholog of C. dubliniensis CD36 : Cd36_33820, C. parapsilosis CDC317 : CPAR2_206210, C. auris B8441
Putative MRP/CFTR-subfamily ABC transporter; member of multidrug resistance-associated protein (MRP)
Protein of unknown function; Spider biofilm induced
Protein of unknown function; transcript upregulated in azole-resistant strain overexpressing MDR1; Spider b
Ortholog of C. dubliniensis CD36 : Cd36_33870, C. parapsilosis CDC317 : CPAR2_204450, C. auris B8441
Putative Arf3p GTPase activating protein; Hap43p-repressed gene; possibly an essential gene, disruptants
Putative patatin-like phospholipase; similar to S. cerevisiae Nte1p, which is predicted to be a membrane pro
S. pombe ortholog SPBC460.04c is a predicted sulfonate/alpha-ketoglutare dioxygenase; induced by nitric
Ortholog(s) have role in inositol metabolic process, protein import into nucleus and nuclear envelope localiz
Ortholog(s) have adenyl-nucleotide exchange factor activity and role in SRP-dependent cotranslational prot
Protein of unknown function; decreased transcription is observed in an azole-resistant strain that overexpre
Ortholog(s) have structural constituent of ribosome activity and mitochondrial small ribosomal subunit locali
Ortholog(s) have role in ribosomal large subunit biogenesis
Putative DnaJ-like heat shock/chaperone; Hap43-repressed; Spider and F-12/CO2 biofilm induced
Protein similar to S. cerevisiae Vac14p; a protein involved in regulated synthesis of PtdIns(3,5)P(2); transpo
Protein of unknown function; rat catheter biofilm induced
Ortholog of C. dubliniensis CD36 : Cd36_34040, C. parapsilosis CDC317 : CPAR2_205850, C. auris B8441
Protein involved in N-glycosylation; Spider biofilm induced; rat catheter biofilm repressed
Ortholog(s) have structural constituent of ribosome activity and cytosolic small ribosomal subunit localizatio

Ortholog(s) have unfolded protein binding activity and role in protein import into nucleus, ribosomal large su
Ortholog of C. parapsilosis CDC317 : CPAR2_205710, C. auris B8441 : B9J08_000119, Candida tenuis NF
Ortholog(s) have fructose-2,6-bisphosphate 2-phosphatase activity and role in glucose metabolic process
Ortholog(s) have SUMO conjugating enzyme activity, SUMO transferase activity and role in DNA repair, mit
Protein of unknown function; Spider biofilm induced
Ortholog(s) have ATPase activity, role in response to drug, ribosomal large subunit biogenesis and preribos
Highly conserved subunit of mitochondrial pyruvate carrier; Hap43-repressed; Spider biofilm repressed
Ortholog of C. dubliniensis CD36 : Cd36_34210, C. parapsilosis CDC317 : CPAR2_205590, C. auris B8441
Ortholog(s) have serine C-palmitoyltransferase activity and SPOTS complex, endoplasmic reticulum, serine
Ortholog(s) have ubiquitin-protein transferase activity and role in cellular response to amino acid stimulus, t
Protein with an enoyl-CoA hydratase related domain; Spider biofilm induced
Ortholog(s) have GTPase activator activity
Protein of unknown function; Spider biofilm repressed
Ortholog of C. dubliniensis CD36 : Cd36_34310
Protein of unknown function
Protein of unknown function; Spider biofilm induced
Protein of unknown function; rat catheter and Spider biofilm induced
Ortholog(s) have role in mRNA polyadenylation, pre-mRNA cleavage required for polyadenylation, regulatio
Protein with predicted oxidoreductase and dehydrogenase domains; Hap43-repressed; Spider biofilm induc
Ortholog(s) have RNA cap binding, chromatin binding, mRNA binding activity and role in deadenylation-dep
Ortholog(s) have tRNA (adenine-N1-)-methyltransferase activity, role in tRNA methylation and nucleus, tRN
Ortholog(s) have protein phosphatase 1 binding activity, role in cortical actin cytoskeleton organization, posi
Plasma membrane protein implicated in stress response; similar to stomatin mechanoreception proteins; ov
Putative cystathionine gamma-synthase; decreased levels in stationary phase cultures; Hog1p-induced; Gc
Protein of unknown function; Spider biofilm induced
Has domain(s) with predicted DNA binding, nucleic acid binding activity
Ortholog of C. dubliniensis CD36 : Cd36_34495, Candida tropicalis NEW ASSEMBLY : CTRG1_05947, Ca
Protein of unknown function; Hap43-induced; transcript induced early in infection of reconstituted human ep
Ortholog of C. dubliniensis CD36 : Cd36_34510, Candida tropicalis NEW ASSEMBLY : CTRG1_05938, Ca
Aldo-keto reductase; increased transcript associated with MDR1 overexpression, benomyl or long-term fluc
Putative oxidoreductase; similar to S. cerevisiae Pga3p; possible Kex2p substrate
Protein with a role in directing meiotic recombination events to homologous chromatids; induced by ciclopiro
Protein of unknown function; Spider biofilm induced
Putative phytanoyl-CoA dioxygenase family protein; mutation confers hypersensitivity to 5-fluorocytosine (5-
Ortholog(s) have role in re-entry into mitotic cell cycle after pheromone arrest and endoplasmic reticulum lo
Protein of unknown function; S. cerevisae ortholog Ypl225w interacts with ribosomes; rat catheter biofilm in
Ortholog(s) have protein-lysine N-methyltransferase activity and role in peptidyl-lysine dimethylation, peptidy
Protein with a Staphylococcal nuclease domain; transcript regulated by Mig1 and Tup1; flow model and Spi
Ortholog(s) have ubiquitin conjugating enzyme activity, ubiquitin-protein transferase activity
Protein with a predicted heme oxygenase domain; Spider biofilm induced
Predicted membrane transporter; member of the drug:proton antiporter (14 spanner) (DHA2) family, major f
Protein with a nischarin related domain and leucine rich repeats; Spider biofilm induced
Protein of unknown function; flow model biofilm induced; ketoconazole-repressed
Protein of unknown function; Spider biofilm induced
Ortholog(s) have role in snoRNA splicing, spliceosomal conformational changes to generate catalytic confo
Ortholog(s) have DNA binding, chromatin binding, histone deacetylase activity and role in chromosome seg
Ortholog(s) have ATP binding activity
Putative mitochondrial protein; Hap43p-induced gene
Ortholog(s) have microtubule binding, microtubule plus end polymerase, microtubule plus-end binding activ
Predicted DDE superfamily endonuclease domain; repression correlates with clinical development of flucon
Ortholog of C. parapsilosis CDC317 : CPAR2_201040, C. auris B8441 : B9J08_001657, Candida tenuis NF
Has domain(s) with predicted integral component of membrane localization
Ortholog of S. cerevisiae Pba1 that is involved in 20S proteasome assembly; upregulated in a cyr1 null mut
Ortholog(s) have role in ubiquinone biosynthetic process, ubiquinone-6 biosynthetic process and mitochond
Protein of unknown function; rat catheter and flow model biofilm induced
Ortholog(s) have phosphatidic acid transfer activity and role in cardiolipin metabolic process, phospholipid tr
Ortholog(s) have role in cytoplasmic translation
Ortholog of S. cerevisiae : YLR287C, C. glabrata CBS138 : CAGL0M09757g, C. dubliniensis CD36 : Cd36_
Putative esterase; possibly transcriptionally regulated by Tac1; induced by Mnl1 under weak acid stress; pro
Predicted membrane transporter, member of the aromatic acid:proton symporter (AAHS) family, major facil
Protein involved in rRNA processing; required for maturation of the 35S primary transcript of pre-rRNA and
Ortholog(s) have phosphatidylinositol-3-phosphate binding, ubiquitin protein ligase activity, ubiquitin-protein
Putative U3-containing small subunit processome complex protein; Hap43-induced gene; repressed in core
Protein of unknown function; rat catheter biofilm repressed

Transporter; similar to the Sit1 siderophore transporter; induced by nitric oxide independent of Yhb1; repres
Ortholog of C. dubliniensis CD36 : Cd36_34965, C. parapsilosis CDC317 : CPAR2_200910, C. auris B8441
Predicted amino acid transport domain; transcript upregulated in clinical strains from HIV+ patients with ora
Protein of unknown function; induced by alpha pheromone in SpiderM medium
Ortholog of S. cerevisiae : SPS4, C. glabrata CBS138 : CAGL0I09834g, C. dubliniensis CD36 : Cd36_3503
Ortholog(s) have ubiquitin ligase complex localization
Ortholog of S. pombe atl1 alkyltransferase-like protein; mutants are viable; Spider biofilm induced
Ortholog(s) have oligosaccharide binding activity and role in endoplasmic reticulum unfolded protein respon
Ortholog of C. dubliniensis CD36 : Cd36_35095, C. parapsilosis CDC317 : CPAR2_200710, C. auris B8441
Protein with a predicted role in assembly of U2 snRNP into the spliceosome; Spider biofilm induced
Ortholog of S. cerevisiae : RRG7, C. glabrata CBS138 : CAGL0I09680g, C. dubliniensis CD36 : Cd36_351
Protein of unknown function; Hap43-repressed gene; transcript induced by elevated CO2
Putative NADH-ubiquinone oxidoreductase; identified in detergent-resistant membrane fraction (possible lip
Putative asparaginase; predicted role in asparagine catabolism; Spider biofilm induced
Protein of unknown function; Spider biofilm induced
Has domain(s) with predicted dynactin complex localization
Protein with a phosphoglycerate mutase family domain; Hap43-repressed gene
Ortholog(s) have histone acetyltransferase activity, role in histone acetylation, replication-born double-stran
Putative mitochondrial 2' O-ribose methyltransferase; predicted role in methylation of U(2791) in 21S rRNA;
Protein with a predicted role in cytochrome c oxidase assembly; rat catheter biofilm induced
Ortholog(s) have role in early endosome to Golgi transport, establishment or maintenance of cell polarity, h
Ortholog of C. dubliniensis CD36 : Cd36_35262, Candida tropicalis NEW ASSEMBLY : CTRG1_05848, Ca
Protein of unknown function; fluconazole-repressed; Spider biofilm induced
Protein of unknown function; Hap43-induced gene; mutant is viable
Protein involved in endoplasmic reticulum (ER) to Golgi vesicle-mediated transport; putative subunit of the t
Ortholog(s) have peptide alpha-N-acetyltransferase activity, peptide-glutamate-N-acetyltransferase activity,
Putative nucleolar protein with a predicted role in pre-18S rRNA processing; Plc1p-regulated; Spider biofilm
Protein with a mitochondrial distribution and morphology domain; possibly an essential gene, disruptants no
Ortholog(s) have ATPase activator activity, role in mRNA splicing, via spliceosome, positive regulation of A
Putative subunit of an alternative replication factor C complex; role in DNA replication, genome integrity, ho
Ortholog(s) have role in maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA,
Ortholog of S. cerevisiae : YNL320W, C. glabrata CBS138 : CAGL0M04125g, C. dubliniensis CD36 : Cd36_
Ortholog(s) have role in positive regulation of TORC1 signaling and Seh1-associated complex, extrinsic co
Ortholog of C. dubliniensis CD36 : Cd36_35360, C. parapsilosis CDC317 : CPAR2_200320, C. auris B8441
Ortholog of S. cerevisiae Vps3; CORVET tethering complex component involved in vacuolar protein sorting
Ortholog(s) have 4-hydroxybenzoate octaprenyltransferase activity, role in ubiquinone biosynthetic process
Ortholog(s) have ubiquitin protein ligase activity, role in anaphase-promoting complex-dependent catabolic
Biotin protein ligase; catalyzes covalent attachment of biotin to biotin-dependent enzymes including acetyl C
Ortholog(s) have role in box C/D snoRNP assembly, protein folding, rRNA processing and R2TP complex lo
Has domain(s) with predicted antiporter activity, xenobiotic transmembrane transporter activity, role in drug
Ortholog(s) have RNA polymerase II complex binding activity, role in DNA damage response, detection of D
Putative component of the monopolin complex with role in rDNA silencing, homologous chromosome segre
Ortholog of S. cerevisiae : YCR087C-A, C. glabrata CBS138 : CAGL0E00517g, C. dubliniensis CD36 : Cd3
Ortholog(s) have role in mitochondrial cytochrome c oxidase assembly and mitochondrial inner membrane
Predicted membrane transporter, member of the anion:cation symporter (ACS) family, major facilitator supe
Putative Ca2+/H+ antiporter; oral infection upregulated gene; mutants have reduced capacity to damage ora
Ortholog(s) have protein-containing complex binding activity and role in endoplasmic reticulum unfolded pro
Ortholog(s) have mRNA binding activity, role in mRNA splicing, via spliceosome and U1 snRNP, U2-type pr
Mitochondrial ribosomal protein of the large subunit; Spider biofilm repressed
Mitochondrial carnitine carrier protein
Metallothionein; for adaptation to growth in high copper; basal transcription is cadmium-repressed; Ssn6 reg
Methyltransferase involved in sphingolipid homeostasis, methylates a drug cantharidin; decreased expressi
GPI-anchored cell wall transglycosylase, putative ortholog of S. cerevisiae Crh1p; predicted glycosyl hydrola
CRH family cell wall protein; transcript regulated by Nrg1 and Tup1; alkaline induced by Rim101; repressed
Protein kinase of the Cdc2 subfamily involved in hyphal development, virulence; promotes hyphal developm
Predicted GTPase of RHO family; CAAX motif geranylgeranylated; expression in S. cerevisiae causes dom
Functional homolog of S. cerevisiae Crm1, which acts in protein nuclear export; predicted to be resistant to
Coronin; cortical actin cytoskeletal component; predicted role in regulation of actin patch assembly; rat cath
Copper transporter; CPx P1-type ATPase; mediates Cu resistance; similar to Menkes and Wilson disease
Calcineurin-regulated C2H2 transcription factor; role in maintenance of membrane integrity, azole tolerance
C2H2 transcription factor, involved in regulation of early adaptation to murine GI tract; Rim101-repressed at
Surface antigen on elongating hyphae and buds; strain variation in repeat number; ciclopirox, filament induc
Extracellular heme-binding protein involved in heme-iron acquisition; regulated by Tsa1, Tsa1B in minimal
Guanyl-nucleotide exchange factor; activator of Ras/adenylyl cyclase pathway; functional homolog of S. cer

Centromeric histone H3 variant; role in structural changes of centromeric nucleosomes during cell cycle; 4 r
Aldo-keto reductase; role in fibronectin adhesion, cell surface hydrophobicity; regulated by temperature, gro
Functional homolog of S. cerevisiae Shr3p, which is a chaperone specific for amino acid permeases; localiz
Putative 66S pre-ribosomal particle component; Hap43-induced; essential for growth; transposon mutation
Putative subunit of a replication fork-pausing checkpoint complex
Protein of unknown function; Hap43-repressed gene; protein not conserved in S. cerevisiae
Putative cell wall associated protein; gene only found in C. albicans and C. dubliniensis; highly upregulated
Putative cell wall associated protein; C. albicans and C. dubliniensis specific gene highly induced during chl
Hyphal cell wall protein; role in progression of mouse systemic infection; predicted P-loop, divalent cation bi
Transcription factor; role in zinc homeostasis and regulation of Spider biofilm matrix; mutation affects filame
Protein kinase of Ste20p/p65PAK family, required for wild-type mating efficiency and virulence in a mouse m
Scaffold protein for the mitogen-activated protein (MAP) kinase cascade that regulates mating; required for
Protein similar to S. cerevisiae Mos10p, which affects S. cerevisiae filamentous growth; activates transcripti
Putative transcription factor; Med2 mediator domain; activates transcription in 1-hybrid assay in S. cerevisia
Putative transcription factor; positive regulator of gene expression; Efg1-repressed; member of a family of t
Putative transcription factor/activator; Med2 mediator complex ddomain; transcript is upregulated in an RHE
Protein similar to S. cerevisiae Ede1p, which is involved in endocytosis; activates transcription in 1-hybrid as
Zn(II)2Cys6 transcription factor; regulates formation of mating projections and same-sex mating; induced by
Protein that activates transcription in 1-hybrid assay in S. cerevisiae
Zn(II)2Cys6 transcription factor; activates transcription in 1-hybrid assay in S. cerevisiae; has similarity to S.
Essential transcription factor, mediates heat shock transcriptional induction; in the absence of heat stress, C
Protein required for normal filamentous growth; induced during the mating process; mRNA binds She3; acti
Putative zinc-finger transcription factor, similar to A. nidulans FarA and FarB; activates genes required for fa
Protein with a predicted role in sister chromatid cohesion; cell-cycle regulated periodic mRNA expression
Predicted component of the kinetochore sub-complex COMA; induced during the mating process; represse
Putative kinetochore protein with a predicted role in sister chromatid cohesion; repressed during the mating
Putative cytochrome c lysine methyltransferase; regulated by Gcn2 and Gcn4; transcript induced by Mnl1 u
Carnitine acetyl transferase; required for growth on nonfermentable carbon sources, not for hyphal growth o
Peroxisomal carnitine acetyl transferase; no obvious metabolic, hyphal, virulence defects in Ura+ strain; ind
Putative citrate transport protein; flucytosine induced; amphotericin B repressed, caspofungin repressed; Ha
Copper transporter; transcribed in low copper; induced Mac1, Tye7, macrophage interaction, alkaline pH via
Putative low-affinity copper transporter of the vacuolar membrane; induced by nitric oxide; clade-associated
Predicted ubiquitin-binding protein; rat catheter biofilm repressed
Metallothionein; involved in copper resistance; copper induced; Spider biofilm induced; flow model biofilm re
Putative copper-binding transcription factor; required for normal resistance to copper; activates transcription
Putative proteolipid subunit of the vacuolar H(+)-ATPase V0 sector; required for vacuolar acidification, secre
Transcription factor; represses SOK1 expression in response to farnesol inhibition; yeast-hypha switch repr
Predicted spliceosome-associated protein; role in pre-mRNA splicing; Spider biofilm induced
Processing alpha glucosidase I, involved in N-linked protein glycosylation and assembly of cell wall beta 1,6
Putative sensor/transporter protein with a predicted role in cell wall biogenesis; possibly an essential gene, d
Putative dolichyl pyrophosphate (Dol-P-P) phosphatase; ketoconazole-induced; expression is increased in a
Zn2Cys6 transcription factor involved in negative regulation of nitrosative stress response; regulates format
Putative cytochrome b2 precursor; induced in high iron; alkaline repressed; colony morphology-related gene
Cytochrome b(5); ortholog of S. cerevisiae Cyb5; induced in high iron; fluconazole-induced; shows colony m
Cytochrome c; complements defects of S. cerevisiae cyc1 cyc7 double mutant; induced in high iron; alkalin
Mitochondrial cytochrome c heme lyase; antigenic cell-wall protein; filament induced; induced on polystyren
Essential protein involved in cytokinesis; contains an SH3 domain
Putative metalloprotease of the mitochondrial intermembrane space; rat catheter biofilm induced
Peptidyl-prolyl cis-trans isomerase; cyclosporin A sensitive activity; soluble in hyphae; biofilm induced, macr
Putative peptidyl-prolyl cis-trans isomerase; macrophage-downregulated protein level; protein level decreas
Class III adenylyl cyclase; mutant lacks cAMP; involved in regulation of filamentation, phenotypic switching a
Cystathionine gamma-lyase; induced by alkaline, amphotericin B, cadmium stress, oxidative stress via Cap
Cystathionine beta-synthase; sulfur amino acid biosynthesis; antigenic in mouse; flow model biofilm induced
Cytochrome c1; induced in high iron; alkaline repressed; possibly an essential gene, disruptants not obtaine
Cytochrome c1 heme lyase; transcript regulated by Nrg1; induced in high iron
Transcription factor; regulates white-opaque switch; hyphal growth regulator; expression in S. cerevisiae ca
N-acetylglucosamine-6-phosphate (GlcNAcP) deacetylase; N-acetylglucosamine utilization; required for wild
Subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to
Essential subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetoc
Subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to
Subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to
Secretory protein; a-specific, alpha-factor induced; mutation confers hypersensitivity to toxic ergosterol anal
Putative dihydroxyacetone kinase; repressed by yeast-hypha switch; fluconazole-induced; caspofungin repr
Putative allantoinase; transcript regulated by Nrg1 and Mig1; macrophage/pseudohyphal-repressed

Putative allantoin permease; fungal-specific (no human or murine homolog)
Allantoate permease; nitrogen catabolite repressed, induced in absence of preferred N sources; nitrogen sc
Putative allantoate permease; mutant is viable; similar but not orthologous to S. cerevisiae Dal5
Putative allantoate permease; mutant is viable
Putative allantoate permease; fungal-specific (no human or murine homolog)
Zn(II)2Cys6 transcription factor; ortholog of S. cerevisiae Dal81, involved in the regulation of nitrogen-degra
Putative allantoate permease; fungal-specific (no human or murine homolog)
Essential subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kineto
Putative D-amino acid oxidase; transcription is regulated upon yeast-hyphal switch
Putative D-amino acid oxidase; rat catheter biofilm induced
Similar to mammalian membrane-associated progesterone receptors involved in DNA damage response; i
Putative dipeptidyl aminopeptidase; transcriptionally regulated during macrophage response
Essential serine/threonine protein kinase involved in mitotic spindle formation and cytokinesis; required for
Regulatory subunit of Cdc7p-Dbf4p protein kinase complex that acts as negative regulator of hyphal develo
Putative DEAD-box family ATP-dependent RNA helicase; flucytosine induced; repressed in core stress resp
Putative ATP-dependent DEAD-box RNA helicase; Hap43-induced; repressed by prostaglandins; Spider bi
Ortholog(s) have ATPase, acting on RNA, RNA helicase activity, inositol hexakisphosphate binding activity
Putative ATP-dependent DEAD-box RNA helicase; Hap43-induced; rat catheter biofilm induced
Protein similar to S. cerevisiae Dbp8p, an ATP-dependent helicase involved in rRNA processing; oxidative
Debranchase; homozygous mutant accumulates lariat intermediates of mRNA splicing; rat catheter biofilm
Protein with a predicted role in sister chromatid cohesion and telomere length maintenance; cell-cycle regul
Protein of unknown function; ortholog of S. cerevisiae Dcg1; transcript regulated by Nrg1 and Mig1
Putative guanine nucleotide exchange factor; required for embedded filamentous growth; activates Rac1; h
Protein similar to S. cerevisiae Ylr422wp; transposon mutation affects filamentous growth; induced by Mnl1
Ortholog(s) have chromatin binding, hydrolase activity, m7G(5')pppN diphosphatase activity, mRNA binding
Putative Dicer RNAse involved in RNA interference, similar to S. cerevisiae Rnt1p but orthologous to S. cas
Protein with predicted GPI modification; dfg5 dcw1 double mutant is inviable; not required for wild-type hyp
Putative DNA damage checkpoint protein; transcript induced during filamentous growth; regulated by Nrg1,
Putative DNA damage inducible v-SNARE binding protein; macrophage/pseudohyphal-repressed
Immunogenic stress-associated protein; filamentation regulated; induced by benomyl/caspofungin/ketocona
Predicted ATP-dependent RNA helicase; RNA strand annealing activity; Spider biofilm induced
Putative tRNA-Asn synthetase; genes encoding ribosomal subunits, translation factors, tRNA synthetases a
RNA polymerase II regulator; role in filamentation, epithelial cell escape, dissemination in RHE model; indu
Putative mitochondrial exonuclease; alpha-factor induced
Putative delta-4 sphingolipid desaturase; planktonic growth-induced gene
Ortholog(s) have role in dolichol biosynthetic process, dolichol-linked oligosaccharide biosynthetic process,
Rim101 pathway protein that acts in Rim101 processing; regulates filamentation in response to alkaline pH;
N-linked mannoprotein of cell wall and membrane; possible signal transducer; role in hyphal growth and HW
Cell-surface associated glycoprotein; promotes activation of Cek1 in a matrix-dependent manner; N-glycosy
Trimethoprim resistant dihydrofolate reductase (DHFR), reduces 7,8-dihydrofolate to 5,4,7,8-tetrahydrofolat
Putative RNA helicase
Ortholog(s) have dolichyl pyrophosphate Glc2Man9GlcNAc2 alpha-1,2-glucosyltransferase activity, role in p
Putative 18S rRNA dimethylase; predicted role in rRNA modification and processing; Hap43-induced; likely
Putative small ribonucleoprotein complex; Tn mutation affects filamentous growth; physically interacts with
Dicarboxylic amino acid permease; mutation confers hypersensitivity to toxic ergosterol analog; induced up
Ortholog(s) have catalytic activity and role in ascospore wall assembly
Monooxygenase of the cytochrome P450 family; produces N,N'-bisformyl dityrosine from N-formyltyrosine;
Similar to bacterial DnaJ; reported to have a role in peroxisome biogenesis; induced in low iron and upon a
Putative D-lactate dehydrogenase; white cell-specific trancript; colony morphology-related gene regulation b
Ortholog(s) have D-lactate dehydrogenase (cytochrome) activity, role in lactate catabolic process and mitoc
Functional homolog of S. cerevisiae Dmc1; a meiosis-specific protein required for repair of double-strand b
Protein similar to S. cerevisiae Dna2p, which is a DNA replication factor involved in DNA repair; induced un
Putative dynamin-related GTPase involved in mitochondrial fission; transcript upregulated inbRHE model of
WD repeat protein; required for ubiquitin-mediated protein degradation; role in control of cellular ubiquitin le
Ortholog of S. cerevisiae Doa4;, a ubiquitin hydrolase involved in recycling ubiquitin from proteasome-boun
Putative 2-deoxyglucose-6-phosphatase; haloacid dehalogenase hydrolase/phosphatase superfamily; simil
Protein of unknown function; induced during planktonic growth
Putative modulator of white-opaque switching
Protein similar to ubiquitin C-terminal hydrolase; localizes to cell surface of hyphal cells, but not yeast-form
Putative nuclear thiol peroxidase; alkaline downregulated; sumoylation target; Spider and flow model biofilm
Protein with a predicted role in telomeric gene silencing and filamentation; repressed by high-level peroxide
Probable subunit of DNA polymerase II (DNA polymerase epsilon), similar to S. cerevisiae Dpb2p; essentia
Putative DNA polymerase epsilon subunit D; null mutant is viable but slow-growing and displays abnormal i
Dolichol-phosphate mannose synthase catalytic subunit; filament induced; Tup1-regulated; flow model and

Dolichol-phosphate mannose synthase subunit, not essential for enzyme activity; flow model and Spider bio
Dolichol-phosphate mannose synthase subunit, essential for enzyme activity; flow model biofilm repressed
Putative diacylglycerol pyrophosphate phosphatase of diacylglycerol production for phospholipid biosynthes
Protein similar to S. cerevisiae pyrophosphate phosphatase Lpp1p; possible role in farnesol biosynthesis
Protein similar to S. cerevisiae pyrophosphate phosphatase Dpp1; required for farnesol biosynthesis; repres
Putative tRNA-Asp synthetase; genes encoding ribosomal subunits, translation factors, tRNA synthetases a
Putative 3-dehydroquinate dehydratase; ketoconazole-repressed; protein abundance downregulated by ma
Putative cytosolic Fe-S protein assembly protein; a-specific transcript; regulated by Sef1, Sfu1, and Hap43;
Member of the DRG family of GTP-binding proteins; involved in regulation of invasive filamentous growth
Putative nucleolar DEAD-box protein; Hap43-induced; mutation confers hypersensitivity to 5-fluorouracil (5-
Essential cell wall protein involved in cell wall integrity and rigidity; periodic mRNA expression peaks at M/G
Protein similar to S. cerevisiae Dsl1p, which is a member of the t-SNARE complex of the endoplasmic retic
Ortholog(s) have D-leucyl-tRNA(Leu) deacylase activity, D-tyrosyl-tRNA(Tyr) deacylase activity and role in D
Putative glutamine amidotransferase (GATase II); role in glutathione catabolism;
Protein similar to S. cerevisiae Dun1p, which is a serine-threonine protein kinase involved in DNA damage
Subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to
Urea amidolyase; hydrolyzes urea to CO2; use of urea as N source and for hyphal switch in macrophage; re
High affinity spermidine transporter; expression is induced by urea; fungal-specific (no human or murine ho
Putative urea transporter; possibly an essential gene, disruptants not obtained by UAU1 method
Putative urea transporter
Putative urea permease; fungal-specific (no human or murine homolog); possibly an essential gene, disrupt
Putative urea transporter; fungal-specific (no human or murine homolog)
Ortholog(s) have tRNA dihydrouridine synthase activity and role in tRNA modification
dUTP pyrophosphatase; cell-cycle regulated if expressed in S. cerevisiae; upstream MluI and SCB element
Dynein heavy chain; motor protein that moves to microtubule minus end; required for yeast cell separation,
Subunit of the NuA4 histone acetyltransferase complex; rat catheter and Spider biofilm induced
Subunit of the NuA4 histone acetyltransferase complex; Hap43-repressed; Spider biofilm repressed
Subunit of the NuA4 histone acetyltransferase complex
GPI-anchored cell wall adhesin; Efg1-regulated; mutant suppresses cell adhesion, filamentation, invasive g
NADPH oxidoreductase; interacts with phenolic substrates (17beta-estradiol); possible role in estrogen resp
Putative NADPH oxidoreductase; mutation confers hypersensitivity to toxic ergosterol analog; oxidative stre
Candidalysin, cytolytic peptide toxin essential for mucosal infection; hypha-specific protein; regulated by Rfg
Protein similar to S. cerevisiae Eci1p, which is involved in fatty acid oxidation; transposon mutation affects f
Putative pre-ribosomal factor; decreased mRNA abundance observed in cyr1 homozygous mutant hyphae;
Has domain(s) with predicted metallocarboxypeptidase activity, zinc ion binding activity and role in proteolys
Protein of unknown function; predicted role in cell wall organization; Hap43-repressed; caspofungin repress
Putative sulfite reductase beta subunit; role in cell wall biogenesis; regulated by Tsa1/Tsa1B in H2O2 stress
Ortholog of S. cerevisiae : ECM18, C. glabrata CBS138 : CAGL0B01969g, C. parapsilosis CDC317 : CPAR
Predicted regulator of endcytosis of plasma membrane proteins; fluconazole induced, alkaline induced by R
Zn(II)2Cys6 transcription factor; rat catheter and Spider biofilm induced
Non-essential protein involved in cell morphogenesis
Putative scaffold protein; assists in association of the proteasome core particle with the regulatory particle;
Has domain(s) with predicted role in transmembrane transport and integral component of membrane localiz
GPI-anchored cell wall protein; mutants show cell-wall defects and reduced adhesion, host cell damage, an
GPI-anchored protein; mainly at plasma membrane, also at cell wall; Hap43, caspofungin-induced; Plc1-reg
Putative gamma-glutamyltransferase; alkaline upregulated; Spider biofilm induced; possibly an essential ge
Putative mannosyltransferase similar to S. cerevisiae Ecm39p, which has a role in Calcofluor white resistan
Cytoplasmic glutathione S-transferase; regulated by Nrg1, Tup1; induced in core stress response, in cyr1 o
Ornithine acetyltransferase; Gcn2, Gcn4-regulated; clade-specific gene expression; possibly essential gene
Protein involved in control of calcium homeostasis and oxidative stress response; mutants show defects in
Protein with mRNA binding activity, involved in regulation of activity of putative metacaspase Mca1p
Translation elongation factor EF-1 beta; repressed by human whole blood or PMNs; macrophage/pseudohy
bHLH transcription factor; required for white-phase cell type, RPMI and Spider biofilm formation, hyphal gro
APSES transcription factor; homodimer; minor role in transcriptional regulation vs Efg1; regulates filamento
Elongation Factor 2 (eEF2); GTPase; essential; highly expressed; target of sordarin antifungals; antigenic i
Putative GAL4 DNA-binding enhancer protein; soluble protein in hyphae; biofilm induced; macrophage/pseu
Nascent polypeptide associated complex protein alpha subunit; soluble protein in hyphae; macrophage/pse
Predicted 3-hydroxyisobutyryl-CoA hydrolase; mitochondrially localized; Spider biofilm induced
Putative acyl-coenzymeA:ethanol O-acyltransferase; regulated by Sef1, Sfu1, and Hap43; induced by alpha
Translation initiation factor eIF4E; genes encoding ribosomal subunits, translation factors, tRNA synthetase
Elongin A; F-box protein; ubiquitin-protein ligase; role in protein ubiquitination and ubiquitin-dependent prote
Putative elongin C; transcript regulated by Nrg1 and Mig1; regulated by Gcn2 and Gcn4
Putative mRNA export protein; Walker A and B (ATP/GTP binding) motifs; required for wild-type morpholog
Predicted histone acetyltransferase; role in regulation of transcription, tRNA wobble uridine modification; Sp

Ortholog of S. cerevisiae Nnf2; possible role in chromosome segregation; mutants are viable, induced durin
COPII-coated vesicle component
Protein similar to S. cerevisiae Emp46, an integral membrane component of ER-derived COPII-coated vesi
Protein with a role in endosome-to-vacuole sorting; rat catheter biofilm repressed
Putative sodium transporter; induced by ciclopirox olamine; alkaline induced by Rim101; repressed by high-
Predicted P-type ATPase sodium pump; Gcn4p-regulated; flucytosine, amphotericin B, or ketoconazole-ind
Regulated by Gcn4p; induced in response to amino acid starvation (3-aminotriazole treatment)
Endo-1,3-beta-glucanase; ortholog of S. cerevisiae Dse4 needed for cell separation; caspofungin, fluconazo
Enolase, involved in glycolysis and gluconeogenesis; also has transglutaminase activity involved in assemb
Protein required for pre-rRNA processing and 40S ribosomal subunit synthesis; associated with U3 and U1
Putative nucleolar protein; essential; heterozygous mutation confers resistance to 5-fluorocytosine (5-FC), 5
Putative epsin; induced during the mating process; transcript is upregulated in an RHE model of oral candic
Subunit of the NuA4 histone acetyltransferase complex
Protein with a predicted role in ribosomal large subunit biogenesis; mutation confers hypersensitivity to 5-flu
Putative membrane protein required for the retention of lumenal endoplasmic reticulum proteins; rat cathete
Putative translation release factor 1, which interacts with stop codons and promotes release of nascent pep
Squalene epoxidase, epoxidation of squalene to 2,3(S)-oxidosqualene; ergosterol biosynthesis; allylamine a
Acetyl-CoA acetyltransferase; role in ergosterol biosynthesis; soluble in hyphae; changes in protein abunda
Lanosterol 14-alpha-demethylase; cytochrome P450 family; role in ergosterol biosynthesis; target of azole a
Ortholog(s) have mevalonate kinase activity and role in ergosterol biosynthetic process, farnesyl diphospha
3-hydroxy-3-methylglutaryl coenzyme A synthase; ergosterol biosynthesis; sumoylation target; Tn mutation
C-8 sterol isomerase; enzyme of ergosterol biosynthesis; converts fecosterol to episterol; mutant is hyperse
Putative farnesyl pyrophosphate synthetase involved in isoprenoid and sterol biosynthesis, based on similar
C-14 sterol reductase, has a role in ergosterol biosynthesis; mutation confers increased sensitivity to dyclor
Putative C-4 methyl sterol oxidase; C4-demethylation of ergosterol biosynthesis intermediates, based on sin
C-4 sterol methyl oxidase; role in ergosterol biosynthesis; Hap43-induced; ketoconazole-induced; amphoter
C-3 sterol dehydrogenase, catalyzes the 2nd of 3 steps required to remove 2 C-4 methyl groups from an int
3-Keto sterol reductase of ergosterol biosynthesis; acts in C-4 sterol demethylation with Erg25p and Erg26p
Ortholog(s) have protein-macromolecule adaptor activity, role in demethylation, ergosterol biosynthetic proc
C-5 sterol desaturase; introduces C-5(6) double bond into episterol; some clinical isolates show increased a
Protein similar to sterol C-24 reductase; shows Mob2p-dependent hyphal regulation; fluconazole-induced; c
Putative C-22 sterol desaturase; fungal C-22 sterol desaturases are cytochrome P450 enzymes of ergoster
Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol, ergosterol biosynthesis; mutation c
2,3-epoxysqualene-lanosterol cyclase (lanosterol synthase), conversion of 2,3-oxidosqualene to lanosterol i
Putative phosphomevalonate kinase; enzyme of the mevalonate pathway of isoprenoid biosynthesis; transc
Putative farnesyl-diphosphate farnesyl transferase (squalene synthase); sterol biosynthesis pathway; likely e
Ortholog of S. cerevisiae Ero1; role in formation of disulfide bonds in the endoplasmic reticulum; fluconazol
Protein involved in ER to Golgi transport; rat catheter and Spider biofilm repressed
Predicted component of the mitochondrial intermembrane space (IMS), involved in protein import into mitoc
Component of COPII-coated vesicles; transcript induced upon filamentous growth; rat catheter biofilm repre
Putative SURF4 family member; plasma membrane-localized; flow model biofilm repressed
Putative ER-derived vesicle protein; COPII-coated vesicle complex subunit; transcript induced by filamentou
Subunit of the NuA4 histone acetyltransferase complex; member of MYST family; Spider biofilm induced
Protein similar to S. cerevisiae Esc4; a protein that represses transposition; transposon mutation affects fila
Separase, caspase-like cysteine protease that cleaves cohesins to allow chromatid separation during anap
Prolyl isomerase (parvulin class); essential; involved in yeast-hyphal switching, Cph1p pathway; has inflexib
Telomerase subunit; allosteric activator of catalytic activity, but not required for catalytic activity; has TPR d
Telomerase subunit; required for telomere maintenance in vivo; separable roles in telomerase activity and p
Putative 2-enoyl thioester reductase; protein present in exponential and stationary growth phase yeast cultu
GPI-anchored cell wall protein, similar to S. cerevisiae exo-1,3-beta-glucosidase Exg2p; predicted Kex2p su
Putative U1 snRNP complex compotent; decreased transcription is observed upon fluphenazine treatment
Putative exodeoxyribonuclease; cell-cycle regulated periodic mRNA expression
Predicted subunit of the exocyst complex, involved in exocytosis; localizes to a crescent on the surface of th
Predicted subunit of the exocyst complex, involved in exocytosis; localizes to a crescent on the surface of th
Putative acyl CoA synthetase; expression regulated upon white-opaque switch; rat catheter biofilm induced;
Predicted acyl CoA synthetase; upregulated upon phagocytosis; transcript regulated by Nrg1 and Mig1
Predicted long chain fatty acid CoA ligase; upregulated upon phagocytosis; induced by nitric oxide indepenc
Predicted acyl CoA synthetase
Acyl CoA synthase involved in uptake of long-chain fatty acids and biofilm formation
Phosphatidylinositol 3-phosphate 5-kinase; required for hyphal growth on solid media, and for wild-type vac
Ortholog(s) have FMN adenylyltransferase activity, role in FAD biosynthetic process and cytoplasm localiza
Delta-12 fatty acid desaturase, involved in production of linoleic acid, which is a major component of membr
Omega-3 fatty acid desaturase; production of alpha-linolenic acid, a major component of membranes; casp
eIF4A subfamily of DEAD-box ATP-dependent RNA helicases; predicted nucleolar protein required for matu

Protein involved in regulation of pheromone-mediated mating; repressed by A1p and Alpha2p in white-phas
Beta subunit of fatty-acid synthase; multifunctional enzyme; Hap43, fluconazole-induced; amphotericin B, ca
Alpha subunit of fatty-acid synthase; required for virulence in mouse systemic infection and rat oropharynge
Predicted enzyme of sphingolipid biosynthesis; upregulated in biofilm
Protein with weak similarity to S. cerevisiae Fus2p; induced by alpha pheromone mating factor in MTLa/MT
Adhesin-like protein; induced by mating factor in MTLa/a opaque cells, in cyr1 null, in filaments; regulated b
Putative alpha-1,6-mannanase; induced by mating factor in MTLa/MTLa opaque cells
Fructose-bisphosphate aldolase; glycolytic enzyme; antigenic in murine/human infection; regulated by yeast
Fructose-1,6-bisphosphatase; key gluconeogenesis enzyme; regulated by Efg1, Ssn6; induced by phagocyt
Cytosine deaminase; enzyme of pyrimidine salvage; functional homolog of S. cerevisiae Fcy1p; mutation is
Transcription factor; repressor of fluconazole/ketoconazole/brefeldin A resistance; Tn mutation enhances fil
bZIP transcription factor; ortholog of S. cerevisiae Yap3; partially complements fluconazole sensitivity of S.
Purine-cytosine permease of pyrimidine salvage; mutation associated with resistance to flucytosine in clinic
High affinity, high capacity, hypoxanthine-adenine-guanine-cytosine/H+ symporter; similar to S. cerevisiae F
Putative transporter; Gcn4p-regulated; more similar to S. cerevisiae Tpn1p, which is a vitamin B6 transporte
Putative transporter; more similar to S. cerevisiae Tpn1, which is a vitamin B6 transporter, than to purine-cy
Formate dehydrogenase; oxidizes formate to CO2; Mig1 regulated; induced by macrophages; fluconazole-r
Glutathione-dependent formaldehyde dehydrogenase; glycine catabolism; repressed by Efg1 in yeast, not h
Putative fatty acid elongase; predicted role in sphingolipid biosynthesis; possibly an essential gene, disrupta
Putative protein with a predicted role in the elongation of fatty acids; amphotericin B, caspofungin represse
Putative ubiquinone reductase; transcriptionally induced by interaction with macrophage; alkaline downregu
Multicopper oxidase; required for growth in low iron and prostaglandin E2 synthesis
Putative multicopper oxidase; ketoconazole/caspofungin/amphotericin B repressed; Sef1/Sfu1/Hap43 regul
Putative multicopper ferro-O2-oxidoreductase; repressed in core caspofungin response; fails to complemen
Multicopper ferroxidase; induced by low iron, ciclopirox olamine, ketoconazole, hypoxia; alkaline induced by
Multicopper oxidase family protein; similar to S. cerevisiae Fet3; does not complement S. cerevisiae fet3 mu
Putative asparaginase; lacks ortholog in S. cerevisiae; transposon mutation affects filamentous growth; Spi
Protein encoded in retrotransposon Zorro3 with a potential zinc finger; lacks an ortholog in S. cerevisiae; tra
Protein encoded in retrotransposon Zorro3 with similarity to retroviral endonuclease-reverse transcriptase p
Putative transcription factor with zinc finger DNA-binding motif; lacks an ortholog in S. cerevisiae; transposo
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth; fluconazole-do
Putative DNA-binding transcription factor; has zinc cluster DNA-binding motif; lacks an ortholog in S. cerevi
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
Protein similar to phosphate transporters; transposon mutation affects filamentous growth; expression is re
Putative phosphatidylinositol-specific phospholipase C (PI-PLC); predicted type 2 membrane protein; no S.
Protein of unknown function; repressed by a1/alpha2 in white-phase cells, a-specific, alpha factor-induced;
Protein encoded in retrotransposon Zorro2 with similarity to retroviral endonuclease-reverse transcriptase p
Zn(II)2Cys6 transcription factor; transposon mutation affects filamentous growth; required for yeast cell adh
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth; possibly an es
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth; rat catheter bi
SUMO E3 ligase for Wor1, involved in CO2-mediated white-opaque phenotypic switching; mutations affect
Protein similar to S. cerevisiae Swa2p; induced upon adherence to polystyrene; transposon mutation affects
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
Protein lacking an ortholog in S. cerevisiae; member of a family of related proteins; transposon mutation aff
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
Putative GPI-anchored adhesin-like protein; transposon mutation affects filamentous growth; Spider biofilm
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
Protein lacking an S. cerevisiae ortholog; transposon mutation affects filamentous growth; induced by by M
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth; Spider biofilm
Protein lacking an ortholog in S. cerevisiae; transposon mutation affects filamentous growth; Hap43p-repres
Protein lacking an ortholog in S. cerevisiae; member of a family encoded by FGR6-related genes in the RB
Protein lacking an ortholog in S. cerevisiae; member of a family encoded by FGR6-related genes in the RB
Fork-head transcription factor; forms a heterodimer with Ifh1 that is tethered to promoters by Tbf1; positivel
S. cerevisiae Fig1 ortholog; an integral membrane protein required for mating; role in thigmotropism; transc
Forkhead transcription factor; morphogenesis regulator; required for wild-type hyphal transcription, cell sep
Protein involved in heme uptake; putative FAD transporter, similar to S. cerevisiae Flc1; regulated by iron;
Protein involved in heme uptake; putative FAD transporter, similar to S. cerevisiae Flc2p
Protein involved in heme uptake; putative FAD transporter, similar to S. cerevisiae Flc3p
Transcription factor; required for hyphal formation and CO2 induced white-opaque switching; regulates hyp
Putative adhesin-like cell wall mannoprotein; repressed during the mating process; mutation confers hypers

Multidrug efflux pump of the plasma membrane; MDR family member of the MFS (major facilitator superfa
Putative oxidoreductase; induced by ciclopirox olamine; upregulation correlates with clinical development o
Putative oxidoreductase; mutation confers hypersensitivity to toxic ergosterol analog, and to amphotericin B
Protein with a monooxygenase domain; Spider biofilm induced
Putative mitochondrial protein; mRNA binds She3
Predicted membrane protein induced during mating; mutation confers hypersensitivity to toxic ergosterol an
Putative methionyl-tRNA transformylase; induced upon adherence to polystyrene
Putative dihydroneopterin aldolase (dihydro-6-hydroxymethylpterin pyrophosphokinase); fungal-specific (no
3-hydroxyacyl-CoA epimerase; fatty acid beta-oxidation; induced by phagocytosis; regulated by Mig1, by wh
Putative peroxisomal 3-oxoacyl CoA thiolase; transcript regulated by white-opaque switch; Spider biofilm in
Formamidopyrimidine DNA glycosylase, involved in repair of gamma-irradiated DNA; Hap43p-repressed ge
Major cell-surface ferric reductase under low-iron conditions; 7 transmembrane regions and a secretion sig
Protein with similarity to ferric reductase Fre10p; possibly an essential gene, disruptants not obtained by U
Protein with similarity to ferric reductases; downregulated in response to amphotericin B, estradiol, or ciclop
Copper-regulated cupric reductase; repressed by ciclopirox olamine or 17-beta-estradiol; induced by alkalin
Ferric reductase; alkaline induced; ciclopirox olamine; Hap43-induced
Ferric reductase; alkaline-induced by Rim101; iron-chelation-induced by CCAAT-binding factor; fluconazole
Putative ferric reductase; alkaline induced by Rim101; fluconazole-downregulated; upregulated in the prese
Putative ammonium transporter; upregulated in the presence of human neutrophils; fluconazole-downregul
Protein with a GPR1/FUN34/yaaH family domain; flucytosine repressed
Putative ammonia transport protein; regulated by Nrg1 and Tup1; regulated by Ssn6; induced by human ne
Phenylalanyl-tRNA synthetase; possible role in early cell wall biosynthesis; downregulated by phagocytosis
Putative tRNA-Phe synthetase; downregulated upon phagocytosis by murine macrophage; protein present i
Protein similar to S. cerevisiae Fth1p, a high affinity iron transporter for intravacuolar stores of iron; repress
Putative iron transporter; similar to S. cerevisiae Fth1p
High-affinity iron permease; required for mouse virulence, low-iron growth; iron, amphotericin B, caspofung
High-affinity iron permease; probably interacts with ferrous oxidase; regulated by iron level, ciclopirox olami
Fumarate hydratase; induced in high iron; protein in exponential and stationary-phase yeast cells, but highe
Putative fumarate hydratase; enzyme of citric acid cycle; fluconazole, Efg1 repressed; induced in high iron;
Functional homolog of S. cerevisiae Fun12 translation initiation factor eIF5B; genes encoding ribosomal su
Putative PAS kinase involved in cell wall damage response; similar to S. cerevisiae Psk1p, a putative serin
Uracil phosphoribosyltransferase; predicted tetrameric enzyme of pyrimidine salvage; mutations associated
Putative uracil permease
Membrane protein required for mating; ortholog of S. cerevisiae Fus1; transcript induced by Cph1 in cells h
Protein with a predicted role maturation of 18S rRNA; rat catheter biofilm induced
Mitochondrial biogenesis protein; rat catheter and Spider biofilm induced
Putative regulatory subunit of ser/thr phosphoprotein phosphatase 1; fluconazole-induced; caspofungin rep
Putative glutamate decarboxylase; alkaline, macrophage-downregulated gene; amphotericin B induced; ind
Galactokinase; galactose, Mig1, Tup1, Hap43 regulated; fluconazole, ketoconazole-induced; stationary pha
UDP-glucose 4-epimerase; galactose utilization; mutant has cell wall defects and increased filamentation;
UDP-glucose 4,6-dehydratase; role in mannosylation of cell wall proteins; mutation confers hypersensitivity
Zn(II)2Cys6 transcription factor; involved in control of glycolysis; ortholog of S. cerevisiae Gal4, but not invo
Putative galactose-1-phoshphate uridyl transferase; downregulated by hypoxia, upregulated by ketoconazol
Amino acid permease; antigenic in human/mouse; 10-12 transmembrane regions; regulated by nitrogen so
General broad specificity amino acid permease; ketoconazole, flucytosine repressed; Ssy1-dependent histi
High-affinity S-adenosylmethionine permease; required for SAM-induced morphogenesis; hyphal induced;
General amino acid permease; fungal-specific (no human or murine homolog)
Broad-specificity amino acid permease; Plc1, Gcn4 regulated; rat catheter biofilm induced
Putative H/ACA snoRNP pseudouridylase complex protein; mutation confers hypersensitivity to tubercidin (
GATA-type transcription factor; regulator of nitrogen utilization; required for nitrogen catabolite repression a
Putative single-strand telomeric DNA-binding protein; protein level decreases in stationary phase cultures;
Extracellular/plasma membrane-associated glucoamylase; expressed in rat oral infection; regulated by carb
Predicted extracellular glucoamylase; induced by ketoconazole; possibly essential, disruptants not obtained
Putative translation initiation factor; transcript regulated by Mig1; repressed upon phagocytosis by murine m
Gamma subunit of translation initiation factor eIF2; involved in identification of the start codon; likely essenti
Putative translation initiation factor; genes encoding ribosomal subunits, translation factors, and tRNA synth
Ortholog of S. cerevisiae Gcd6; catalytic epsilon subunit of the translation initiation factor eIF2B; genes enc
Putative translation initiator; downregulated in the presence of human whole blood or polymorphonuclear (
HMG box mitochondrial protein; binds to mt DNA and the HWP1 promoter; mutant phenotype and functiona
Ortholog(s) have protein kinase activator activity, protein kinase regulator activity
Translation initiation factor 2-alpha (eIF2alpha) kinase; has nonessential role in amino acid starvation respo
YEF3-subfamily ABC family protein, predicted not to be a transporter
Putative translation initiator; downregulated in the presence of human whole blood or polymorphonuclear (
bZIP transcription factor; amino acid control response; required for Efg1-dependent pseudohyphal inductio

Histone acetyltransferase; required for hyphen elongation and cell wall organization; mutation confers hyper
Functional homolog of S. cerevisiae Gcr3, which acts in regulation of glycolytic genes; no intron predicted, i
Gamma-glutamylcysteine synthetase; glutathione synthesis, required for virulence;induced in low iron, H2O
Putative T subunit of glycine decarboxylase; transcript negatively regulated by Sfu1; Spider biofilm represse
Glycine decarboxylase P subunit; protein of glycine catabolism; repressed by Efg1; Hog1-induced; induced
Glycine decarboxylase, subunit H; protein level decrease in stationary phase cultures
Aldo/keto reductase; mutation confers hypersensitivity to toxic ergosterol analog; farnesol-repressed; statio
Golgi membrane GDPase, required for wild-type O-mannosylation, not N-glycosylation; required for wild-typ
Putative glycogen debranching enzyme; expression is regulated upon white-opaque switch; regulated by N
Glycerophosphocholine phosphodiesterase; mutation confers hypersensitivity to 5-fluorouracil (5-FU); F-12
Mitochondrial NAD-dependent glutamate dehydrogenase; catalyzes deamination of glutamate to alpha-keto
NADP-glutamate dehydrogenase; Nrg1, Plc1 regulated; hypha, hypoxia, Efg1-repressed; Rim101-induced
Putative Rab GDP-dissociation inhibitor; GlcNAc-induced protein; Spider biofilm repressed
Putative mitochondrial protein; Hap43-repressed gene; Spider biofilm induced
Golgi Ca2+/H+ exchanger, plays a compensatory role for the calcium pump Pmr1p in regulation of calcium
Putative ARF GTP/GDP exchange factor; induced in low iron; flow model biofilm repressed
Member of the voltage chloride channel family; Hap43p-repressed gene
Glucosamine-6-phosphate synthase, homotetrameric enzyme of chitin/hexosamine biosynthesis; inhibited
Protein involved in Golgi trafficking; rat catheter and Spider biofilm repressed
Protein induced by N-acetylglucosamine (GlcNAc); localized in cytoplasm; mutation causes increased resis
Putative heterohexameric cochaperone prefoldin complex subunit; macrophage/pseudohyphal-repressed g
Protein involved in regulation of DNA-damage-induced filamentous growth; putative component of DNA rep
Autophosphorylated kinase; role in pseudohyphal-hyphal switch and cytokinesis; phosphorylates Cdc11p o
Ortholog of S. cerevisiae Gir2; transposon mutation affects filamentous growth
Translational activator for mRNAs with internal ribosome entry sites; induced in high iron; repressed by yea
Glycerophosphoinositol permease; involved in utilization of glycerophosphoinositol as a phosphate source;
Putative glycerophosphoinositol permease; fungal-specific; repressed by alpha pheromone in SpiderM med
Glycerophosphocholine permease; white cell specific transcript; fungal-specific; alkaline repressed; caspofu
Glycerophosphocholine transporter; fungal-specific (no human or murine homolog); possibly an essential g
Putative 1,4-glucan branching enzyme; fluconazole-induced; colony morphology-related gene regulation by
Putative catalytic subunit of type 1 serine/threonine protein phosphatase; regulated by Shp1; induced in hig
Putative nucleoporin; moderately induced at 42 degrees C
Putative nuclear pore complex; possibly an essential gene, disruptants not obtained by UAU1 method; rat c
Putative self-glucosylating initiator of glycogen synthesis; expression regulated upon white-opaque switch;
Putative glucokinase; transcript regulated upon yeast-hyphal switch; Efg1 regulated; fluconazole-induced; i
Putative glucokinase; decreased expression in hyphae compared to yeast-form cells
Putative glutamate synthase; regulated by Tsa1, Tsa1B under H2O2 stress conditions; Spider biofilm induc
GATA transcription factor, involved in regulation of nitrogen starvation-induced filamentous growth; regulate
Putative tRNA-Gln synthetase; genes encoding ribosomal subunits, translation factors, tRNA synthetases a
Putative monomeric glyoxalase I; oxidative stress-induced via Cap1; flow model and rat catheter biofilm rep
Ortholog(s) have hydroxyacylglutathione hydrolase activity, role in methylglyoxal catabolic process to D-lact
Putative ARF GTPase activator; role in COPI coating of Golgi vesicle, ER to Golgi vesicle-mediated transpo
Glutathione reductase; upregulated by human neutrophils; oxidative stress-induced regulation via Cap1p; o
Putative glutamate synthase; regulated by Sef1, Sfu1, and Hap43; rat catheter biofilm repressed
Glutathione-independent glyoxalase; binds human immunoglobulin E; alkaline, fluconazole, Hog1 represse
L-threonine aldolase; complements glycine auxotrophy of S. cerevisiae shm1 shm2 gly1-1 triple mutant; ma
Glucosamine-6-phosphate acetyltransferase; enzyme of UDP-GlcNAc biosynthesis; required for viability in
6-phosphogluconate dehydrogenase; soluble in hyphae; farnesol, macrophage-induced protein; antigenic in
Similar to asparagine and glutamine permease; fluconazole, caspofungin induced; regulated by Nrg1, Mig1
Putative high-affinity glutamine permease; fungal-specific (no human or murine homolog)
Protein required for respiratory growth, resistance to oxidants, chlamydospore formation, hyphal growth und
Ortholog(s) have glyoxylate reductase (NAD+) activity, role in glyoxylate catabolic process and extracellular
G-protein alpha subunit; regulates filamentous growth, copper resistance; involved in cAMP-mediated gluco
Glycerol-3-phosphate dehydrogenase; glycerol biosynthesis; regulated by Efg1; regulated by Tsa1, Tsa1B
Surface protein similar to glycerol 3-P dehydrogenase; binds host Factor H, FHL-1, plasminogen; regulated
Putative glycogen phosphorylase; role in glycogen metabolism; regulated by Ssk1, Mig1, Tup1, Hap43; fluc
Putative protein of GPI synthesis; expression is reduced in a fluconazole-resistant isolate
Major facilitator superfamily protein; has phosphodiesterase/nucleotide pyrophosphatase domain; similar to
Subunit of GPI-GlcNAc transferase; role in synthesis of N-acetylglucosaminyl phosphatidylinositol (GlcNAc-
Subunit of the GPI-N-acetylglucosaminyl transferase (GPI-GnT) that catalyzes the first step in GPI anchor
Protein involved in attachment of GPI-linked proteins to cell wall; member of major facilitator superfamily; p
Metal-dependent endopeptidase, a subunit of the GPI transamidase complex that adds GPI anchors to prot
Phosphoglycerate mutase; surface protein that binds host complement Factor H and FHL-1; antigenic; fluco
Putative phosphoglycerate mutase; repressed in hyphae; macrophage/pseudohyphal-repressed; induced b

Plasma membrane G-protein-coupled receptor of the cAMP-PKA pathway; detects lactate and triggers sign
GABA/polyamine transporter; 9 to 11 membrane spanning segments; complements GABA uptake defect of
Putative thiol peroxidase; rat catheter and Spider biofilm induced
Similar to glutathione peroxidase; induced in high iron; alkaline induced by Rim101; induced by alpha factor
Putative glutathione peroxidase involved in Cap1p-dependent oxidative stress response, required for Cap1
Putative reductase; Nrg1 and Tup1-regulated; benomyl- and hyphal-induced; macrophage/pseudohyphal-re
Putative D-xylose reductase; antigenic in murine systemic infection; soluble protein in hyphae; induced by fa
Putative homeodomain transcription factor, involved in control of filamentous growth; null mutant is an aden
Protein similar to dihydroflavonol-4-reductases
NAD(H)-linked methylglyoxal oxidoreductase involved in regulation of methylglyoxal and pyruvate levels; reg
F-box protein component of the SCF ubiquitin-ligase complex required for cell cycle progression; involved in
Putative tRNA-Gly synthetase; genes encoding ribosomal subunits, translation factors, tRNA synthetases a
Putative glutaredoxin; induced in low iron
Putative glutaredoxin; flucytosine induced; regulated by Gcn4p; repressed in response to amino acid starva
Essential beta-1,3-glucan synthase subunit; gsc1 allele determines resistance/sensitivity to echinocandins;
Putative subunit of the TRAPP complex; involved in targeting of ER-to-Golgi transport vesicles; flow model
Putative glutathione synthase; induced in high iron; heavy metal (cadmium) stress-induced
Beta-1,3-glucan synthase subunit; 10 predicted transmembrane regions; caspofungin induced; repressed b
Protein similar to beta-1,3-glucan synthase; 16 predicted membrane-spanning regions; transcript regulated
Small RAN G-protein; essential; no prenylation predicted; can rescue S. cerevisiae gsp1 viability; macropha
Putative glutathione S-transferase; upregulated in the presence of human neutrophils; expression is regulat
Glutathione S transferase; induced by benomyl and in populations of cells exposed to fluconazole over mult
Glutathione S-transferase; expression regulated upon white-opaque switch; induced by human neutrophils;
Glycogen synthase (UDP glucose/starch glucosyltransferase); transcript repressed by yeast-hyphal switch,
Putative GTP-binding protein; involved in activation of TOR1C during starvation response; transcript is upre
Putative glutathione S-transferase; downregulated upon adherence to polystyrene; regulated upon white-op
Glutathione S-transferase, localized to ER; induced in exponentially growing cells, under oxidative stress; in
Ortholog(s) have glutathione peroxidase activity, glutathione transferase activity, role in glutathione metabol
Putative glutathione S-transferase; opaque-specific transcript; repressed by alpha pheromone in SpiderM m
Putative GMP synthase, involved in the final step of guanine biosynthesis; soluble protein in hyphae; flucyto
Putative guanylate kinase; identified in extracts from biofilm and planktonic cells; protein level decrease in s
Putative O-acyltransferase with a role in glycerol uptake; functionally complements growth of S. cerevisiae g
Putative glutamine-tRNA ligase; stationary phase enriched protein; Spider biofilm repressed
Putative glycerol kinase; downregulated upon adherence to polystyrene; greater mRNA abundance observe
Glycerol-3-phosphate dehydrogenase; Plc1p-regulated; rat catheter biofilm induced; Spider biofilm induced
BAR domain protein; ocalizes to early and late Golgi vesicles; predicted role in adaptation to varying nutrien
Inositol acyltransferase with role in early steps of GPI anchor biosynthetic process; antifungal drug target
Putative Cis-golgi GTPase-activating protein; required for hyphen growth and virulence; transcript regulated
Ortholog(s) have GTPase activator activity, role in activation of GTPase activity and cytoplasm localization
Putative Rab GTPase activator; role in ER to Golgi vesicle-mediated transport; Spider biofilm induced
Protein similar to S. cerevisiae Gyp7p (GTPase-activating protein for Ypt1p); caspofungin-induced
Ortholog(s) have GTPase activator activity, role in vesicle-mediated transport and cytoplasm localization
GATA-type transcription factor; oxidative stress-induced via Cap1; mutant has abnormal colony morphology
bZIP transcription factor; role in unfolded protein response and control of morphology; transcript undergoes
Putative potassium transporter; similar to Schwanniomyces occidentalis Hak1p; amphotericin B induced; in
Putative phosphoadenosine-5'-phosphate or 3'-phosphoadenosine 5'-phosphosulfate phosphatase; possibl
Putative phosphoadenosine-5'-phosphate or 3'-phosphoadenosine 5'-phosphosulfate phosphatase; possibl
Putative Zn(II)2Cys6 transcription factor; gene in zinc cluster region of Chr. 5; induced by Mnl1 in weak acid
Putative deoxyribonucleoside triphosphate pyrophosphohydrolase; caspofungin repressed; regulated by Gc
CCAAT-binding transcription factor; regulates low-iron induction of FRP1; in these conditions CBF comprise
Predicted CCAAT-binding transcription factor that regulates respiration; Cap2-dependent induction in low iro
Putative CCAAT-binding transcription factor; regulates CYC1; required for resistance to rapamycin, copper;
Putative Hap4-like transcription factor; Hap43-repressed; not required for response to low iron; induced by
Predicted transcription factor; possibly an essential gene, disruptants not obtained by UAU1 method
CCAAT-binding factor-dependent transcription factor; repressor; also called CAP2; required for low iron res
Component of CCAAT-binding transcription factor; roles in filamentous growth, low-iron induction of FRP1;
Functional homolog of S. cerevisiae Has1p, which is a nucleolar protein of the DEAD-box ATP-dependent R
Hat1-Hat2 histone acetyltransferase complex subunit; involved in DNA damage repair and morphogenesis;
Putative Hat1-Hat2 histone acetyltransferase complex subunit; role in DNA damage repair and morphogene
Essential protein involved in regulation of MTL gene expression; hemoglobin-regulated inhibitor of white-opa
Essential protein; regulated by hemoglobin; S. cerevisiae ortholog is essential; Hap43p-induced gene
Putative role in regulation of cell wall biogenesis; Hap43p-induced gene; possibly an essential gene, disrupt
Ortholog of S. cerevisiae Hch1, a regulator of heat shock protein Hsp90; regulated by Gcn4; induced in resp
Protein with forkhead domain; similar to S. cerevisiae Hcm1p; Hap43p-induced gene

Putative translation initiation factor; repressed upon phagocytosis by murine macrophage; Spider biofilm rep
Histone deacetylase; inducer of filamentation; conserved deacetylation motif; regulates white-to-opaque sw
Putative 5-aminolevulinate synthase; caspofungin repressed; induced by high iron, nitric oxide; regulated by
Coproporphyrinogen III oxidase; antigenic; on yeast cell surface, not hyphae; iron-regulated expression; Ha
Putative protoporphyrinogen oxidase; involved in heme biosynthesis; predicted Kex2p substrate; iron regula
Putative ferrochelatase involved in heme biosynthesis; transcript not regulated by iron levels and not affecte
Putative porphobilinogen synthase; induced in high iron; protein level decrease in stationary phase cultures;
Hydroxymethylbilane synthase; converts 4-porphobilinogen to hydroxymethylbilane in heme biosynthesis; in
Putative uroporphyrinogen III synthase; induced in high iron or elevated CO2; alkaline, Hap43-repressed
Putative sphingolipid transfer protein; involved in localization of glucosylceramide which is important for viru
Beta-N-acetylhexosaminidase/chitobiase, highly glycosylated enzyme that is secreted to the periplasm and
Protein similar to S. cerevisiae Hex3p, which is involved in DNA damage response; transposon mutation aff
HAP5-like; ortholog of S. cerevisiae Dpb3; third-largest subunit of DNA polymerase II (DNA polymerase eps
HAP5-like; ortholog of S. cerevisiae Bur6, a heterodimeric NC2 transcription regulator complex subunit; fluc
Hypha-specific G1 cyclin-related protein involved in regulation of morphogenesis, biofilm formation; Cdc28-
Putative HMG1/2-related protein; transcript regulated by Mig1
High-affinity MFS glucose transporter; induced by progesterone, chloramphenicol, benomyl; likely essential
Glycerol permease involved in glycerol uptake; member of the major facilitator superfamily; induced by osm
Glucose, fructose, mannose transporter; major facilitator superfamily; role in macrophage-induced hyphal g
Predicted sugar transporter, involved in glycerol utilization; member of the major facilitator superfamily; 12 t
Putative MFS glucose transporter; 20 member C. albicans glucose transporter family; 12 probable membra
Putative glucose transporter of the major facilitator superfamily; the C. albicans glucose transporter family c
Putative MFS family glucose transporter; 20 members in C. albicans; 12 probable membrane-spanning seg
Putative glucose transporter of the major facilitator superfamily; the C. albicans glucose transporter family c
Putative MFS glucose/myo-inositol transporter; 20 member family; 12 transmembrane segments, extended
Putative MFS glucose transporter; 20 member C. albicans glucose transporter family; 12 probable membra
Putative glucose transporter of the major facilitator superfamily; the C. albicans glucose transporter family c
Putative glucose transporter of the major facilitator superfamily; the C. albicans glucose transporter family c
Glucose and galactose sensor; fermentation, filamentation, virulence roles; 20-member glucose transporter
Putative glucose transporter of the major facilitator superfamily; the C. albicans glucose transporter family c
Putative high-affinity MFS glucose transporter; 20 family members; induced in core stress response; flucona
Putative MFS glucose transporter; glucose, fluconazole, Snf3 induced, expressed at high glucose; 20 memb
High-affinity glucose transporter of the major facilitator superfamily; 20 members in the C. albicans glucose
Putative glucose transporter of the major facilitator superfamily; the C. albicans glucose transporter family c
Putative histone H4; repressed in fkh2 mutant; regulated by Efg1; fluconazole induced; amphotericin B repr
Putative histone H4; regulated by Efg1; flucytosine, fluconazole-induced; amphotericin B, caspofungin repre
Putative histone H1; farnesol regulated; Hap43-induced; contains 5' UTR intron; Spider biofilm repressed
Histone H3 variant, specific to CTG-clade species; acts in regulation of planktonic and biofilm growth; reduc
Putative histone H3; farnesol regulated; Hap43-induced; rat catheter and Spider biofilm repressed
Putative histone H3; amphotericin B repressed; regulated by Efg1, farnesol; Hap43-induced; rat catheter an
Amino acid permeases; alkaline, flucytosine induced; regulated by Plc1, Gcn2 and Gcn4; fungal-specific; Sp
Component of the HIR complex, a nucleosome assembly factor involved in chromatin formation; involved in
ATP phosphoribosyl transferase; enzyme of histidine biosynthesis; acid upregulated/alkaline repressed by R
Imidazoleglycerol-phosphate dehydratase, enzyme of histidine biosynthesis; functionally complements S. ce
Multifunctional enzyme that catalyzes three steps of histidine biosynthesis, with phosphoribosyl-AMP cycloh
Putative histidinol-phosphate aminotransferase; Gcn4p-regulated; protein present in exponential and station
Putative imidazole glycerol phosphate synthase; histidine biosynthesis; no human/murine homolog; transcri
Ortholog of S. cerevisiae Hit1; protein of unknown function required for high temperature growth; flow mode
Putative HSP40 co-chaperone; repressed during the mating process
HMG-CoA reductase; enzyme of sterol pathway; inhibited by lovastatin; gene not transcriptionally regulated
ATP-dependent 3' - 5' helicase involved in maintenance of mitochondrial DNA; ortholog of S. cerevisiae Hm
HMG-box transcription factor; binds upstream of hexose and ergosterol metabolism and cell cycle genes; a
hLh domain Myc-type transcript factor; required for morphogenesis induced by elevated temperature or Hsp
Major type I protein arginine methyltransferase (PRMT); involved in asymmetric dimethylation of arginine re
Heme oxygenase; utilization of hemin iron; transcript induced by heat, low iron, or hemin; repressed by Efg1
Putative choline/ethanolamine transporter; mutation confers hypersensitivity to toxic ergosterol analog; colo
Putative transporter; Hap43, flucytosine repressed; possibly essential, disruptants not obtained by UAU1 m
Putative choline permease; fungal-specific (no human or murine homolog)
Histidine triad nucleotide-binding protein; protein level decreases in stationary phase cultures
Putative dinucleoside triphosphate hydrolase; induced upon low-level peroxide stress
Protein with similarity to mannosyltransferases; similar to S. cerevisiae Hoc1p and C. albicans Och1p
Protein involved in cytokinesis and DNA damage response; interacts genetically with Rad53p-dependent ch
MAP kinase of osmotic-, heavy metal-, and core stress response; role in regulation of response to stress; p
Putative MFS transporter; regulated by Nrg1; macrophage/pseudohyphal-repressed; induced by alpha pher

Putative ion transporter; alkaline induced by Rim101; Plc1-regulated; caspofungin repressed; rat catheter a
Aspartate-semialdehyde dehydrogenase; forms a homodimer; conserved in bacteria, archaea, and fungi bu
Putative L-aspartate 4-P-transferase; fungal-specific (no human or murine homolog); regulated by Gcn2 an
Putative homoserine dehydrogenase; Gcn4-regulated; induced by amino acid starvation (3-ATtreatment); m
Histone deacetylase; similar to S. cerevisiae Hos1; has conserved deacetylation motif; slightly greater expre
Putative protein deacetylase, deacetylates tubulin in vitro; genetic evidence suggests that Set3p and Hos2p
Histone deacetylase; similar to S. cerevisiae Hos3p; greater expression and longer mRNA in white cells, co
Ortholog(s) have D-amino-acid N-acetyltransferase activity, N-acetyltransferase activity and role in D-amino
Ortholog(s) have DNA binding, nucleosome binding activity
3-hydroxypropionate dehydrogenase; involved in degradation of toxic propionyl-CoA; rat catheter and Spide
Putative hypoxanthine-guanine phosphoribosyltransferase; protein abundance affected by URA3 expression
Putative serine/threonine kinase; predicted role in cellular ion homeostasis; Spider biofilm repressed
Protein of unknown function; mutants are viable; rat catheter and Spider biofilm induced
Predicted protein serine/threonine kinase; Spider biofilm induced
Ortholog of S. cerevisiae Hrt1; component of a nuclear ubiquitin-protein ligase complex involved in cell cycle
Protein described as having a role in Ty3 transposition; repressed in hyphae; stationary phase enriched pro
ESCRT-0 complex subunit; SH3-domain-containing protein
Subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to
Probable protein kinase involved in determination of morphology during the cell cycle of both yeast-form and
Ortholog(s) have role in mismatch repair, proteasome regulatory particle assembly and cytosol, nucleus loc
Heat-shock protein; roles in biofilm and virulence; complements chaperone, prion activity in S. cerevisiae; g
Heat-shock protein; induced by osmotic/oxidative/cadmium stress, fluphenazine treatment, low iron, CDR1
Small heat shock protein; role in stress response and virulence; fluconazole-downregulated; induced in cyr1
Putative heat shock protein; fluconazole repressed; amphotericin B induced; Spider biofilm induced; rat cath
Putative 30 kda heat shock protein; repressed during the mating process; rat catheter biofilm induced
Heat shock protein; soluble in hyphae; regulated by Nrg1 and by iron; induced in high iron; heavy metal (cad
Putative hsp70 chaperone; role in entry into host cells; heat-shock, amphotericin B, cadmium, ketoconazole
Heat-shock protein; regulated by macrophage response, Nrg1, Mig1, Gcn2, Gcn4, Mnl1p; heavy metal (cad
Essential chaperone, regulates several signal transduction pathways and temperature-induced morphogene
Putative histone deacetylase, involved in regulation of white-opaque switching
Putative histone deacetylase; role in regulation of white-opaque switch; Spider biofilm induced
Histone H3K56 deacetylase; reduced copy number increases opaque cell formation; repressed by MMS, hy
ABC transporter related to mammalian P-glycoproteins; functional homolog of S. cerevisiae Ste6p (a-phero
MAP kinase kinase involved in mating and hyphal growth signal transduction pathways; phosphorylates Cek
UDP-glucose:ceramide glucosyltransferase (glucosylceramide synthase [GCS], EC 2.4.1.80); involved in gl
Histone H2A; repressed in fkh2 mutant; amphotericin B repressed; farnesol regulated; RNA abundance reg
Putative histone H2A; farnesol regulated; rat catheter biofilm repressed; Spider biofilm repressed; Hap43-in
Putative histone H2A; amphotericin B repressed; flucytosine induced; RNA abundance regulated by tyrosol
Histone H2B; induced by adherence to polystyrene; amphotericin B, caspofungin repressed; flucytosine, fluc
Putative tRNA-His synthetase; downregulated upon phagocytosis by murine macrophage; stationary phase
Ortholog(s) have UDP-galactose transmembrane transporter activity and role in UDP-galactose transmemb
Hyphal cell wall protein; host transglutaminase substrate; opaque-, a-specific, alpha-factor induced; at MTL
GPI-anchored, glycosylated cell wall protein; required for biofilm formation, adhesion, filamentous growth or
N-acetylglucosamine (GlcNAc) kinase; involved in GlcNAc utilization; required for wild-type hyphal growth a
Hexokinase II; antigenic in humans; repressed by human neutrophils; Efg1-regulated; fluconazole-induced;
Putative sugar transporter; induced by ciclopirox olamine; Snf3-induced; alkaline repressed; colony morpho
Protein of RAM cell wall integrity signaling network; involved in regulation of Ace2 activity and cellular morph
GPI-anchored hyphal cell wall protein; macrophage-induced; repressed by neutrophils; resistance to killing
Putative GPI-anchored adhesin-like protein; similar to Hyr1p induced in high iron; clade-specific repeat varia
Putative GPI-anchored adhesin-like protein; Rim101-repressed; constitutive expression independent of MTL
Putative DNA polymerase III (delta) subunit with a predicted role in DNA replication and DNA repair; cell-cyc
Putative hydantoin utilization protein A; induced upon adherence to polystyrene; regulated by Gcn2p and Gc
Protein similar to S. cerevisiae Iah1p, which is involved in acetate metabolism; mutation confers hypersensi
Isocitrate lyase; glyoxylate cycle enzyme; required for virulence in mice; induced upon phagocytosis by mac
Putative mitochondrial NAD-isocitrate dehydrogenase subunit 1; soluble protein in hyphae; protein level dec
Putative mitochondrial NAD-isocitrate dehydrogenase subunit; induced by ciclopirox; induced in high iron; p
Ortholog(s) have isopentenyl-diphosphate delta-isomerase activity and role in farnesyl diphosphate biosynth
Putative isocitrate dehydrogenase; transcriptionally induced by interaction with macrophage; alkaline induce
Isocitrate dehydrogenase; white-opaque switch regulated; morphology-regulation by Ssn6; protein in expon
Putative LPF family protein; Plc1-regulated; induced by alpha pheromone in SpiderM medium
IPF family A protein; mutants are viable; Spider biofilm induced
Protein of unknown function; oxidative stress-induced via Cap1
Putative aldo/keto reductase; Mig1-regulated
Aldo-keto reductase; similar to aryl alcohol dehydrogenases; protein increase correlates with MDR1 overexp

Putative medium-chain alcohol dehydrogenase; rat catheter and Spider biofilm repressed
Putative alcohol dehydrogenase; yeast-enriched transcript; Efg1-regulated; induced by prostaglandins, Hog
Secreted protein required for normal cell wall structure and for virulence; member of the IFF family; Hap43p
Putative GPI-anchored protein
Adhesin-like cell surface protein; putative GPI-anchor; null mutant germ tubes show decreased adhesion to
Putative GPI-anchored protein; adhesin-like protein; possibly an essential gene, disruptants not obtained by
Putative GPI-anchored adhesin-like protein; opaque-specific transcript; macrophage-induced gene; Hap43-
Putative GPI-anchored adhesin-like protein; decreased transcription is observed in an azole-resistant strain
Predicted GPI-linked cell-wall protein; similar to Hyr1; induced in low iron; possibly an essential gene, disrup
Putative D-amino acid oxidase; Spider biofilm induced
Transcription factor; forms a heterodimer with Fhl11 that is tethered to promoters by Tbf1; positively regulat
Protein of unknown function; constitutive expression independent of MTL or white-opaque status
Putative thiol-specific monooxygenase; mutant is viable; flow model biofilm induced
Putative mitochondrial translation initiation factor; transcript regulated by Nrg1, Mig1, and Tup1
Protein with a 2-hydroxyacid dehydrogenase catalytic domain; Hap43-repressed; Plc1-regulated; overlaps c
Predicted oxidoreductase/dehydrogenase; induced by nitric oxide; rat catheter and Spider biofilm induced
Zinc-binding dehydrogenase; induced by benomyl, ciclopirox olamine, alpha pheromone, Hap43; regulated
Predicted membrane protein involved in cell wall maintenance; estradiol-induced; upregulation associated w
GPI-anchored protein; alkaline, hypha-induced; regulated by Nrg1, Rfg1, Tup1 and Tsa1, Tsa1B in minimal
Protein of unknown function; induced during hyphae development; induced in low iron; Spider biofilm induce
Putative isoleucyl-tRNA synthetase, the target of drugs including the cyclic beta-amino acid icofungipen/PLD
Putative threonine dehydratase; regulated by Gcn4 and Gcn2; induced by amino acid starvation (3-AT); pro
Putative acetolactate synthase; regulated by Gcn4p; induced by amino acid starvation (3-AT treatment); sta
Dihydroxyacid dehydratase; repressed by nitric oxide; macrophage-induced protein; protein in exponential a
Ketol-acid reductoisomerase; antigenic; regulated by Gcn4; GlcNAc, amino acid starvation (3-AT)-induced;
Putative regulatory subunit of acetolacetate synthase; alkaline induced; regulated by Gcn2 and Gcn4; prote
Putative serine/threonine protein kinase; mutation confers hypersensitivity to amphotericin B
Mitochondrial ribosomal protein of the large subunit; rat catheter biofilm induced
Inosine monophosphate (IMP) dehydrogenase; enzyme of GMP biosynthesis; target of mycophenolic acid a
Putative protein with a role in autophagy; rat catheter biofilm induced
Protein of unknown function; early-stage flow model biofilm induced; Hap43-repressed; Spider biofilm repre
Predicted subunit of the mitochondrial inner membrane peptidase complex involved in protein targeting to m
Predicted subunit of the mitochondrial inner membrane peptidase complex involved in protein targeting to m
Putative SSU processome component; Hap43-induced; repressed by prostaglandins; Spider biofilm induce
Protein with similarity to S. cerevisiae Inn1p, which is an essential protein of the contractile actomyosin ring
Inositol-1-phosphate synthase; antigenic in human; repressed by farnesol in biofilm or by caspofungin; upst
Transcriptional activator that forms a heterodimer with Ino4p; likely regulates genes involved in phosphatidy
Transcription factor; activator that forms a heterodimer with Ino2; likely regulates genes involved in phospha
Putative phosphatidylinositol-4,5-bisphosphate phosphatase; involved in maintenance of phosphoinositide l
Protein structurally similar to alpha-subunit of human leukocyte integrin; role in morphogenesis, adhesion, a
Ortholog of S. cerevisiae/S. pombe Ipk1; an inositol pentakisphosphate 2-kinase, a nuclear protein require
Putative inositol polyphosphate multikinase; involved in regulation of calcium homeostasis, secretion and hy
Putative Aurora kinase; Hap43-induced; induced during planktonic growth; possibly an essential gene, disru
Putative inorganic pyrophosphatase; antigenic; soluble protein in hyphae; macrophage-induced protein; pro
Inositol phosphoryl transferase; catalyzes the synthesis of the most abundant sphingolipid, mannose-(inosit
Actomyosin ring component at bud neck; cell-cycle regulated ser phosphorylation at CDK sites regulate ass
GTPase-activating protein; negatively regulates RAS by converting it from the GTP- to the GDP-bound inac
Protein kinase involved in regulation of unfolded protein response; role in cell wall regulation; mutant is hype
Protein with a role in iron utilization, pathogenesis; both IRO1 and adjacent URA3 are mutated in strain CAI
Putative cohesin complex subunit; cell-cycle regulated periodic mRNA expression
Protein with roles in cell wall integrity, systemic (but not oral) murine infection, adherence, hyphal growth, ar
Putative mitochondrial iron-sulfur protein; alkaline repressed; induced in high iron; regulated by Sef1, Sfu1,
Protein required for maturation of mitochondrial [4Fe-4S] proteins; role in biotin biosynthetic process; rat cat
Mitochondrial membrane localized inositol phosphosphingolipid phospholipase C; hydrolyzes complex sphin
Putative inosine 5'-monophosphate 5'-nucleotidase; fungal-specific (no human or murine homolog)
Protein with a positive role in the multivesicular body sorting pathway; rat catheter biofilm repressed
Ortholog(s) have lipid binding activity and role in endoplasmic reticulum membrane organization, protein loc
Protein with similarity to NifU; possible role in iron-sulfur cluster biogenesis; induced in low iron; rat catheter
Ortholog of S. cerevisiae Isw2; an ATPase involved in chromatin remodeling; required for chlamydospore fo
Putative pre-mRNA-splicing factor; mutation confers resistance to 5-fluorocytosine (5-FC); rat catheter biofi
MFS inositol transporter; uptake of exogenous inositol; 12 transmembrane motifs; expressed in rich mediur
Component of the COP9 signalosome (CSN) complex, provides catalytic activity for deneddylation that clea
Functional homolog of S. cerevisiae Jem1p, which acts with Scj1p and Kar2p (BiP) in protein folding and E
Lactate transporter; induced by lactic acid, activated by Cat8; alkaline repressed by Rim101; localizes to pla

Dicarboxylic acid transporter; regulated by glucose repression; induced by Rgt1; disruptants not obtained b
Ortholog of S. cerevisiae Jip5; predicted role in biogenesis of the large ribosomal subunit; repressed in core
Putative karyopherin; mutation confers hypersensitivity to cytochalasin D
Similar to Hsp70 family chaperones; role in translocation of proteins into the ER; induced in high iron; prote
Kinesin-like microtubule motor protein; required for nuclear fusion during mating; C-terminal motor domain;
Transcription factor; required for gene regulation in response to pheromones; ortholog of S. cerevisiae Kar
Ortholog of S. cerevisiae Kar5; involved in nuclear membrane fusion during karyogamy; induced by alpha f
Ortholog of S. cerevisiae Kar9; role in mitotic spindle positioning; nonessential; localizes to bud tip, bud nec
Ortholog of Kch1 a potassium transporter; mediates K+ influx and activates high-affinity Ca2+ influx system
Predicted inositol polyphosphate kinase; Spider biofilm induced
Kelch repeat domain-containing protein; localizes to sites of polarized growth; mutant colonies exhibit slight
5'->3' exoribonuclease of cytoplasmic stress granules; role in filamentous growth; complements slow growt
Subtilisin-like protease (proprotein convertase); processes aspartyl proteinase Sap2; required for hyphal gr
Putative 2-oxoglutarate dehydrogenase; regulated by Efg1 under yeast but not hyphal growth conditions; tr
Putative dihydrolipoamide S-succinyltransferase; induced in high iron; Hap43-repressed; Spider biofilm rep
Member of the GCK-III subfamily of eukaryotic Ste20p kinases; in RAM cell wall integrity signaling network;
Protein with similarity to S. cerevisiae Kin2p, transcription is positively regulated by Tbf1
Protein similar to S. cerevisiae Kin3p; induced under Cdc5p depletion; shows Mob2p-dependent hyphal reg
Non-essential kinesin from the bipolar (Kinesis-5) family; involved in formation of the mitotic spindle
Putative kinesin-related motor protein involved in mitotic spindle positioning; repressed by alpha pheromon
Putative kinesin, involved in mitotic spindle organization
S. cerevisiae Smy1 ortholog; Tn mutation affects filamentous growth; filament induced; has Mob2-depende
Snf1p complex scaffold protein; similar to S. cerevisiae Gal83p and Sip2p with regions of similarity to Sip1p
Scaffold protein of Snf1p complex; similar to S. cerevisiae Gal83p and Sip2p; interacts with Snf4p; interacti
Protein kinase involved in negative regulation of PolIII transcription; effector kinase of the TOR signaling pa
Putative TORC1 subunit; heterozygous null mutant displays sensitivity to rapamycin; likely to be essential f
Cell wall glycoprotein; beta glucan synthesis; increases glucan content in S. cerevisiae kre1, complements
YEF3-subfamily ABC family protein; predicted not to be a transporter; repressed in core stress response; m
UDP-glucose:glycoprotein glucosyltransferase; 1,6-beta-D-glucan biosynthesis, hyphal growth, virulence in
Essential beta-1,6-glucan synthase subunit; change in mRNA length, not abundance, at yeast-hypha transit
Putative subunit of glucan synthase; macrophage-induced gene; Bcr1-regulated in a/a RPMI biofilms
Protein of beta-1,6-glucan biosynthesis; required for serum-induced hyphal growth; required for efficient util
Putative nucleolar protein; repressed benomyl treatment or in an azole-resistant strain that overexpresses
Putative tRNA-Lys synthetase; repressed upon phagocytosis by murine macrophages; stationary phase enr
Putative serine/threonine protein kinase; mRNA binds She3 and is localized to hyphal tips; mutation confers
3-ketosphinganine reductase, catalyzes the second step in phytosphingosine synthesis
Zn-ribbon protein; required for synthesis of diphthamide on translation factor eEF2; involved in modification
Protein similar to S. cerevisiae Kti12p, which associates with Elongator complex; has a role in resistance to
Mannosyltransferase; transcription elevated in chk1, nik1, and sln1 homozygous null mutants; fungal-specif
Mannosyltransferase; induced during cell wall regeneration; fungal-specific (no human or murine homolog);
Ortholog(s) have role in protein lipoylation
Ceramide synthase; required for biosynthesis of ceramides with C18:0 fatty acids, which serve as precurso
Putative ceramide synthase component; Hap43p-repressed gene; amphotericin B repressed
Putative aminopeptidase; positively regulated by Sfu1; clade-associated gene expression; virulence-group-
Protein similar to aminopeptidase I; mutation confers hypersensitivity to amphotericin B; transcript regulate
Putative aminopeptidase yscI precursor; mutant is viable; protein present in exponential and stationary gro
Putative bud formation and morphogenesis protein; mutation confers hypersensitivity to 5-fluorocytosine (5-
Putative dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex; sumoyla
Putative serine palmitoyltransferase component; mutation confers hypersensitivity to aureobasidin A
Putative sphingosine kinase; Tac1p-regulated expression; rat catheter biofilm induced
Putative LDG family protein; F-12/CO2 early biofilm induced
Predicted component of U2 snRNP; induced by alpha pheromone in SpiderM medium
Putative membrane protein; mutation increases resistance to miltefosine; early-stage flow model biofilm ind
3-isopropylmalate dehydratase; antigenic in humans; repressed in hyphae; alkaline repressed; upregulated
Isopropyl malate dehydrogenase; leucine biosynthesis; induced by human whole blood or PMNs; protein le
Zn(II)2Cys6 transcription factor; predicted regulator branched-c ofhain amino acid biosynthesis genes; alka
Putative 2-isopropylmalate synthase; regulated by Nrg1, Mig1, Tup1, Gcn4; induced by human whole blood
Putative alpha-isopropylmalate synthase; fungal-specific; induced by human blood or polymorphonuclear c
Putative mitochondrial carrier protein; Hap43-repressed; rat catheter biofilm induced
Ortholog(s) have RNA binding, RNA strand annealing activity, tRNA binding activity, role in tRNA 3'-trailer c
Protein similar to S. cerevisiae Hsp70p; predicted Kex2p substrate; possibly essential, disruptants not obta
tRNA ligase; functional homolog of S. cerevisiae Trl1
DNA ligase; mRNA detected in yeast-form and pseudohyphal cells, induced upon hyphal induction; suppre
Secreted lipase, member of a lipase gene family whose members are expressed differentially in response

Secreted lipase, member of a lipase gene family whose members are expressed differentially in response t
Secreted lipase; member of a differentially expressed lipase gene family; expressed in alimentary tract, but
Secreted lipase; gene family member whose members are expressed differentially in response to carbon s
Secreted lipase, member of a differentially expressed lipase gene family with possible roles in nutrition and/
Cold-activated secreted lipase, differentially expressed lipase gene family member with possible roles in nu
Secreted lipase, member of family of lipase genes expressed differentially in response to carbon source an
Probable lipase, part of a gene family whose members are differentially expressed during infection; lacks a
Secreted lipase, member of a differentially expressed lipase gene family with possible roles in nutrition and/
Secreted lipase, member of a lipase gene family whose members are expressed differentially in response t
Putative leukotriene A(4) hydrolase; repressed during the mating process; Hog1p-induced
Protein involved together with Dck1p and Rac1p in invasive filamentous growth and cell wall integrity; acts
Putative dihydrolipoamide dehydrogenase; soluble in hyphae; antigenic in human oral infection and murine
Aldo-keto reductase family protein; similar to aryl alcohol dehydrogenases; osmotic stress-induced, correlat
Protein phosphatase type 1 regulator; role in chromosome segregation, regulation of phosphoprotein phos
Lysophospholipid acyltransferase, involved in phospholipid remodeling; role in glycerophospholipid biosynth
GTPase activator (GAP) that negatively controls small GTPases Cdc42p and Ras1p, involved in signaling
Acyltransferase that catalyzes diacylglycerol esterification of phospholipids; role in lipid storage, triglyceride
Putative succinate-CoA ligase subunit; induced by high iron; fluconazole-induced; protein present in expone
Putative succinate-CoA ligase beta subunit; regulated by Mig1, Tup1; induced in high iron; protein present i
Putative Lsm protein; flucytosine induced
Eisosome component with a predicted role in endocytosis; protein present in exponential and stationary gro
Protein similar to GDP/GTP exchange factors; repressed by alpha pheromone in SpiderM medium; flow m
Putative protein phosphatase of the PTP family (tyrosine-specific), similar to S. cerevisiae Ltp1p
Putative GSE complex component; repressed by prostaglandins
Putative permease; amphotericin B induced; flucytosine repressed; possibly an essential gene, disruptants
Saccharopine dehydrogenase (biosynthetic); enzyme of alpha-aminoadipate lysine biosynthesis pathway; f
Homoisocitrate dehydrogenase; catalyzes 4th step in the alpha-aminoadipate pathway of lysine biosynthesi
Zn(II)2Cys6 transcription factor; has similarity to S. cerevisiae Lys14, which is a transcription factor involve
Zn(II)2Cys6 transcription factor; has similarity to S. cerevisiae Lys14, involved in the regulation of lysine bio
Zn(II)2Cys6 transcription factor; ortholog of S. cerevisiae Lys14 involved in the regulation of lysine biosynthe
Zn(II)2Cys6 transcription factor; has similarity to S. cerevisiae Lys14, involved in the regulation of lysine bio
Heterodimeric alpha-aminoadipate reductase large subunit; lysine biosynthesis; predicted binding sites for
Homocitrate synthase, major isoform; lysine biosynthesis; expression increased in a fluconazole-resistant i
Homocitrate synthase, minor isoform; repressed by nitric oxide and by hypoxia; protein level decreases in s
Homoaconitase; regulated by Gcn4, Gcn2; induced in response to amino acid starvation (3-AT); induced b
Phosphopantetheinyl transferase; enzyme of lysine biosynthesis; modifies, and thereby activates, Lys2p al
Saccharopine dehydrogenase; lysine biosynthesis; soluble protein in hyphae; amphotericin B repressed; G
Copper fist transcription factor; regulator of CTR1 copper transporter; induces CTR1 in low-copper conditio
Protein required for the spindle assembly checkpoint of the cell cycle; necessary for survival in host cell ma
Malic enzyme, mitochondrial; transcription regulated by Mig1, Tup1; colony morphology-related gene regula
Putative negative regulator of RNA polymerase III; decreased expression in hyphae vs yeast cells; caspofu
Putative constituent of 66S pre-ribosomal particles; Hap43-induced; repressed by prostaglandins; Spider bi
Putative 66S pre-ribosomal particle subunit; mutation confers hypersensitivity to tubercidin (7-deazaadenos
Putative protein involved in the structural stability of L-A double-stranded RNA-containing particles; downre
Putative nucleolar DEAD-box RNA helicase; oxidative stress-repressed via Cap1; repressed by prostaglan
Alpha-glucosidase; hydrolyzes sucrose for sucrose utilization; transcript regulated by Suc1, induced by mal
Putative high-affinity maltose transporter; transcript is upregulated in clinical isolates from HIV+ patients wit
Putative mitochondrial acidic matrix protein; regulated by Ssn6p; protein present in exponential and station
Putative mitochondrial processing protease; Hap43-repressed; transcript regulated by Nrg1; oxidative stres
Putative processing peptidase, catalytic (alpha) subunit; protein level decreases in stationary phase culture
Putative transcriptional coactivator; caspofungin repressed; involved in virulence
Putative component of the MBF transcription complex involved in G1/S cell-cycle progression; non-periodic
Putative metacaspase, cysteine protease involved in apoptosis in response to stresses; has similarity to S.
Alpha-kleisin cohesin complex subunit; for sister chromatid cohesion in mitosis and meiosis; repressed by
Mannose-ethanolamine phosphotransferase, essential gene involved in GPI anchor biosynthesis
Putative NADH-ubiquinone dehydrogenase; Hap43p-repressed gene
Transcription factor; regulator of hyphal growth; may act with Wor1p; canonical and non-canonical binding
Phosphorylated protein of unknown function; transcription is periodic with a peak at M/G1 phase of the cell
Putative DNA replication protein; periodic mRNA expression, peak at cell-cycle M/G1 phase; Spider biofilm
Putative MCM DNA replication initiation complex component; mRNA expression peak at cell-cycle M/G1 ph
NADH-cytochrome-b5 reductase; soluble in hyphae; alkaline downregulated; farnesol, ketoconazole or fluc
Putative malonyl-CoA acyl carrier protein acyltransferase
Mitochondrial protein involved in utilization of carbon sources, filamentous growth and virulence
Ortholog(s) have role in pheromone-dependent signal transduction involved in conjugation with cellular fusi

Mitochondrial malate dehydrogenase; regulated by Mig1, Tup1, white-opaque switch, phagocytosis; induced
Predicted malate dehydrogenase precursor; macrophage-induced transcript; protein present in exponential
Predicted malate dehydrogenase; farnesol regulated; protein present in exponential and stationary growth p
Putative member of the HSP40 (DnaJ) family of chaperones; rat catheter and Spider biofilm induced
Predicted component of the mitochondrial import motor; involved in protein import into mitochondrial matrix
Putative mitochondrial, half-size MDR-subfamily ABC transporter
Putative mitochondrial, half-size MDR-subfamily ABC transporter
Predicted component of the mitochondrial sorting and assembly machinery (SAM complex) and ER-mitocho
Putative zinc finger transcription factor; macrophage-downregulated; flow model biofilm induced; flow mode
Putative midasin, a very large dynein-related AAA-type ATPase; induced during the mating process
Plasma membrane MDR/MFS multidrug efflux pump; methotrexate is preferred substrate; overexpression i
TOR signaling pathway component; required for growth and hyphal formation at alkaline pH, for full virulenc
Protein similar to A. nidulans MesA, which is involved in localization of actin cables; Hap43p-induced gene
Cell cycle checkpoint protein with a role in genome integrity; RNA abundance regulated by tyrosol and cell d
Putative DNA damage and meiotic pachytene checkpoint protein; increased transcription is observed upon
RNA polymerase II mediator complex subunit; RNA polymerase II transcription cofactor
RNA polymerase II mediator complex subunit; possibly an essential gene, disruptants not obtained by UAU
Subunit of the RNA polymerase II mediator complex
RNA polymerase II mediator complex subunit
RNA polymerase II mediator complex subunit; possibly an essential gene, disruptants not obtained by UAU
Putative RNA polymerase II mediator complex subunit; induced by nitric oxide
Putative RNA polymerase II mediator complex subunit; possibly an essential gene, disruptants not obtained
RNA polymerase II mediator complex subunit; rat catheter biofilm repressed
RNA polymerase II mediator complex subunit
Subunit of the RNA polymerase II mediator complex; involved in control of filamentous growth and Spider b
Ortholog(s) have transcription coactivator activity, transcription corepressor activity and role in negative regu
RNA polymerase II mediator complex subunit
RNA polymerase II mediator complex subunit
RNA polymerase II core mediator complex subunit
RNA polymerase II mediator complex subunit; transcription positively regulated by Tbf1p
Subunit of the RNA polymerase II mediator complex
Ortholog(s) have RNA polymerase II cis-regulatory region sequence-specific DNA binding, TBP-class prote
RNA polymerase II mediator complex subunit; Hap43p-repressed gene
Putative mitochondrial translation elongation factor; caspofungin induced
Ammonium permease; Mep1 more efficient permease than Mep2, Mep2 has additional regulatory role; 11 p
Ammonium permease and regulator of nitrogen starvation-induced filamentation; 11 predicted transmembra
Cytoplasmic methionyl-tRNA synthetase; zinc-binding motif; ribosomal subunits, translation factors, tRNA sy
Putative uroporphyrin-3 C-methyltransferase, methionine biosynthesis enzyme; upregulated by human whol
Sulfite reductase; role in sulfur amino acid metabolism; induced by human whole blood or PMNs; Hog1-indu
Putative methionine biosynthesis protein; ketoconazole-induced; amphotericin B repressed; Spider biofilm r
Putative adenylylsulfate kinase; predicted role in sulfur metabolism; possibly adherence-induced; protein pre
O-acetylhomoserine O-acetylserine sulfhydrylase; sulfur amino acid synthesis; immunogenic; Hog1, adhere
Putative 3'-phosphoadenylsulfate reductase; sulfur amino acid metabolism; reports differ on regulation durin
Putative protein with a predicted role in nucleotide excision repair (NER) and RNA polymerase II (RNAP II) t
Homoserine acetyltransferase; Hap43p-, Gcn4p-regulated; macrophage/pseudohyphal-repressed; not highl
Predicted bZIP domain-containing transcription factor; protein induced during the mating process; possibly e
ATP sulfurlyase; sulfate assimilation; repressed by Met, Cys, Sfu1, or in fluconazole-resistant isolate; Hog1
Putative transcription coactivator; predicted role in sulfur amino acid metabolism; required for yeast cell adh
Essential 5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase (cobalamin-independent m
Putative bifunctional dehydrogenase and ferrochelatase with a predicted role in siroheme biosynthesis; regu
Putative methylthioadenosine phosphorylase; protein level decreases in stationary phase cultures
Nuclear export protein; has NTF2-like domain; interacts with Mtr2p via the NTF2-like domain
a-factor mating pheromone; produced in opaque MTLa cells; required for mating competence of MTLa cells
Regulator of filamentous growth; required for biofilm formation, virulence; interacts with Flo8 and Mss11
Putative mitochondrial matrix cochaperone; overexpression increases resistance to fluconazole; macrophag
Putative mitochondrial genome maintenance protein; fungal-specific (no human or murine homolog); mutati
Protein similar to S. cerevisiae Mhp1p, which is involved in microtubule stabilization; transposon mutation a
Predicted component of the mitochondrial intermembrane space import machinery; Hap43p-repressed gen
Putative stretch-activated Ca2+ channel of the high affinity calcium uptake system; role in thigmotropism; d
Centromere-associated protein; similar to CENP-C proteins; Cse4p and Mif2p colocalize at C. albicans cen
C2H2 transcription factor; repressor; regulates genes for carbon source utilization; Tup1-dependent and ind
Putative protein phosphatase of the PTP family (tyrosine-specific); ortholog of S. cerevisiae Mih1; mRNA bi
Predicted mitochondrial protein involved in outer membrane protein import; rat catheter biofilm repressed
Putative mitochondrial phosphate transporter; caspofungin repressed; expression is increased in a fluconaz

Predicted mitochondrial C1-tetrahydrofolate synthase precursor; putative protein of glycine catabolism; repr
Mitochondrial C1-tetrahydrofolate synthase precursor
Mannosylinositol phosphorylceramide (MIPC) synthase catalytic subunit; sphingolipid biosynthesis; fluconaz
MAP kinase; role in biofilm formation, contact-induced invasive filamentation, systemic virulence in mouse,
Ortholog of S. cerevisiae Mkk2; MAP kinase kinase involved in signal transduction; macrophage-downregul
Microtubule-dependent localized protein; at Spitzenkorper and cytokinetic ring in hyphae; cell-cycle depend
Putative mismatch repair protein; cell-cycle regulated periodic mRNA expression
Ortholog(s) have role in meiotic mismatch repair, mismatch repair, reciprocal meiotic recombination and Mu
Ortholog(s) have ribonucleoprotein complex binding activity
Malate synthase; glyoxylate cycle enzyme; no mammalian homolog; regulated upon white-opaque switch; p
Vacuolar membrane transporter; MRP subfamily of ABC family; may transport organic anions conjugated to
Mitochondrial protein; possibly required for transamination of isoleucine; macrophage-downregulated protei
Putative SUMO E3 ligase, MMS21-SMC5-SMC6 complex component; involved in regulation of invasive and
Putative adapter subunit of E3 ubiquitin ligase complex, acts with cullin subunit Rtt101p in response to DNA
Transcription factor; induces transcripts of stress response genes via SLE (STRE-like) elements; required f
Putative alpha-1,3-mannosyltransferase; of the mannosyltransferase complex; negatively regulated by Rim1
Alpha-1,6-mannosyltransferase involved in biosynthesis and organization of cell wall polysaccharides
Ortholog(s) have alpha-1,6-mannosyltransferase activity, role in protein N-linked glycosylation, protein glyco
Predicted alpha-1,3-mannosyltransferase activity with a role in protein glycosylation
Predicted alpha-1,3-mannosyltransferase activity with a role in protein glycosylation; regulated by Sef1p-, St
Predicted alpha-1,3-mannosyltransferase activity with a role in protein glycosylation; Hap43-repressed; Spic
Putative alpha-1,3-mannosyltransferase; predicted role in protein O-linked glycosylation; Spider biofilm indu
Alpha-1,2-mannosyltransferase; similar to S. cerevisiae Mnn2; role in cell wall integrity, temperature sensitiv
Ortholog(s) have alpha-1,2-mannosyltransferase activity, role in protein glycosylation and Golgi apparatus lo
Alpha-1,2-mannosyltransferase; required for normal cell wall mannan; regulated by Tsa1, Tsa1B at 37 deg;
Alpha-1,2-mannosyltransferase; mutants hypersensitive to toxic ergosterol analog, amphotericin B, calcoflu
Alpha-1,2-mannosyltransferase; required for normal cell wall mannan content
Putative alpha-1,2-mannosyltransferase; mutant sensitive to calcofluor, SDS and growth at 42 deg; present
Regulator of mannosylphosphorylation of N-linked mannans to cell wall proteins; no role in virulence or norm
Mannosyltransferase; transcript upregulated in Ssk1 response regulator mutant or in nik1 null mutant, but n
Protein of N-linked outer-chain mannan biosynthesis; mutant has defective cell wall; required for wild-type h
Putative ion transporter; fungal-specific (no human or murine homolog)
Alpha-1,2-mannosidase; processes Man9GlcNAc2 to Man8GlcNAc2 isomer B; member of ER localized gly
Alpha-1,2-mannosyl transferase; predicted type II Golgi membrane protein; adds 2nd mannose during cell-w
Alpha-1,2-mannosyl transferase; adds 3rd mannose in cell-wall mannoprotein biosynthesis; partially redund
Mannosyltransferase; transcription elevated in cyr1, chk1, nik1, and sln1 homozygous null mutants; fungal-s
Predicted alpha-1,3-mannosyltransferase with a role in protein glycosylation; induced in low iron
Putative mitotic exit network component; periodic mRNA expression, peak at cell-cycle G2/M phase
Mob1/phocein domain protein of RAM signaling network; cell wall integrity; role in cell separation, cortical ac
Has domain(s) with predicted ATP binding, ATPase, nucleoside-triphosphatase activity
Ortholog of S. cerevisiae Moh1, essential for staionary phase growth; induced by alpha pheromone in Spide
Peripheral membrane protein; role in endocytosis and vacuole integrity; flow model and rat catheter biofilm
Cell surface mannoprotein; cell-wall glucan metabolism, adhesion; adhesin motif; O-glycosylation; induced
Protein similar to S. cerevisiae Mph1p, which is a DNA helicase involved in DNA repair; induced under hydr
Putative SSU processome and 90S preribosome component; repressed in core stress response; repressed
Monopolar spindle protein, putative spindle assembly checkpoint kinase; essential for growth; involved in ox
Putative RNA-binding protein; Hap43p-repressed gene; protein induced during the mating process
Putative DNA double-strand break repair factor; involved in response to oxidative stress and drug resistanc
Putative mitochondrial respiratory protein; induced by farnesol, benomyl, nitric oxide, core stress response;
Predicted mitochondrial ribosomal protein
Protein similar to S. cerevisiae Mrp2p, which is a component of the small subunit of the mitochondrial ribos
Component of mitochondrial ribosome; decreased expression in hyphae compared to yeast-form cells
Mitochondrial ribosomal protein of the large subunit; rat catheter biofilm induced
Mitochondrial ribosomal protein; ortholog of S. cerevisiae Mrp8; transcript induced in hyphal form; mutant is
Putative mitochondrial large subunit ribosomal protein; colony morphology-related gene regulation by Ssn6
Putative ribosomal protein; induced upon adherence to polystyrene; Spider biofilm repressed
Putative 60S ribosomal protein L27, mitochondrial precursor
Ribosomal protein of the large subunit, mitochondrial; repressed in core stress response; protein present in
Putative mitochondrial ribosomal protein of the large subunit; Ssr1-repressed; rat catheter biofilm induced
Mitochondrial ribosomal protein of the large subunit; rat catheter biofilm induced
Putative mitochondrial large subunit ribosomal protein; shows colony morphology-related gene regulation by
Putative mitochondrial ribosomal protein; Spider biofilm repressed
Putative mitochondrial ribosomal protein
Mitochondrial 60S ribosomal protein subunit; Hap43p-repressed gene

Mitochondrial ribosomal protein S9; has N-terminal mitochondrial targeting signal and an S9 consensus mo
Putative Zn(II)2Cys6 transcription factor; regulator of MDR1 transcription; gain-of-function mutations cause
Zn(II)2Cys6 transcription factor involved in regulation of multidrug resistance via control of CDR1 expressio
Putative magnesium ion transporter, mitochondrial; fungal-specific (no human or murine homolog)
Mitochondrial carrier family member, involved in iron homeostasis; putative membrane transporter localizec
Member of the LETM1-like protein family, mitochondrial membrane protein
Putative mRNA turnover protein; Hap43-induced; mutation confers hypersensitivity to tubercidin (7-deazaac
Ortholog of Candida albicans WO-1 : CAWG_03682
Protein of unknown function; repressed by fluphenazine treatment or in an azole-resistant strain that overex
Ortholog of Candida albicans WO-1 : CAWG_04793
Protein of unknown function; Spider biofilm induced
Planktonic growth-induced gene
Ortholog of Candida albicans WO-1 : CAWG_04796
Membrane protein involved in mycelial growth, biofilm formation and epithelial damage; Spider biofilm induc
Putative regulator of transcription; expression in S. cerevisiae flo8 and flo11 mutants suggests a role in regu
Mucin family adhesin-like protein; cell wall damage sensor; required for Cek1 phosphorylation by cell wall st
S. cerevisiae ortholog Mcs7 has a role in reciprocal meiotic recombination; Spider biofilm repressed
Putative phenylalanine-tRNA ligase; protein level decreases in stationary phase cultures; Hap43p-represse
Putative DNA mismatch repair factor; transcript regulated by Nrg1; flucytosine repressed; transcript regulate
Mismatch repair protein; predicted role in repair of insertion or deletion mutations and removal of nonhomol
Protein similar to S. cerevisiae Msh6p, which is involved in mismatch repair; repressed under Cdc5p deplet
Essential HSP70 family protein; required for fluconazole resistance and calcineurin-dependent transcription
Putative mitochondrial lysine-tRNA synthetase; flucytosine repressed
Mitochondrial methionyl-tRNA synthetase (MetRS); functionally complements methionine auxotrophy of an
Zinc finger transcription factor; similar to S. cerevisiae Msn4, but not a significant stress response regulator
Predicted karyopherin involved in nuclear import and export of proteins; flow model biofilm induced; Spider
Putative secretory protein involved in S. cerevisiae sporulation; repressed during pseudohyphal growth in th
Transcription factor; activator that binds to Flo8 via a LisH motif to cooperatively activate transcription of hy
Putative DEAD-box protein; required for efficient splicing of mitochondrial Group I and II introns; Hap43-indu
Phosphatidylinositol-4-phosphate 5-kinase; activity induced by phosphatidic acid (Pld1 product); macrophag
Putative mRNA maturation factor; fungal-specific (no human or murine homolog)
Ortholog(s) have threonine-tRNA ligase activity, role in mitochondrial threonyl-tRNA aminoacylation and mit
NA
NA
NA
NA
Exoribonuclease, along with helicase Suv3p forms a two-component complex (mtEXO) responsible for mito
Protein similar to S. cerevisiae Msw1p, which is mitochondrial tryptophanyl-tRNA synthetase; Hap43p-repre
Putative mitochondrial GTPase; likely essential for respiratory competence and in large ribosomal subunit a
Putative Obg family GTPase member; peripheral protein of the mitochondrial inner membrane; associates v
Homeodomain protein of the MTLa mating type locus; a1 and alpha2 together repress white-opaque switch
Master regulator (activator) of a-type mating; has HMG domain, which is predicted to bind DNA; gene has ir
Ortholog(s) have pyridoxal phosphate binding activity, role in cellular iron ion homeostasis, pyridoxal phospl
Putative mitochondrial protein; rat catheter biofilm induced
Putative importin; member of a family of fungal-specific nuclear importins; Mig1-regulated
Nuclear export protein; member of NTF2 family; monomeric in solution; interacts with Mex67p via the NTF2
Sphingolipid C9-methyltransferase; catalyzes methylation of the 9th carbon in the long chain base compone
Kinetochore component; amount of Nuf2p and Mtw1p protein detected at each centromere is consistent wit
Predicted protein required for ubiquitination; role in meiosis, regulation of cell budding in S. cereviae; Spider
Protein similar to S. cerevisiae Muc1; a cell surface glycoprotein involved in filamentous growth; repressed
Protein similar to S. cerevisiae Mum2, a protein essential for meiotic DNA replication and sporulation; induc
High affinity methionine permease; required for morphogenesis; alkaline upregulated by Rim101; Spider bio
Putative choline phosphate cytidylyltransferase/phosphoethanolamine cytidylyltransferase; repressed in hyp
ESCRT-I complex subunit with a role in multivesicular body (MVB) trafficking; mutant displays growth defec
Mevalonate diphosphate decarboxylase; functional homolog of S. cerevisiae Erg19; possible drug target; re
Putative methionine sulfoxide reductase; Plc1-regulated; induced by human neutrophils, flucytosine; macro
Component of actomyosin ring at neck of newly-emerged bud
Class V myosin; nonessential; sole class V myosin in C. albicans; required for WT actin cytoskeletal polarity
Class I myosin; nonessential; role in cortical actin patch polarity and polar budding; required for hyphal grow
Putative nuclear polyadenylated RNA-binding protein; flucytosine repressed
Glucosamine-6-phosphate deaminase; required for normal hyphal growth and mouse virulence; converts gl
Putative MFS transporter; similar to Nag4; required for wild-type mouse virulence and cycloheximide resista
Putative transporter; fungal-specific; similar to Nag3p and to S. cerevisiae Ypr156Cp and Ygr138Cp; require
Protein required for wild-type mouse virulence and wild-type cycloheximide resistance; putative GTP-bindin

Mitochondrial leucyl-tRNA synthetase					
Putative role in nonsense-mediated mRNA decay; similar to S. cerevisiae Nam7p; gene induced by ciclopir					
Putative U3 snoRNP protein; Hap43p-induced gene; physically interacts with TAP-tagged Nop1p					
Nucleosome assembly protein; mutants show constitutive filamentous growth; present in exponential and s					
Putative cytosolic iron-sulfur (FeS) protein assembly machinery protein; induced by nitric oxide; oxidative st					
Putative N-terminal acetyltransferase; Hap43p-repressed gene; mutation confers hypersensitivity to toxic e					
Putative histone acetyltransferase; involved in regulation of white-opaque switch; early-stage flow model bi					
Subunit of the N-terminal acetyltransferase NatA; Spider biofilm repressed					
Subunit of the NuA4 histone acetyltransferase complex; Plc1p-regulated					
Protein containing an SH3 domain; involved in vacuolar fusion in hyphae; mutants form multiple germ tubes					
Beta subunit of NC2, heterodimeric regulator of transcription; activates CDR1 transcription; possibly an ess					
Non classical protein export protein; localized to plasma membrane; Hap43-induced gene; flow model biofil					
Carbonic anhydrase; converts of CO2 to bicarbonate; essential for virulence in host niches with limited CO					
Putative RecQ-mediated genome instability protein; Hap43-repressed gene; periodic mRNA expression, pe					
NADPH-cytochrome P450 reductase, acts with Erg11p in sterol 14 alpha-demethylation in ergosterol biosy					
Putative vacuolar membrane protein; predicted role in sphingolipid metabolism; transcript regulated by Nrg					
Putative cytosolic thiouridylase subunit; Spider biofilm induced					
Putative NADH dehydrogenase; may act alternatively to complex I in respiration; caspofungin repressed; ra					
Nicotinamide adenine dinucleotide dehydrogenase complex I subunit of the mitochondrial electron transpor					
Ortholog of Ndt80; meiosis-specific transcription factor; activator of CDR1 induction by antifungal drugs; re					
Ortholog(s) have rRNA (pseudouridine) methyltransferase activity					
Ortholog(s) have histone acetyltransferase activity and role in chromatin organization, histone acetylation, r					
N-acetyltransferase related to Gcn5p, acts as N-acetylglucosamine (GlcNAc) sensor required for GlcNAc-i					
N-acetylglucosamine (GlcNAc)-specific transporter; role in GlcNAc (but not serum) induced hyphal growth;					
Putative H/ACA snoRNP protein; macrophage/pseudohyphal-induced					
Putative non-histone chromatin component; RNA abundance regulated by tyrosol,cell density; Hap43-induc					
Protein similar to S. cerevisiae Nhx1p, which is an Na+/H+ exchanger required for intracellular sequestratio					
Protein of unknown function; ortholog of S. cerevisiae Nif3; rat catheter biofilm repressed					
Histidine kinase involved in a two-component signaling pathway that regulates cell wall biosynthesis; requir					
Putative translation initiation factor; mutation confers hypersensitivity to roridin A and verrucarin A; genes e					
p150 subunit of dynactin; required for normal spindle formation and position					
Putative nucleolar protein with role in ribosomal assembly; hyphal-induced; Hap43-induced; Spider biofilm i					
Putative carbon-nitrogen hydrolase; rat catheter biofilm repressed					
Putative nitrilase; regulated by Gcn2p and Gcn4p; protein present in exponential and stationary growth pha					
Putative serine protease and general molecular chaperone; macrophage-induced gene; repressed in core					
Putative nonsense-mediated mRNA decay protein; repressed in core stress response; repressed by prosta					
Karyopherin; carrier protein involved in nuclear import of proteins; repressed in core stress response; Hap4					
Myristoyl-CoA:protein N-myristoyltransferase; attaches the fatty acid myristate to a small number of protein					
Putative nucleolar complex protein; Hap43-induced; transposon mutation affects filamentous growth; mutat					
Putative nucleolar protein; Hap43-induced; mutation confers resistance to 5-fluorocytosine (5-FC), 5-fluoro					
Putative GTPase; mutation confers hypersensitivity to 5-fluorocytosine (5-FC), 5-fluorouracil (5-FU), and tu					
Putative nucleolar GTPase; repressed by prostaglandins; Hap43-induced, rat catheter and Spider biofilm in					
Nucleolar protein; flucytosine induced; Hap43-induced; Spider biofilm repressed					
Small nucleolar ribonucleoprotein; flucytosine induced					
Ortholog of S. cerevisiae Nop13; a nucleolar protein found in preribosomal complexes; Hap43-induced gen					
Putative nucleolar protein; Hap43-induced; mutation confers resistance to 5-fluorocytosine (5-FC), 5-fluoro					
Nucleolar ribosome biogenesis factor; hyphal-induced expression; Hap43-induced; rat catheter biofilm indu					
Putative nucleolar protein; Hap43-induced; mutation confers hypersensitivity to 5-fluorocytosine (5-FC), 5-fl					
Ortholog of S. cerevisiae Nop58; involved in pre-rRNA process; Tn mutation affects filamentous growth; ma					
Putative ortholog of S. cerevisiae Nop6; role in ribosomal small subunit biogenesis; Spider biofilm induced					
Ortholog of S. cereviiae Nop8; has a role in ribosomal large subunit biogenesis; rat catheter and Spider bio					
Transcriptional regulator; not required for buccal epithelial cell adherence or virulence in mouse systemic in					
Putative E3 ubiquitin-protein ligase; required for maintenance, but not induction, of hyphal development; ho					
Protein with similarity to S. cerevisiae Not5p, a member of the transcription regulatory CCR4-NOT complex					
Putative RNA-binding protein; required for normal flow model biofilm growth; nuclear export is facilitated by					
Putative ubiquitin-binding protein; regulated by Gcn2p and Gcn4p					
Component of the RSC chromatin remodeling complex; Hap43-induced; Spider biofilm repressed					
Predicted serine/threonine protein kinase, involved in regulation of ammonium transport; induced in core st					
Putative urea transporter; induced during infection of murine kidney, compared to growth in vitro; has murin					
Putative nicotinate phosphoribosyltransferase, involved in NAD salvage pathway; fungal-specific (no huma					
Transcription factor/repressor; regulates chlamydospore formation/hyphal gene induction/virulence and res					
Transcription factor; transposon mutation affects filamentous growth					
Transcriptional regulator of cell cycle gene expression; regulates expression of genes involved in DNA repli					
Ortholog(s) have cytoplasmic stress granule localization					

Putative 66S pre-ribosomal particles conmponent; Hap43-induced; repressed by prostaglandins
Putative protein constituent of 66S pre-ribosomal particles; Hap43-induced; repressed by prostaglandins
Essential component of the nuclear pore complex; sumoylation target; stationary phase enriched protein; ra
Putative nuclear envelope protein; regulated by Ssn6; rat catheter biofilm repressed
Protein with strong similarity to both S. cerevisiae Ntg1 and Ntg2 DNA repair glycosylases; transcript induce
Neutral trehalase; hyphal induction in mutant delayed but not reduced overall; not required for virulence in m
Putative NADH-ubiquinone oxidoreductase; identified in detergent-resistant membrane fraction (possible lip
Kinetochore component; amount of Nuf2p and Mtw1p protein detected at each centromere is consistent wit
NADH-ubiquinone oxidoreductase subunit with roles in mitochondrial respiratory chain complex I assembly
NADH-ubiquinone oxidoreductase subunit; Hap43p-repressed gene; repressed by nitric oxide; identified in
Nucleoside permease; adenosine and guanosine are substrates, whereas cytidine, adenine, guanine, uridir
FG-nucleoporin component of central core of the nuclear pore complex (NPC); contributes to nucleocytopla
Putative nuclear pore complex subunit; transcript regulated by Nrg1 and Mig1
Nuclear pore protein
Ortholog of S. cerevisiae Nup60p; a subunit of the nuclear pore complex; mutants are viable
Linker nucleoporin of the nuclear pore complex; role in mRNA andexport from nucleus, protein import into n
Ortholog(s) have structural constituent of nuclear pore activity
Ortholog of S. cerevisiae Nup85; a structural constituent of the nuclear pore; required for alkaline-induced h
Putative mitochondrial inner membrane transporter; rat catheter biofilm induced
Similar to oxysterol binding protein; non-sex gene located within the MTLa mating-type-like locus; Plc1p-reg
Putative protein phosphatase of the PTP family (tyrosine-specific); ortholog of S. cerevisiae Oca1; mutant is
Putative protein phosphatase of the PTP family (tyrosine-specific), similar to S. cerevisiae Oca6p; mutant sl
Alpha-1,6-mannosyltransferase; initiates N-glycan outer chain branch addition; similar to S. cerevisiae Och1
Putative prolyl hydroxylase family member; regulates Ume6p stability in response to oxygen; inhibited by hy
Putative transcription factor with zinc finger DNA-binding motif, involved in regulation of white-opaque switcl
Protein involved in regulation of white-opaque switching; Hap43-repressed gene; rat catheter biofilm repres
Mitochondrial glycosylase/lyase; repairs oxidative damage to mitochondrial DNA, contributes to UVA resista
Fatty acid desaturase, essential protein involved in oleic acid synthesis; required for aerobic hyphal growth a
Protein with similarity to fatty acid desaturase (stearoyl-CoA desaturase); homozygous null mutant shows de
Ala- Leu- and Ser-rich protein; secreted; N-terminal hydrophobic region; possible glycosylation; opaque-spe
Leucine zipper transcription factor; involved in regulation of filamentous growth; has putative Opi1-Sin3 inte
Phosphatidylethanolamine N-methyltransferase; acts in phosphatidylcholine biosynthesis; downregulation c
Oligopeptide transporter; transports 3-to-5-residue peptides; alleles are distinct, one has intron; suppresses
Oligopeptide transporter; induced upon phagocytosis by macrophage; macrophage/pseudohyphal-represse
Oligopeptide transporter; transcript induced by macrophage phagocytosis, BSA or peptides; fluconazole-inc
Oligopeptide transporter; detected at germ tube plasma membrane; transcript inducede during phagocytosi
Oligopeptide transporter; fungal-specific (no human or murine homolog); induced by BSA, but not by tetrape
Putative oligopeptide transporter; fungal-specific (no human or murine homolog); expression of OPT6, OPT
Putative oligopeptide transporter; possibly transports GSH or related compounds; Hog1-induced; expressio
Oligopeptide transporter; similar to Opt1 and to S. cerevisiae Ygl114wp, but not other OPTs; induced by nitr
Predicted transmembrane protein; role in cell wall biogenesis; required for Cek1 phosphorylation; Spider bio
Putative origin recognition complex large subunit; essential for viability; similar to S. cerevisiae Orc1p origin
Protein similar to S. cerevisiae Orc3p, which is a component of the origin recognition complex involved in D
Phosphorylated protein similar to S. cerevisiae Orc4, subunit of the origin recognition complex (ORC); induc
Putative endoplasmic reticulum membrane protein; Hap43p-repressed gene; mutation confers hypersensitiv
Protein required for wild-type filamentation; has oxysterol binding protein domain and pleckstrin homology n
Putative flavoprotein subunit of fumarate reductase; soluble protein in hyphae; caspofungin repressed; stati
Putative mitochondrial fumarate reductase; regulated by Ssn6p, Gcn2p, and Gcn4p; Hog1p-downregulated
Alpha subunit of the oligosaccharyltransferase complex of the ER lumen; catalyzes asparagine-linked glyco
Ortholog(s) have role in cellular response to oxidative stress and mitochondrion localization
Putative NAPDH dehydrogenase; induced by nitric oxide; Spider biofilm induced
Putative NADPH dehydrogenase; rat catheter biofilm induced
Putative NAPDH dehydrogenase; induced by nitric oxide, benomyl; oxidative stress-induced via Cap1; Hap4
NAD(P)H oxidoreductase family protein; induced by nitric oxide, amphotericin B, oxidative stress via Cap1;
Putative phenylacrylic acid decarboxylase; repressed by Rgt1p
Putative maltase; regulated by Gcn4; repressed by amino acid starvation (3-AT); rat catheter biofilm induce
Predicted component of the presequence translocase-associated import motor (PAM complex) involved in p
Predicted component of the presequence translocase-associated import motor (PAM complex) involved in p
Essential protein involved in endocytosis and polarized growth; ortholog of S. cerevisiae Pan1, which is a pa
Ortholog(s) have RNA binding, poly(A) binding, poly(A)-specific ribonuclease activity, role in DNA repair, nu
Ortholog(s) have pantoate-beta-alanine ligase activity and role in pantothenate biosynthetic process
Poly(A) polymerase, likely involved in mRNA polyadenylation; PAP is inhibited by parnafungin antifungals; n
Putative RNA binding protein; transcript regulated by Nrg1, Mig1, and Tup1
Protein of unknown function; required for cohesion, adhesion, and RPMI biofilm formation; induced by alpha

MAPK kinase (MAPKK); role in osmotic and oxidative stress responses, oxidative stress adaptation; require
Ortholog(s) have 8-oxo-7,8-dihydroguanosine triphosphate pyrophosphatase activity, pyrophosphatase acti
Phosphoenolpyruvate carboxykinase; glucose, C-source, yeast-hypha, Hap43 regulated; fluconazole, phag
Cyclin homolog; transcript induced by filamentous growth; induced by alpha pheromone in SpiderM medium
Cyclin homolog; reduced expression observed upon depletion of Cln3; farnesol regulated; periodic mRNA e
Putative cyclin for Pho85 kinase; Gcn4-induced; suppresses toxicity of C. albicans Gcn4 overproduction in
Putative cyclin-like protein; possible Pho85 cyclin; hyphal repressed; induced by Mnl1 under weak acid stre
Putative choline-phosphate cytidylyl transferase, antigenic during human oral infection
Putative pyruvate dehydrogenase alpha chain; fluconazole-induced; protein present in exponential and stati
Putative pyruvate dehydrogenase; fluconazole-induced; protein level decreases in stationary phase cultures
Pyruvate decarboxylase; antigenic; on hyphal not yeast cell surface; Hap43, Gcn4, Efg1, Efh1, Hsf1 regulat
Putative pyruvate decarboxylase; fungal-specific (no human or murine homolog)
Homeodomain-like transcription factor; regulator of pyruvate decarboxylase; contains a putative C-terminal
Low affinity cyclic nucleotide phosphodiesterase; mediates cAMP signaling in response to glucose or intrac
High affinity cyclic nucleotide phosphodiesterase; moderates signaling by cAMP; required for virulence, swi
Putative protein disulfide-isomerase; antigenic in human infection; soluble protein in hyphae; induced by fila
Putative pyruvate dehydrogenase kinase; mutation confers hypersensitivity to amphotericin B
Phosphatidylinositol transfer protein; induction correlates with CDR1, CDR2 overexpression/azole resistanc
Fungal-specific protein (no human or murine homolog); role in sensitivity to fluconazole, specifically
Putative pleiotropic drug resistance regulatory protein 6; transcript regulated by Nrg1; induced by alpha phe
Putative protein with a predicted role in establishment and maintenance of sister chromatid condensation a
Pyruvate dehydrogenase complex protein X; essential component of the mitochondrial pyruvate dehydroge
Pyridoxamine-phosphate oxidase; transcript regulated by yeast-hypha switch and by Nrg1, Mig1, Tup1; Ha
Putative coiled-coil polarisome; predicted role in polarized morphogenesis, cell fusion, and low affinity Ca2+
Predicted enzyme of mitochondrial phospholipid biosynthesis; rat catheter and flow model biofilm induced
Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles between late-Golgi and pre
Predicted target membrane receptor (t-SNARE) involved in vacuolar transport, endocytosis, and secretion;
Peptidase; activity useful for strain identification by multilocus enzyme electrophoresis (MLEE); clade-asso
Vesicle transport protein; acts in endosomal transport; roles in metal ion resistance, virulence, adhesion, hy
Protein similar to S. cerevisiae Pep8p, which is involved in retrograde transport; transposon mutation affect
Pescadillo homolog required for dispersal of biofilm cells into planktonic yeast cells; essential in yeast cells,
Chaperone that facilitates the assembly of cytochrome c oxidase; plasma membrane protein
Protein with a predicted role in 5'-end processing of mitochondrial RNAs; ortholog of S. cerevisiae Pet127;
Mitochondrial ADP/ATP carrier protein involved in ATP biosynthesis; possible lipid raft component; 3 predic
Peroxisomal ATPase involved in import of peroxisomal matrix proteins; involved in oxidative stress toleranc
Putative peroxisomal membrane protein; role in fatty acid oxidation; expression is Tac1-regulated; Hms1p-
Ortholog(s) have ubiquitin protein ligase activity, role in protein import into peroxisome matrix, protein mono
Protein required for peroxisomal protein import mediated by PTS1 and PTS2 targeting sequences; transcri
Ortholog(s) have protein-macromolecule adaptor activity, role in protein import into peroxisome matrix, doc
Putative peroxin
Ortholog(s) have peroxisome membrane targeting sequence binding activity
Ortholog(s) have ubiquitin protein ligase activity, role in fatty acid metabolic process, protein import into per
Putative peroxin
Putative peroxisomal protein involved in targeting proteins into peroxisomes; possibly an essential gene, dis
Putative peroxisomal ubiquitin conjugating enzyme; regulated by Sef1, Sfu1, and Hap43; rat catheter biofil
Pex5p family protein; required for PTS1-mediated peroxisomal protein import, fatty acid beta-oxidation; sim
Ortholog(s) have ATPase activity, role in fatty acid metabolic process, protein import into peroxisome matri
Ortholog(s) have peroxisome matrix targeting signal-2 binding activity, role in fatty acid metabolic process,
Putative peroxisomal biogenesis factor; expression regulated during planktonic growth
Phosphofructokinase alpha subinit; activated by fructose 2,6-bisphosphate, AMP, ATP inhibited; activity red
Phosphofructokinase beta subunit; fructose 2,6-bisphosphate, AMP activated; ATP inhibited; phagocytosis,
Putative 6-phosphofructo-2-kinase; protein repressed during the mating process
Profilin; functional homolog of S. cerevisiae Pfy1; hyphae, macrophage/pseudohyphal-induced; regulated b
Putative GPI-anchored protein; induced during cell wall regeneration; required for normal adhesion to host
GPI anchored membrane protein; utilization of hemin and hemoglobin for Fe in host; Rim101 at ph8/hypoxi
Putative GPI-anchored protein
Putative GPI-anchored protein
GPI-anchored cell wall protein involved in cell wall synthesis; required for normal cell surface properties; inc
Putative GPI-anchored protein; induced during cell wall regeneration; regulated by Ssn6p
Putative GPI-anchored protein
Putative GPI-anchored protein
Putative GPI-anchored protein; exogenously expressed protein substrate for Kex2 processing in vitro; repre
Putative GPI-anchored protein; regulated by Nrg1, Tup1; rat catheter biofilm repressed
Putative GPI-anchored protein; macrophage-induced gene; mutants are viable

Putative GPI-anchored protein; adhesin-like protein
Putative GPI-anchored protein of unknown function; Rim101-repressed; Cyr1-regulated; colony morphology
Putative GPI-anchored adhesin-like protein; fluconazole-downregulated; induced in oralpharyngeal candida
GPI-anchored adhesin-like protein of the cell wall; role in cell wall integrity; required for normal virulence; in
Putative GPI-anchored protein
Protein similar to S. cerevisiae Wsc2p, which has roles in stress- and cell-wall-related processes; predicted
GPI-anchored protein of cell wall
Cell wall protein; putative GPI anchor; expression regulated upon white-opaque switch; induced by Congo
Putative GPI-anchored adhesin-like protein; induced in high iron; Spider biofilm induced
Putative GPI-anchored protein of unknown function; Spider biofilm repressed
Putative GPI-anchored protein; transcript repressed by alpha pheromone in SpiderM medium; induced in o
Putative GPI-anchored protein; Hap43-repressed; Spider biofilm induced
Putative adhesin-like GPI-anchored protein; repressed during cell wall regeneration; possibly an essential g
Putative GPI-anchored protein
GPI-anchored cell surface protein; beta-1,3-glucanosyltransferase with similarity to the A. fumigatus GEL fa
Putative GPI-anchored protein; adhesin-like protein
Putative GPI-anchored adhesin-like protein; decreased transcription is observed in azole-resistant strains t
Putative GPI-anchored protein
Putative GPI-anchored protein
Putative GPI-anchored cell wall protein; repressed in core caspofungin response; Hog1-induced; regulated
Putative GPI-anchored protein; secreted; fluconazole-induced
Putative GPI-anchored adhesin-like protein; similar to S. cerevisiae Spi1p, which is induced at stationary ph
Putative GPI-anchored protein
Putative GPI-anchored beta-1,3-glucanosyltransferase with similarity to the A. fumigatus GEL family; fungal
Putative GPI-anchored protein; adhesin-like protein
GPI-anchored cell surface protein of unknown function; Hap43p-repressed gene; fluconazole-induced; poss
GPI-anchored cell surface protein of unknown function; greater mRNA abundance observed in a cyr1 hom
GPI-anchored protein; Hog1-repressed; induced in cyr1 or efg1 mutant or in hyphae; colony morphology-rel
GPI-anchored adhesin-like protein; filament induced; regulated by Nrg1, Tup1; regulated upon hyphal form
Regulator of sorbose utilization; putative GPI-anchor; hypha and cell wall regeneration induced; colony mor
Putative GPI-anchored protein; Hap43p-induced gene
Putative GPI-anchored protein; transcription is positively regulated by Tbf1p
Adhesin-like cell wall protein; putative GPI-anchor; colony morphology-related gene regulation by Ssn6; Ha
GPI-anchored cell wall adhesin-like protein; induced by high iron; upregulated upon Als2 depletion; mRNA
Putative GPI-anchored adhesin-like protein; hyphal-induced expression
Putative GPI-anchored protein
Adhesin-like cell wall protein; putative GPI-anchor; fluconazole-induced; induced in high iron; induced durin
Component COPII vesicle coat; required for vesicle formation in ER to Golgi transport; predicted GPI-anch
GPI-linked hyphal surface antigen; induced by ciclopirox olamine, ketoconazole, Rim101 at pH 8; Hap43, fl
Glucose-6-phosphate isomerase; enzyme of glycolysis; antigenic; Efg1-regulated; induced upon adherence
Phosphoglycerate kinase; localizes to cell wall and cytoplasm; antigenic in murine/human infection; flow m
Ortholog of S. cerevisiae Pgm2; induced in planktonic culture; Tye7p-regulated; flow model biofilm induced;
Putative prephenate dehydratase; Hap43p-repressed gene; expression downregulated in an ssr1 null muta
Putative prohibitin; identified in detergent-resistant membrane fraction (possible lipid raft component); predi
Prohibitin 2; plasma membrane localized
Putative 4a-hydroxytetrahydrobiopterin dehydratase; transposon mutation affects filamentous growth; flow
Ortholog(s) have endopolyphosphatase activity, exopolyphosphatase activity, hydrolase activity, role in poly
Putative transporter, possibly involved in ion homeostasis, drug tolerance, filamentous growth, virulence; fu
Putative inducible acid phosphatase; DTT-extractable and observed in culture supernatant in low-phosphat
Phytase, implicated in hyphal morphogenesis and virulence; associated with cell surface; Rim101-represse
Putative constitutive acid phosphatase; Rim101-repressed; DTT-extractable; N-glycosylated; possibly an es
Acid phosphatase; induced by Mnl1 under weak acid stress; Spider biofilm induced
Putative 4-nitrophenylphosphatase; Hap43p-repressed gene; transcription is regulated upon yeast-hyphal s
HAD-family 2-phosphoglycolate phosphatase, likely involved in a metabolic repair system, not in protein de
Ortholog(s) have methylated histone binding activity
bHLH transcription factor of the myc-family; required for phosphate acquisition and for resistance to stresse
Putative repressible vacuolar alkaline phosphatase; Rim101-induced transcript; regulated by Tsa1, Tsa1B i
Protein involved in regulation of hyphal development; required for response to farnesoic acid; possibly adhe
High-affinity phosphate transporter; transcript regulated by white-opaque switch; Hog1, ciclopirox olamine o
Functional homolog of S. cerevisiae Pho85p, a cyclin-dependent kinase that regulates transcription of PHO
Putative endoplasmic reticulum protein; possibly adherence-induced
Putative phosphate permease; transcript repressed by Rim101 at pH 8; regulated by white-opaque switch;
Protein with a role in phosphate transport; biofilm-regulated expression; amphotericin B repressed
Putative phosphate permease; transcript regulated upon white-opaque switch; alkaline induced by Rim101;

Putative low-affinity phosphate transporter; fungal-specific (no human or murine homolog)
Cell surface glycosidase; may act on cell-wall beta-1,3-glucan prior to beta-1,6-glucan linkage; role in syste
Glycosidase; role in vaginal not systemic infection (low pH not neutral); low pH, high iron, fluconazole, Hap4
Putative beta-1,3-glucanosyltransferase with similarity to the A. fumigatus GEL family; fungal-specific (no h
DNA helicase and 3'-5' exonuclease; decreased transcription is observed upon fluphenazine treatment
Phosphatidylinositol 4-kinase; controls levels of phosphatidylinositol-4-phosphate (PI(4)P) in the Golgi; non-
Eisosome component; predicted role in endocytosis; echinocandin-binding protein; localizes to cell surface
ATP-dependent Lon protease; role in degradation of misfolded proteins in mitochondria, biogenesis and ma
Putative SH3-domain-containing protein; predicted role in actin cytoskeleton organization; Spider biofilm re
Protein with similarity to S. cerevisiae Pin4p; transposon mutation affects filamentous growth
1,3-beta-glucan-linked cell wall protein; N-mannosylated, O-glycosylated by Pmt1; cell wall defect in het mu
Cell wall protein, putative structural component of the cell wall; mutation leads to increased chitin content, i
Protein kinase C; functional homolog of S. cerevisiae Pkc1p; mutant has abnormal yeast-form cell morphol
Putative serine/threonine protein kinase; predicted role in sphingolipid-mediated signaling pathway that con
Ortholog(s) have role in cell wall integrity MAPK cascade
Phospholipase B; host cell penetration and virulence in mouse systemic infection; Hog1-induced; signal se
Putative phospholipase B; conserved catalytic region; 6 putative N-glycosylation motifs; predicted secretion
GPI-anchored cell surface phospholipase B; possibly secreted; fungal-specific (no mammalian homolog); i
Phospholipase B; Hog1-induced; regulated by Ssn6; putative GPI-anchor; repressed during cell wall regene
Putative GPI-linked phospholipase B, fungal-specific (no mammalian homolog); null mutation eliminates ce
Phosphoinositide-specific phospholipase C (PI-PLC), delta-form; essential; roles in stress resistance, hyph
Phosphatidylinositol (PtdIns)-specific phospholipase C (PI-PLC); predicted type 2 membrane protein; role i
Phospholipase D1; required for phosphatidic acid and for most diacylglycerol production; required for wild-t
Plasma membrane H(+)-ATPase; highly expressed, comprises 20-40% of total plasma membrane protein;
Vacuolar calcium P-type ATPase; transcript regulated by calcineurin and fluconazole; mutant shows increa
Phosphomannose isomerase; cell wall biosynthesis enzyme; drug target; functional homolog of S. cerevisia
Phosphomannomutase; enzyme of O- and N-linked mannosylation; interconverts mannose-6-phosphate a
Secretory pathway P-type Ca2+/Mn2+-ATPase; calcium pump involved in control of calcium homeostasis;
Putative DNA mismatch repair factor; ortholog of S. cerevisiae PMS1 which is an ATP-binding protein invol
Protein mannosyltransferase; required for virulence in mice and for adhesion to epithelial cells; role in hyph
Protein mannosyltransferase (PMT) with roles in hyphal growth and drug sensitivity; member of the PMT fa
Protein mannosyltransferase; required for WT cell wall composition and virulence in mice; roles in hyphal g
Protein mannosyltransferase (PMT), expressed at extremely low levels; not required for wild-type hyphal gr
Protein mannosyltransferase; required for virulence in mice, adhesion to endothelium; role in hyphal growth
Putative nicotinamidase, involved in NAD salvage pathway; decreased transcription is observed in an azole
Putative peptide:N-glycanase; gene has variable numbers of 12-bp repeats; induced by caspofungin, ciclop
Purine nucleoside phosphorylase; metabolizes inosine and guanosine nucleosides; in the nicotinamide ribo
Protein involved in chromatin assembly and disassembly; ortholog of S. cerevisiae Pob3; transposon mutat
Putative DNA directed DNA polymerase alpha; RNA abundance regulated by cell cycle, tyrosol and cell den
DNA polymerase epsilon; transcript induced by interaction with macrophage; transcript is regulated by Tup1
Large subunit of DNA polymerase III; partially complements defects of an S. cerevisiae cdc2 mutant; differi
Proliferating cell nuclear antigen (PCNA), forms homotrimeric sliding clamp for DNA polymerases; RNA ab
Putative subunit of DNA polymerase delta, involved in chromosomal DNA replication; cell-cycle regulated p
Putative DNA Polymerase phi; F-12/CO2 early biofilm induced
Predicted ORF in retrotransposon Tca8 with similarity to the Pol region of retrotransposons encoding rever
Putative nuclear pore membrane glycoprotein
Component of the Ccr4-Pop2 mRNA deadenylase; heterozygous null mutant exhibits resistance to parnafu
Putative RNase MRP and nuclear RNase P component; decreased repressed by prostaglandins; Spider bio
Ortholog of S. cerevisiae Pop4; a subunit of both RNase MRP and nuclear RNase P; filament induced; reg
Mitochondrial outer membrane porin; in detergent-resistant membrane fraction (possible lipid raft compone
Protein similar to S. cerevisiae Pos5p, a mitochondrial NADH kinase involved in the oxidative stress respon
Putative peroxisomal 3-oxoacyl CoA thiolase; transcript regulated by Nrg1 and Mig1; farnesol regulated; Ha
Putative peroxisomal 3-ketoacyl CoA thiolase; Hap43-repressed
Predicted acyl-CoA oxidase; regulated upon white-opaque switch; upregulated upon phagocytosis; Spider b
Predicted acyl-CoA oxidase; farnesol regulated; stationary phase enriched protein; Spider biofilm induced
Similar to Pox18, a peroxisomal protein; induced during chlamydospore formation in C. albicans and C. dub
Protein similar to S. cerevisiae Ppe1p; shows genetic interaction with some genes involved in diploid filame
Protein phosphatase of the Type 2A-related family (serine/threonine-specific) involved in control of filament
Catalytic subunit of protein phosphatase of the Type 2A-related family (serine/threonine-specific), involved i
Putative catalytic subunit of protein phosphatase complex; functions with regulatory subunit Psy2p in depho
Transcription factor with zinc cluster DNA-binding motif involved in regulation of purine catabolism; has simi
Putative dual specificity protein phosphatase, similar to S. cerevisiae Pps1p; mutant shows virulence defect
Putative serine/threonine phosphatase; induced in high iron
Phosphopantetheinyl transferase (PPTase); Spider biofilm induced

Protein phosphatase Z; fungal-specific type 1 family serine/threonine protein phosphatase involved in catio
Protein with similarity to proteasomal 26S regulatory subunit of S. cerevisiae, H. sapiens, Methanobacteriu
Cell surface protein that sequesters zinc from host tissue; enriched at hyphal tips; released extracellularly; b
Endoprotease B; regulated by heat, carbon source (GlcNAc-induced), nitrogen, macrophage response, hu
Putative carboxypeptidase; induced by human neutrophils; Spider biofilm induced
Putative carboxypeptidase Y precursor; transcript regulated by Nrg1 and Mig1; regulated by Gcn2 and Gcn
Putative proteinase; transcript regulated by Nrg1, Mig1, and Tup1; Hogp-induced; stationary phase enriche
Putative beta 4 subunit of the 20S proteasome; Rim101-induced at acid pH; flucytosine induced; amphoteri
Alpha7 (C8) subunit of the 20S proteasome; multiple phosphorylated residues; transcript induced upon fila
Putative proteasome beta-5 subunit; macrophage-induced protein
Putative beta-1 proteasome subunit; macrophage-induced protein; regulated by Gcn2p and Gcn4p; GlcNA
Alpha6 subunit of the 20S proteasome; regulated by Gcn4; induced in response to amino acid starvation (3
Putative alpha-4 subunit of the proteasome; reported as macrophage-induced protein and macrophage/pse
Putative alpha-2_sc subunit of proteasome; macrophage-induced protein; regulated by Gcn2p and Gcn4p;
Alpha3 (C9) subunit of the 20S proteasome; transcript regulated by Mig1; flow model biofilm repressed
Putative DNA primase; gene adjacent to and divergently transcribed with CDC68; Hap43-induced; Spider b
Putative protein serine/threonine kinase; mutants sensitive to growth on hydrogen peroxide medium
Putative membrane protein with a predicted role in membrane fusion during mating; Hap43p-repressed ge
Protein described a similar to S. cerevisiae Prm9; not the ortholog though; mutant is viable
Protein with similarity to pirins; induced by benomyl and in response to alpha pheromone in SpiderM mediu
Protein similar to pirin; Hap43p-repressed gene
Protein similar to pirin; induced by Mnl1 under weak acid stress; Hap43-repressed; Spider biofilm induced
Protein with similarity to pirins; induced by benomyl treatment; flow model biofilm repressed
Putative gamma-glutamyl kinase; transcript regulated by Nrg1; regulated by Gcn2 and Gcn4; Hap43-repres
Putative gamma-glutamyl phosphate reductase with a predicted role in proline biosynthesis; regulated by G
Delta 1-pyrroline-5-carboxylate reductase; protein induced during the mating process; alkaline induced; stat
Putative integral inner mitochondrial membrane protein with similarity to exonucleases
Putative RNA-dependent ATPase; induced upon adherence to polystyrene; induced by Mnl1p under weak a
Predicted splicing factor, component of the U4/U6-U5 snRNP complex; Hap43-induced gene; rat catheter b
Putative component of the U1 snRNP; involved in splicing; Hap43-induced gene; Spider biofilm induced
Putative component of the U1 snRNP, involved in splicing; ortholog of S. cerevisiae PRP42
Protein required for pre-mRNA splicing; Spider biofilm induced
Putative pre-mRNA processing RNA-helicase; induced upon adherence to polystyrene; rat catheter and Sp
Protein similar to S. cerevisiae Prp8, a component of the U4/U6-U5 snRNP complex; repressed by alpha p
Putative serine/threonine protein kinase; mutation confers resistance to 5-fluorocytosine (5-FC)
Putative prolyl-tRNA synthetase; monofunctional Class II synthetase; gene is constitutively expressed
Phosphoribosylpyrophosphate synthetase; enzyme of purine, pyrimidine, histidine, and tryptophan biosynth
Putative 5-phospho-ribosyl-1(alpha)-pyrophosphate synthetase; Hap43-induced; repressed during core stre
Putative translation initiation factor eIF3; mutation confers hypersensitivity to roridin A, verrucarin A; genes
Thioredoxin peroxidase; transcriptionally induced by interaction with macrophage; fluconazole induced; Fkh
Pry family pathogenesis-related protein; extracellular; opaque specific transcript; repressed by alpha phero
Mannose-1-phosphate guanyltransferase; Hap43, macrophage-repressed; stationary phase enriched prote
Phosphatidylserine decarboxylase; involved in phosphatidylethanolamine synthesis; Spider biofilm represse
Ortholog(s) have phosphatidylserine decarboxylase activity, role in phosphatidylcholine biosynthetic proces
Putative GINS complex subunit which is localized to DNA replication origins; implicated in assembly of the
Ortholog(s) have role in DNA-dependent DNA replication, double-strand break repair via break-induced rep
Putative GINS complex subunit; cell-cycle regulated periodic mRNA expression; Spider biofilm induced
Putative DNA cross-link repair protein; expressed in opaque or white MTLa/MTLa or MTLalpha/MTLalpha,
Protein repressed during the mating process
Flavodoxin-like protein involved in oxidative stress protection and virulence; putative 1,4-benzoquinone redu
Flavodoxin-like protein involved in oxidative stress protection and virulence; putative NADH:quinone oxidore
Flavodoxin-like protein involved in oxidative stress protection and virulence; YNB biofilm induced; stationary
Putative protein phosphatase PP4 complex subunit; macrophage-induced gene
Putative protein phosphatase of the Type 2C-related family (serine/threonine-specific), similar to S. cerevisi
Protein phosphatase of the Type 2C-related family (serine/threonine-specific); with protein kinase Ssn3p co
Type PP2C serine/threonine phosphatase; localized to mitochondria; mutation causes sensitivity to sodium,
Mitochondrial protein phosphatase of the Type 2C-related family (serine/threonine-specific), involved in dru
Mitochondrial protein phosphatase of the Type 2C-related family (serine/threonine-specific), functional hom
Protein phosphatase, type 2C; has S/T phosphatase activity, Mn2+/Mg2+ dependent; predicted membrane-
Predicted type 2C protein phosphatase, ser/thr-specific; required for hyphal growth; transcript induced by st
Putative gluconate transport protein; antigenic during human oral infection; possibly an essential gene, disru
Putative cAMP-independent regulatory protein; constitutive expression independent of MTL or white-opaqu
Putative protein kinase of polyamine import; mutation confers hypersensitivity to high concentrations of tun
Phosphotyrosine-specific protein phosphatase; rat catheter biofilm induced

Predicted protein tyrosine phosphatase; involved in regulation of MAP kinase Hog1 activity; induced by Mnl
Putative protein tyrosine phosphatase; hypha induced; alkaline induced; regulated by Efg1, Ras1, cAMP pa
Oligopeptide transporter involved in uptake of di-/tripeptides; highly induced during chlamydospore formatio
Oligopeptide transporter involved in uptake of di-/tripeptides; regulated by Stp2 and Stp3; transcript induce
Protein similar to S. cerevisiae Ptr3p, which is a sensor of external amino acids; expression upregulated in
RNA-binding protein involved in regulation of mitochondrial biogenesis
Putative beta 2 subunit of the 20S proteasome; macrophage/pseudohyphal-repressed; Spider biofilm repres
Alpha5 subunit of the 20S proteasome; macrophage/pseudohyphal-repressed; regulated by Gcn2p and Gc
Putative beta 3 subunit of the 20S proteasome; macrophage/pseudohyphal-repressed
Putative pseudouridine synthase; transcript regulated by Nrg1, Mig1, and Tup1
Pseudouridine synthase; catalyzes pseudouridylation in U2 snRNA, 5S rRNA, cytoplasmic tRNAs and in pre
Putative proline oxidase; alkaline upregulated by Rim101; flow model biofilm induced; Spider biofilm induce
Putative delta-1-pyrroline-5-carboxylate dehydrogenase; alkaline upregulated; protein present in exponentia
Zn(II)2Cys6 transcription factor; has similarity to S. cerevisiae Put3, a transcription factor involved in the re
Putative proline permease; fungal-specific (no human or murine homolog); repressed during the mating pro
Putative rRNA processing protein; Hap43-induced; repressed in core stress response
Putative 90S pre-ribosomal component; repressed in core stress response; repressed by prostaglandins; p
Putative peroxisomal, half-size adrenoleukodystrophy protein (ALD or ALDp) subfamily ABC family transpo
Putative peroxisomal, half-size adrenoleukodystrophy protein (ALD or ALDp) subfamily ABC transporter; G
Putative acyl-CoA oxidase; enzyme of fatty acid beta-oxidation; induced during macrophage infection; opaq
Putative pyruvate carboxylase; binds biotin cofactor; repressed by Ssk1 response regulator, by benomyl tre
C2H2 transcription factor; Hap43-induced; rat catheter and Spider biofilm induced
Ubiquinol-cytochrome-c reductase; antigenic; induced by interaction with macrophage; repressed by nitric o
Putative ubiquinol-cytochrome-c reductase, subunit 7; Hap43p-repressed gene
Putative ubiquinol cytochrome c reductase; macrophage and pseudohyphal-induced protein; colony morpho
Putative ubiquinol cytochrome c reductase; shows colony morphology-related gene regulation by Ssn6p
Putative antibiotic resistance transporter; regulated by white-opaque switch, Nrg1, Tup1; Hap43, caspofung
Predicted MFS membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) family; S
Predicted membrane transporter, member of the drug:proton antiporter (12 spanner) (DHA1) family, major
G-protein of RAC subfamily; required for embedded filamentous growth, not for serum-induced hyphal grow
Putative single-stranded DNA endonuclease; transcript regulated by Nrg1; macrophage-induced gene
Ortholog of S. cerevisiae Rad10, an endonuclease involved in nucleotide excision repair; mutant is extreme
Putative DNA repair protein; transcription is regulated upon yeast-hyphal switch; flucytosine repressed
Ortholog of S. cerevisiae Rad16; a protein that recognizes and binds damaged DNA; flucytosine induced; ra
Putative transcription factor with zinc finger DNA-binding motif; Hap43p-repressed gene
Ortholog of S. cerevisiae Rad2, a nucleotide excision repair nuclease; null mutant is extremely sensitive to
S. cerevisiae Rad23 ortholog; binds damaged DNA; Spider biofilm repressed
Ortholog of S. cerevisiae Rad3; 5' to 3' DNA helicase, nucleotide excision repair and transcription, subunit
DNA polymerase eta with role in DNA repair; required for transition to hyphal growth; down-regulation asso
Putative DNA double-strand break repair factor; involved in response to oxidative stress and drug resistanc
Protein involved in homologous recombination and DNA repair; flucytosine induced; slow growth and increa
Required for homologous DNA recombination, repair of UV- or MMS-damaged DNA, telomere length, UV-i
Protein involved in regulation of DNA-damage-induced filamentous growth; putative component of cell cycle
Putative DNA-dependent ATPase involved in DNA repair; induced under hydroxyurea treatment; plays an e
Putative DNA recombination and repair protein; induced by interaction with macrophage; transcript is regula
Protein involved in homologous recombination and DNA breaks repair; similar to S. cerevisiae Rad59p; N-t
Functional ortholog of S. cerevisiae Rad6; negative regulator of hyphal growth; required for wild-type UV re
Protein similar to S. cerevisiae Rad7p, which is a subunit of the Nucleotide Excision Repair Factor 4; induce
DNA damage-dependent checkpoint protein; involved in regulation of DNA-damage-induced filamentous gr
Protein that acts in prenylation; transcription is alpha-factor induced; regulated in response to lovastatin an
Alpha subunit of heterodimeric protein geranylgeranyltransferase type I and farnesyltransferase; a-specific
Transcription factor; binds telomeres and regulatory sequences in DNA; involved in telomere maintenance;
RAS signal transduction GTPase; regulates cAMP and MAP kinase pathways; role in hyphal induction, virul
Protein similar to S. cerevisiae Ras2; has opposite effects to Ras1; Tn mutation affects filamentous growth;
5'-->3' exoribonuclease; similar to S. cerevisiae nuclear exoribonuclease Rat1p; suppresses S. cerevisiae
Protein similar to S. cerevisiae Rav2; a regulator of (H+)-ATPase in vacuolar membrane; transposon mutat
Protein with a predicted role in bud site selection; hypha-induced expression; Spider biofilm induced
Plasma membrane protein involved in establishment of bud sites and linear direction of hyphal growth; fila
Rhomboid-like protein; similar to putative intramembrane serine proteases; role in filamentous growth; Gcn
Pry family cell wall protein; Rim101, Efg1, Ssn6, alkaline repressed; O-glycosylation; no GPI anchor predict
Transcription factor; glutamine-rich activation domain; binds RPG-box DNA sequences; predominantly nucl
Has domain(s) with predicted ribokinase activity and role in D-ribose metabolic process
Peptidyl-prolyl cis-trans isomerase; rapamycin-binding protein; homozygous null mutation confers rapamyci
Glycosylphosphatidylinositol (GPI)-anchored cell wall protein; required for filamentous growth at acidic pH;

Cell wall protein; expression repressed by Rim101; transcript regulated upon white-opaque switching; repre
Cell wall adhesin-like protein; repressed by Rim101; possibly an essential gene, disruptants not obtained by
Cell wall protein with similarity to Hwp1; required for virulence; predicted glycosylation; fluconazole, Tup1 re
Pry family protein; required for virulence in mouse systemic/rabbit corneal infections; not filamentation; mRN
GPI-linked cell wall protein; hemoglobin utilization; Rfg1, Rim101, Tbf1, Fe regulated; Sfu1, Hog1, Tup1, se
Protein with similarity to RNase T2 enzymes; has putative secretion signal; expression is Tup1-repressed
Protein involved in regulation of carbonic anhydrases; controls CO2 sensing; bZIP domain-containing transc
Putative Type II CAAX prenyl protease; induced during the mating process
Plasma membrane protein; involved in regulation of cytosolic calcium homeostasis; null mutation confers se
Predicted MAP kinase-activated protein kinase, similar to S. cerevisiae serine/threonine protein kinase Rck
Putative U3-containing 90S preribosome processome complex subunit; Hap43-induced; essential; S. cerev
Protein involved in calcineurin-dependent signaling that controls stress response and virulence; inhibits calc
Fluconazole-induced protein; Ras1, Cyr1 repressed and Efg1 induced; regulated by Nrg1, Tup1, Tbf1, Ssn6
Putative F-box protein involved in endocytic membrane traffic and/or recycling; fungal-specific (no human o
Putative DNA-dependent ATPase with a predicted role in DNA recombination and repair; transcriptionally in
Putative rho GDP dissociation inhibitor; transposon mutation affects filamentous growth; farnesol, filament-i
Putative protein phosphatase regulatory subunit; Hap43-repressed gene; macrophage/pseudohyphal-induc
Putative cytoplasmic pre-60S factor; Hap43-induced; repressed by prostaglandins
Putative transcription factor involved in transcription of N-acetylglucosamine-inducible genes; involved in ne
Putative cis-prenyltransferase involved in dolichol synthesis; participates in endoplasmic reticulum (ER) pro
Delta subunit of the coatomer complex (COPI); coats Golgi-derived transport vesicles; involved in retrograd
Ortholog(s) have DNA-directed DNA polymerase activity, role in error-free translesion synthesis, error-prone
Putative 3'-5' RNA exonuclease with a predicted role in 3'-end processing of U4 and U5 snRNAs, 5S and 5.
Ortholog(s) have 3'-5'-exoribonuclease activity
Putative DNA replication factor A; RNA abundance regulated by cell cycle, tyrosol and cell density
Putative DNA replication factor A; RNA abundance regulated by cell cycle, tyrosol and cell density
Putative DNA replication factor C subunit; ortholog of S. cerviaie Rfc1; likely essential, based on an insertion
Putative heteropentameric replication factor C subunit; periodic mRNA expression, peak at cell-cycle G1/S
Putative heteropentameric replication factor C subunit; transcription is induced upon filamentous growth
Putative heteropentameric replication factor C subunit; flucytosine induced; periodic mRNA expression, pea
Putative heteropentameric replication factor C subunit; periodic mRNA expression, peak at cell-cycle G1/S
HMG domain transcriptional repressor of filamentous growth and hyphal genes; in Tup1-dependent and -ind
Transcription factor; involved in DNA damage responses, morphogenesis, and virulence; Spider biofilm indu
Transcriptional repressor; regulator of filamentation, response to DNA damage, adhesion, virulence in murin
Putative GTPase-activating protein (GAP) for Rho-type GTPase Cdc42; involved in cell signaling pathways
GTPase activator protein; transcript induced in low iron; alkaline upregulated; localized to the bud emergenc
Putative Rho GTPase activating protein; fungal-specific (no human or murine homolog)
Protein of RGS superfamily; mutants are viable; rat catheter and Spider biofilm induced
Zn(II)2Cys6 transcription factor; transcriptional repressor involved in the regulation of glucose transporter ge
Putative small G protein from the Ras superfamily involved in cell wall integrity and control of filamentous gr
Putative beta-mannosyltransferase required for the addition of beta-mannose to the acid-labile fraction of ce
Predicted ORF in retrotransposon Tca4 with similarity to the Gag region encoding nucleocapsid-like protein
GPI-anchored yeast-associated cell wall protein; induced in high iron; clade-associated gene expression; no
Small GTPase of Rho family; regulates beta-1,3-glucan synthesis activity and binds Gsc1p; essential; expe
Ortholog(s) have GTPase activity and role in establishment or maintenance of actin cytoskeleton polarity, re
Putative Rho family GTPase; possible substrate of protein farnesyltransferase and geranylgeranyltransferas
Glycerol 3-phosphatase; roles in osmotic tolerance, glycerol accumulation in response to salt; Spider/flow m
Putative translation elongation factor; genes encoding ribosomal subunits, translation factors, and tRNA syn
GTP cyclohydrolase II, rate-limiting enzyme of riboflavin biosynthesis; fungal-specific (no human or murine
3,4-Dihydroxy-2-butanone 4-phosphate synthase; homodimeric enzyme of riboflavin biosynthesis; converts
Lumazine synthase (6,7-dimethyl-8-ribityllumazine synthase, DMRL synthase); catalyzes the penultimate st
Putative riboflavin synthase; fungal-specific (no human or murine homolog); farnesol-downregulated; protei
Ortholog of S. cerevisiae Ric1 guanyl-nucleotide exchange factor; mutant is viable; rat catheter biofilm repre
Putative single-stranded DNA-binding protein; protein level decreases in stationary phase cultures; rat cathe
Transcription factor; alkaline pH response; required for alkaline-induced hyphal growth; role in virulence in r
Ortholog of S. cerevisiae Rim11; a protein kinase involved in meiosis and sporulation in S. cerevisiae; muta
Protease of the pH response pathway; likely to mediate activation of Rim101 via C-terminal cleavage; requi
Ortholog(s) have protein kinase activity, protein serine/threonine kinase activity
Putative mitochondrial carrier protein; induced by alpha pheromone in SpiderM medium; Spider biofilm indu
Protein involved in the pH response pathway; binds to the transcription factor Rim101 and may serve as a s
Plasma membrane pH-sensor involved in the Rim101 pH response pathway; required for processing and a
Beta-arrestin-like protein; involved in pH response; required for pathogenesis, activation of Rim101 and alka
Protein required for alkaline pH response via the Rim101 signaling pathway; ortholog of S. cerevisiae Rim9
Putative serine kinase with a predicted role in the processing of the 20S pre-rRNA into mature 18S rRNA; n

Putative ubiquinol cytochrome c-reductase; induced by high iron; Hap43, nitric oxide, alkaline repressed; Sp
Putative initiator tRNA methionine ribosyltransferase; fungal-specific (no human or murine homolog)
Putative ATPase of the AAA family; role in ribosomal subunit export from the nucleus; mutation impairs hyp
Ortholog(s) have ribose-5-phosphate isomerase activity and role in pentose-phosphate shunt, pyridoxine bi
Member of RNase L inhibitor (RLI) subfamily of ABC family; predicted not to be a transporter; regulated by
Transcription factor required for wild-type resistance to cell wall perturbation caused by caspofungin treatme
Putative ribosomal protein; Hap43-induced; essential gene; heterozygous mutation confers hypersensitivity
Zinc finger protein, controls asexual sporulation; white-specific transcript; upregulation correlates with clinica
Ortholog of Rmp1; subunit of RNase MRP subunit that processes pre-rRNA and has a role in cell cycle-regu
Putative lysine methyltransferase; Hap43-induced; protein induced during mating; possibly essential, disrup
Minor protein arginine methyltransferases (PRMT) involved in methylation of arginine residues
Putative GTPase-activating protein; protein level decreases in stationary phase cultures; Spider biofilm repr
Ribonuclease H (RNAse H); hyphal-induced; flucytosine induced; similar to orf19.5564 (see Locus History);
Putative ribonuclease H2 catalytic subunit; flucytosine induced; Spider biofilm repressed
Ribonucleotide reductase large subunit; induced in low iron; transposon mutation affects filamentous growth
Ribonucleoside-diphosphate reductase; regulated by tyrosol and cell density; ciclopirox olamine, fluconazol
Putative ribonucleoside diphosphate reductase;colony morphology-related gene regulation by Ssn6; transcr
Putative ribonucleotide reductase large subunit; transcript induced in low iron; rat catheter and Spider biofil
Ortholog(s) have endoribonuclease activity, role in RNA catabolic process, apoptotic process, cell morphog
Putative PDR-subfamily ABC transporter involved in sensitivity to azoles; Spider biofilm induced
Zn(II)2Cys6 transcription factor; required for Spider model biofilm formation; mutant displays abnormal colo
Protein similar to S. cerevisiae Rod1;a membrane protein with a role in drug tolerance; repressed by Rgt1;
Putative GDP/GTP exchange factor; possibly an essential gene, disruptants not obtained by UAU1 method;
Similar to S. cerevisiae Rot1p, which is involved in cell wall 1,6-beta-glucan biosynthesis; has predicted tran
Alpha-glucosidase II, catalytic subunit, required for N-linked protein glycosylation and normal cell wall synth
Putative DNA-directed RNA polymerase I; induced upon adherence to polystyrene
Putative RNA polymerase I subunit A135; repressed by prostaglandins
Putative RNA polymerase I subunit A190; Hap43p-induced gene; flucytosine induced
Putative RNA polymerase I subunit; rat catheter biofilm induced
Putative RNA polymerase II subunit; flucytosine induced
Protein similar to S. cerevisiae Rpb4p, which is a component of RNA polymerase II; transposon mutation af
Functional homolog of S. cerevisiae Rpb7; essential subunit of RNA Polymerase II; enhances hyperfilamen
Putative subunit of RNA polymerases I, II, and III; regulated by Gcn4p; repressed in response to amino aci
Putative RNA polymerase subunit ABC10-alpha of RNA polymerase complexes I, II, and III; flucytosine indu
Putative RNA polymerase III subunit C11; repressed in core caspofungin response; Spider biofilm induced
Putative RNA polymerases I and III subunit AC19; Hap43-induced; rat catheter biofilm induced
Putative RNA polymerase III subunit C31; repressed by nitric oxide; induced during infection of murine kidn
Putative RNA polymerase; protein level decreases in stationary phase cultures; Hap43p-induced gene
Ortholog(s) have RNA polymerase III activity, role in tRNA transcription by RNA polymerase III and RNA po
Histone deacetylase; regulates frequency of white-to-opaque and opaque-to-white switching; greater expres
Putative histone deacetylase; involved in regulation of white-opaque switch; Spider biofilm repressed
Putative nucleolar protein with a predicted role in the assembly and export of the large ribosomal subunit; e
Putative pre-rRNA processing protein; Hap43p-induced gene; mutation confers hypersensitivity to 5-fluoroc
Putative translation initiation factor; mutation confers hypersensitivity to roridin A and verrucarin A; represse
Ribosomal protein L10; intron in 5'-UTR; downregulated upon phagocytosis by murine macrophage; transcr
Predicted ribosomal protein; downregulated upon phagocytosis by murine macrophages; Hap43-induced; S
Ribosomal protein; repressed by phagocytosis; colony morphology-related gene regulation by Ssn6; Hap43
Ribosomal protein L12, 60S ribosomal subunit; downregulated by human whole blood or polymorphonuclea
Putative ribosomal subunit; antigenic during murine infection; downregulated upon phagocytosis by murine
Ribosomal protein L14; promoter bound directly by Tbf1p; Hap43p-induced gene
Putative ribosomal protein; repressed upon phagocytosis by murine macrophage; positively regulated by Tb
Ribosomal protein; transposon mutation affects filamentous growth; repressed upon phagocytosis by murin
Ribosomal protein L17; mutation confers hypersensitivity to 5-FU, tubercidin; repressed upon phagocytosis
Predicted ribosomal protein; Plc1p-regulated, Tbf1-activated; repressed upon phagocytosis by murine macr
Ribosomal protein L19; repressed upon phagocytosis by murine macrophages; Hap43-induced gene; Spide
Putative 60S ribosomal protein L2; Hap43-induced gene; repressed in infected rabbit kidney in SC5314, bu
Ribosomal protein L20; repressed upon phagocytosis by murine macrophage; alternatively spliced intron in
Putative ribosomal protein; repressed upon phagocytosis by murine macrophage; Spider biofilm repressed
Ribosomal protein; downregulated upon phagocytosis by murine macrophage; Hap43-induced; sumoylation
Predicted ribosomal protein; downregulated upon phagocytosis by murine macrophage; intron in 5'-UTR; Ha
Putative rRNA-binding ribosomal protein component of the 60S ribosomal subunit; Hap43-induced; colony
Ribosomal protein L27; Spider biofilm repressed
Putative ribosomal protein; Plc1-regulated; downregulated upon phagocytosis by murine macrophage; Spid
Ribosomal protein L29; induced upon germ tube formation; colony morphology-related gene regulation by

Ribosomal protein, large subunit; induced by ciclopirox olamine treatment; genes encoding cytoplasmic ribo
Ribosomal 60S subunit protein; pre-rRNA processing; pre-mRNA alternatively spliced to productive/unprodu
Component of the large (60S) ribosomal subunit; Spider biofilm repressed
Ribosomal protein; downregulation correlates with clinical development of fluconazole resistance; colony m
Ribosomal protein L37; Hap43-induced; Spider biofilm repressed
60S ribosomal ribosomal protein subunit; genes encoding cytoplasmic ribosomal subunits, translation facto
Ribosomal protein L39; transcript induced upon germ tube formation; colony morphology-related gene regu
Protein with similarity to the ribosomal protein portion of S. cerevisiae Rpl40Bp; colony morphology-related
Putative 60S ribosomal subunit protein; colony morphology-related gene regulation by Ssn6; Spider biofilm
Putative ribosomal protein, large subunit; repressed by human whole blood or PMNs; colony morphology-re
Ribosomal protein 4B; repressed upon phagocytosis by murine macrophage; Spider biofilm repressed
Ribosomal protein; repressed upon phagocytosis by murine macrophages; Hap43-induced; Spider biofilm r
Ortholog of S. cerevisiae ribosomal subunit, Rpl6B; transposon mutation affects filamentous growth; transla
Ribosomal protein L7; repressed upon phagocytosis by murine macrophages; Hap43-induced; rat catheter
Predicted ribosomal protein; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA
Predicted ribosomal protein; regulated upon yeast-hypha switch; repressed upon phagocytosis by murine m
Ribosomal protein L9; repressed upon phagocytosis by murine macrophages; repressed by nitric oxide; pro
Mitochondrial RNase P subunit; roles in nuclear transcription, cytoplasmic and mitochondrial RNA processi
Putative 19S regulatory particle of the 26S proteasome; regulated by Gcn2p and Gcn4p
Putative 19S regulatory particle of the 26S proteasome; macrophage/pseudohyphal-repressed; regulated by
Putative 26S proteasome subunit; transcript regulated by Mig1; caspofungin repressed; regulated by Gcn2
Putative non-ATPase regulatory subunit of the 26S proteasome lid; amphotericin B repressed; oxidative str
C2H2 transcription factor; putative regulator of proteasome genes; DNA recognition sequence (GAAGGCA
Putative COP9 signalosome component; macrophage/pseudohyphal-repressed
Putative 26S proteasome subunit; Hap43p-induced gene; regulated by Gcn2p and Gcn4p
Subunit of the proteasome regulatory particle; regulated by Gcn2p and Gcn4p; protein present in exponenti
Putative regulatory subunit of the 26S proteasome; mutation confers hypersensitivity to amphotericin B; reg
RNA polymerase II; ortholog of S. cerevisiae Rpo21, transposon mutation affects filamentous growth; flow r
Putative RNA polymerase subunit; heterozygous null mutant exhibits resistance to parnafungin in the C. alb
Putative mitochondrial RNA polymerase; repressed in core stress response; Spider biofilm induced
Putative ribosomal protein; antigenic in mouse; repressed upon phagocytosis by murine macrophage; induc
Putative ortholog of S. cerevisiae Rpp1; subunit of both RNase MRP and nuclear RNase P; rat catheter and
Conserved acidic ribosomal protein; likely role in regulation of translation elongation; interacts with Rpp2B;
Conserved acidic ribosomal protein, likely involved in regulation of translation elongation; interacts with Rpp
Acidic ribosomal protein; likely role in translation elongation regulation; interacts with Rpp1B; 1 of 4 similar r
Conserved acidic ribosomal protein; possibly involved in regulation of translation elongation; interacts with R
Ortholog(s) have ribonuclease P activity, role in intronic box C/D RNA processing, tRNA processing and nu
Putative ribosomal protein 10 of the 40S subunit; elicits host antibody response during infection; transcript i
Ribosomal protein S10; downregulated in the presence of human whole blood or PMNs; Spider biofilm repr
Acidic ribosomal protein S12; regulated by Gcn4, activated by Tbf1; repressed by amino acid starvation (3-
Putative ribosomal protein of the small subunit
Putative ribosomal protein; repressed upon phagocytosis by murine macrophage; transcript positively regul
Putative ribosomal protein; macrophage/pseudohyphal-induced after 16 h; repressed upon phagocytosis by
Putative 40S ribosomal subunit; macrophage/pseudohyphal-induced after 16 h; Spider biofilm repressed
Ribosomal protein 17B; downregulated upon phagocytosis by murine macrophages; Hap43-induced; Spide
Predicted ribosomal protein; repressed upon phagocytosis by murine macrophage; repressed by nitric oxide
Putative ribosomal protein S19; protein level decreases in stationary phase cultures; Spider biofilm represse
Putative ribosomal protein; repressed upon phagocytosis by murine macrophage; transcript positively regul
Protein component of the small (40S) subunit; repressed upon phagocytosis by murine macrophage; positi
Ribosomal protein S21; regulated by Nrg1, Tup1; colony morphology-related gene regulation by Ssn6; posit
Predicted ribosomal protein; repressed upon phagocytosis by murine macrophage; Spider biofilm represse
Putative ribosomal protein; repressed upon phagocytosis by murine macrophage; Spider biofilm repressed
Predicted ribosomal protein; hyphal downregulated; repressed upon phagocytosis by murine macrophage; t
Ribosomal protein; macrophage/pseudohyphal-induced after 16 h; repressed upon phagocytosis by murine
Ribosomal protein; regulated by Nrg1, Tup1; repressed upon phagocytosis by murine macrophage; alternat
Putative ribosomal protein; repressed upon phagocytosis by murine macrophage; Spider biofilm repressed
Ribosomal protein S27; rat catheter and Spider biofilm induced
Putative ribosomal protein S28B
Ribosomal protein S3; Hog1, Hap43-induced; grepressed upon phagocytosis by murine macrophage; prese
Putative 40S ribosomal protein S30; colony morphology-related gene regulation by Ssn6; rat catheter biofil
Predicted ribosomal protein S4, component of the small ribosomal subunit; has paralog RPS41
Predicted ribosomal protein, component of the small ribosomal subunit; repressed upon phagocytosis by m
Ribosomal protein S5; macrophage/pseudohyphal-induced after 16 h; downregulated upon phagocytosis by
Ribosomal protein 6A; localizes to cell surface of yeast cells but not hyphae; repressed upon phagocytosis

Ribosomal protein S7; genes encoding cytoplasmic ribosomal subunits, translation factors, and tRNA synth
Small 40S ribosomal subunit protein; induced by ciclopirox olamine; repressed upon phagocytosis by murin
Predicted ribosomal protein; repressed upon phagocytosis by murine macrophage; transcript possibly regul
Putative 26S proteasome regulatory subunit 7; Hap43p-repressed gene; regulated by Gcn2p and Gcn4p; o
Putative ATPase of the 19S regulatory particle of the 26S proteasome; oxidative stress-induced via Cap1; S
26S proteasome regulatory subunit; regulated by Gcn2p and Gcn4p; protein level decreases in stationary p
26S proteasome regulatory subunit; transcript regulated by Nrg1 and Mig1; regulated by Gcn2 and Gcn4; p
Putative ATPase of the 19S regulatory particle of the 26S proteasome; transcript regulated by Mig1; regulat
Putative peptidyl-prolyl cis/trans-isomerase; caspofungin induced
Putative RNA polymerase I subunit; rat catheter biofilm induced; Spider biofilm induced
Protein with a predicted role in recruitment of RNA polymerase I to rDNA; caspofungin induced; flucytosine
Putative nucleolar protein; constituent of pre-60S ribosomal particles; Hap43-induced; repressed by prostag
Putative exosome non-catalytic core component; involved in 3'-5' RNA processing; rat catheter biofilm induc
Putative nuclear exosome exonuclease component; Hap43p-induced gene; mutation confers hypersensitivi
Ribosomal protein; Hap43-induced; F-12/CO2 early biofilm and rat catheter biofilm induced
Ribosomal protein; mutation confers resistance to 5-fluorocytosine (5-FC), 5-fluorouracil (5-FU), and tuberc
Putative ribosome biogenesis and nuclear export protein; Hap43p-induced gene; mutation confers hyperse
Predicted mitochondrial small ribosomal subunit; rat catheter and Spider biofilm induced
Protein of unknown function; flow model biofilm induced; Spider biofilm induced; induced during the mating
Putative NEDD4 family E3 ubiquitin ligase; induced during infection of murine kidney, compared to growth i
RAS-related protein; GTP/GDP cycling required for wild-type polar bud site selection, hyphal growth guidan
Flippase involved in sphingolipid long chain base release; mediates calcineurin-dependent ER stress respo
7-transmembrane receptor protein involved in regulation of asymmetric lipid distribution in plasma membra
Protein similar to S. cerevisiae Rsb1p, involved in fatty acid transport; transposon mutation affects filament
Putative RNA polymerase II-associated Paf1 complex subunit; induced during the mating process
RNA polymerase II transcription factor involved in regulation of galactose catabolism genes; as result of tra
Transcription factor with bZIP motif involved in regulation of galactose catabolism genes; performs role ana
Putative serine/threonine-protein phosphatase B-type regulatory subunit; transcription is regulated upon yea
Putative cullin subunit of E3 ubiquitin ligase complex, involved in response to DNA damage; induced by alp
Histone acetyltransferase, mutants are sensitive to DNA damage, show decreased virulence in mice, decre
Ubiquitin-related protein with similarity to mammalian NEDD8; reversible conjugation (neddylation) of the cu
Putative trancription modulator; RuvB-like protein family member; heterozygous null mutant displays sensiti
Protein required for endocytosis; contains a BAR domain, which is found in proteins involved in membrane
Protein containing a BAR domain, which is found in proteins involved in membrane curvature; null mutant d
SH3-domain- and BAR domain-containing protein involved in endocytosis; null mutant exhibits defects in hy
Putative transcriptional repressor
Putative phosphatidylinositol phosphate (PtdInsP) phosphatase, involved in cell wall integrity and morphoge
Putative nuclear pore-associated protein, required for small ribosomal subunit biogenesis; possibly an esse
Fimbrin; actin filament bundling protein; involved in hyphal growth, oxidative stress response and virulence;
Putative GTPase activating protein (GAP) for Rho1; repressed upon adherence to polystyrene; macrophage
S-adenosyl-L-homocysteine hydrolase; sulfur amino acid metabolism; antigenic in human; alkaline-, flucona
Putative protein phosphatase of the Type 1 family; serine/threonine-specific; similar to S. cerevisiae Ppq1;
S-adenosylmethionine synthetase; localizes to surface of hyphae, not yeast cells; alkaline, Hog1-induced; fa
Predicted component of the sorting and assembly machinery (SAM complex) of the mitochondrial outer me
Protein of the mitochondrial outer membrane, component of the Sorting and Assembly Machinery (SAM) in
Putative S-adenosylmethionine-homocysteine methyltransferase; Hap43-repressed; alkaline induced; Spide
Predicted component of the SAM complex involved in mitochondrial protein import
Component of the SAM complex involved in mitochondrial protein import, involved in beta-barrel protein ass
Secreted aspartyl proteinase; acts in utilization of protein as nitrogen source; assessment of virulence role
Secreted aspartyl protease; roles in adhesion, virulence (RHE model), cell surface integrity; distinct specific
Major secreted aspartyl proteinase; utilization of protein as nitrogen source; role in virulence complicated by
Secreted aspartyl proteinase, acts in utilization of protein as nitrogen source; assessment of virulence role
Aspartic-type endopeptidase; involved in degradation of alpha pheromone; functional equivalent of S. cerev
Secreted aspartyl proteinase; sap4,5,6 mutant defective in protein utilization for nitrogen; virulence role com
Biofilm-specific aspartyl protease; virulence role effected by URA3; expressed during infection; mRNA local
Biofilm-specific aspartyl protease; expressed during hyphal growth, oral carriage, infection; virulence role af
Pepstatin A-insensitive secreted aspartyl protease; self-processing; expressed in human oral infection; Ssn
Secreted aspartyl protease; regulated by growth phase, temperature, white-opaque switch; highly express
Secreted aspartyl protease; roles in adhesion, cell surface integrity; induced by antifungal drugs, stationary
Glycosyl-phosphatidylinositol-anchored aspartic endopeptidase; regulated by Gcn2p and Gcn4p; expresse
Putative secreted aspartyl protease; possible Kex2 substrate; induced by low iron; repressed by alpha pher
Functional homolog of S. cerevisiae Sar1; which is required for ER-to-Golgi protein transport; binds GTP; s
Putative U3-containing small subunit processome complex subunit; Hap43p-induced gene; mutation confe
Predicted histone acetyltransferase involved in histone H4 acetylation; member of MYST family

Similar to silencing proteins; increased transcription is observed upon fluphenazine treatment; rat catheter b
Similar to co-chaperones; induced in high iron; farnesol-, heavy metal (cadmium) stress-induced; protein lev
Similar to RNA binding proteins; downregulated upon adherence to polystyrene; stationary-phase enriched
Protein kinase; involved in growth control, ribosomal protein synthesis, cell size, resistance to rapamycin,, c
Proteasome subunit YC7alpha; protein present in exponential and stationary growth phase yeast cultures; f
Putative copper transporter; Hap43p-repressed gene
Putative cortical actin cytoskeleton protein; constitutive expression independent of MTL or white-opaque sta
Putative ceramide hydroxylase; regulated by Nrg1; induced in high iron; fluconazole-induced; Hap43-repres
Putative glycerol-3-phosphate O-acyltransferase; fungal-specific (no human or murine homolog)
Putative glycerol-3-phosphate acyltransferase; fungal-specific (no human or murine homolog)
Cell wall protein; repressed in ace2 mutant; repressed in core caspofungin response; induced in high iron; p
Putative cell wall protein; substrate for Kex2p processing in vitro; expression regulated by white-opaque swi
Predicted nuclear protein involved in actin cytoskeleton organization, passage through Start, 60S ribosome
Putative COMPASS/SET1C histone methyltransferase complex subunit
Putative mitochondrial succinate dehydrogenase; macrophage/pseudohyphal-induced; repressed by nitric o
Succinate dehydrogenase; soluble protein in hyphae; macrophage-downregulated protein level; downregula
Succinate dehydrogenase, Fe-S subunit; localizes to surface of yeast cells, but not hyphae; induced in high
Succinate dehydrogenase, membrane subunit; induced in high iron
Putative regulatory subunit of the PP1 phosphatase Glc7p; involved in dephosphorylation of Rad53p in orde
Protein similar to S. cerevisiae Sds24 involved in cell separation during budding; transcript regulated by Mig
Ortholog(s) have SNARE binding activity, role in exocytosis, positive regulation of vesicle fusion, vesicle doc
Ortholog(s) have role in Golgi to plasma membrane transport, exocytosis and cell division site, cell tip, exoc
Putative guanyl-nucleotide exchange factor; induced in high iron; Hap43-repressed
Putative protein transport factor; antigenic during murine systemic infection; macrophage-downregulated pr
Essential protein; functional homolog of S. cerevisiae Sec14p, a Golgi phosphatidylinositol/phosphatidylcho
Exocyst subunit, involved in polarized growth; cellular bud tip-associated protein; interacts with Ras-related
Functional homolog of S. cerevisiae Sec18p, which acts in protein transport; conserved ATP binding site; n
Guanyl-nucleotide exchange factor for the small G-protein Sec4; delivery of post-Golgi secretory vesicles to
Essential protein; similar to S. cerevisiae Sec20p; depletion causes membrane accumulation and drug sens
Ortholog(s) have role in endoplasmic reticulum to Golgi vesicle-mediated transport, retrograde vesicle-med
Ortholog(s) have SNAP receptor activity and role in endoplasmic reticulum to Golgi vesicle-mediated transp
Putative GTPase-activating protein; regulated upon yeast-hypha switch; Spider biofilm repressed
Protein with a possible role in ER to Golgi transport; induced upon yeast-hyphal switch; sumoylation target;
Secretory vesicles coatomer complex protein
Ortholog(s) have ubiquitin binding activity
Predicted subunit of the exocyst complex, involved in exocytosis; required for hyphal growth after the first se
Ortholog(s) have cargo adaptor activity
Small GTPase of Rab family; role in post-Golgi secretion; possible C-terminal palmitoylation; downregulated
Predicted exocyst component; ortholog of S. cerevisiae Sec5p; merged with orf19.75 in Assembly 21
Predicted subunit of the exocyst complex, involved in exocytosis; localizes to a crescent on the surface of th
ER protein-translocation complex subunit; essential; 10 predicted transmembrane regions; chimeric mutant
Putative endoplasmic reticulum (ER) protein-translocation complex subunit
Component of the protein-targeting Signal Recognition Particle (SRP); similar to mammalian Srp19; functio
Putative guanine nucleotide exchange factor (GEF); mutation confers hypersensitivity to Brefeldin A; caspo
ER protein-translocation complex component; regulated by Gcn4p; repressed in response to amino acid sta
Predicted subunit of the exocyst complex, involved in exocytosis; localizes to a crescent on the surface of th
t-SNARE protein required for secretory vesicle-membrane fusion
Zn2-Cys6 transcription factor; regulates iron uptake; negatively regulated by Sfu1p, positively regulated by T
Zn(II)2Cys6 transcription factor, required for normal resistance to copper; repressed by Sfu1 in high-iron co
Ortholog(s) have role in positive regulation of TORC1 signaling and Seh1-associated complex, extrinsic com
Putative helicase; repressed by prostaglandins
Similar to delta subunit of tRNA splicing endonuclease; increased transcription is observed upon fluphenazi
Putative tRNA splicing endonuclease subunit; mutation confers hypersensitivity to toxic ergosterol analog a
Protein with similarity to permeases; Sfu1-repressed; flucytosine induced; induced by Mnl1 under weak acid
Putative 3-phosphoserine aminotransferase; predicted role in serine and glycine biosynthesis; protein prese
Ortholog(s) have phosphoserine phosphatase activity and role in L-serine biosynthetic process
Predicted enzyme of amino acid biosynthesis; Gcn4p-regulated; upregulated in biofilm; protein present in ex
Seryl-tRNA synthetase; charges the tRNA that recognizes the CUG codon, which typically specifies Leu, bu
Lysine histone methyltransferase; methylates histone H3 K4; regulates of white-opaque switch, epithelial ce
Ortholog(s) have histone methyltransferase activity (H3-K36 specific) activity
NAD-dependent histone deacetylase; mutations affect filamentous growth; genetic evidence suggests Set3
Ortholog of S. cerevisiae Set6, a SET domain protein of unknown function; Hap43-induced; rat catheter and
Putative succinate-fumarate transporter; involved in repression of growth on sorbose; alkaline induced; rat c
Putative phosphatidylinositol transporter; rat catheter and Spider biofilm repressed

Putative centrin-binding protein; predicted role in spindle pole body duplication; induced by alpha pheromon
Transcription factor involved in negative regulation of morphogenesis, flocculation and virulence; induced in
Transcription factor involved in regulation of morphogenesis; regulates transcription in response to carbon
C2H2 transcription factor involved in regulation of biofilm formation; regulates carbon source-dependent str
Putative Golgi v-SNARE; Plc1-regulated; Spider biofilm induced
Putative membrane protein; transcript regulated by Mig1; Spider biofilm induced
GATA-type transcription factor; regulator of iron-responsive genes; represses iron utilization genes if iron is
Putative glucoamylase; induced in oralpharyngeal candidasis; rat catheter and Spider biofilm induced
Predicted small ribosomal subunit biogenesis protein; repressed in core stress response; transcript increas
Putative multidrug resistance factor; induced in low iron; regulated by Sef1, Sfu1, and Hap43
Component of the spindle checkpoint; cell-cycle regulated periodic mRNA expression
RecQ-related DNA helicase; Bloom's syndrome-related gene; haploinsufficient for wild-type lifespan; upregu
Putative co-chaperone protein with a predicted role in kinetochore assembly; mutation confers hypersensiti
Putative small tetratricopeptide repeat (TPR)-containing protein; protein abundance is affected by URA3 ex
Putative ser/thr kinase involved in glucose transport; Tn mutation affects filamentous growth; fluconazole-in
mRNA-binding protein that localizes specific mRNAs to daughter yeast cells and to hyphal tips; required for
Protein with similarity to S. cerevisiae She9p, which inhibits growth when overproduced; gene has possible
Mitochondrial serine hydroxymethyltransferase; complements the glycine auxotrophy of an S. cerevisiae sh
Cytoplasmic serine hydroxymethyltransferase; complements glycine auxotrophy of S. cerevisiae shm1 shm
Regulator of the type 1 protein phosphatase Glc7p activity, involved in control of morphogenesis, progressi
Cytochrome c oxidase biosynthesis protein; transcript regulated by Nrg1 and Mig1
Putative U3 snoRNP protein; Hap43p-induced gene; physically interacts with TAP-tagged Nop1p
Adhesin-like protein; involved in cell wall maintenance, redundant with Sun41; possibly secreted; macropha
Protein similar to S. cerevisiae Sin3p (transcriptional corepressor involved in histone deacetylase recruitme
Protein of unknown function; flow model, rat catheter and Spider biofilm induced
Histone deacetylase, sirtuin, required for wild-type lifespan, asymmetric inheritance of oxidatively damaged
Putative Type II HSP40 co-chaperone; macrophage/pseudohyphal-repressed; heavy metal (cadmium) stres
Transporter of ferrichrome siderophores, not ferrioxamine B; required for human epithelial cell invasion in v
Serine/threonine protein phosphatase catalytic subunit; has a role in cell wall maintenance, hyphal growth,
Putative protein phosphatase of the PTP family (tyrosine-specific), similar to S. cerevisiae Siw14p; mutant
Possible SUMO/Smt3 ligase; Rim101-repressed
Ortholog(s) have role in endoplasmic reticulum unfolded protein response, nuclear-transcribed mRNA cata
Ortholog(s) have role in nuclear-transcribed mRNA catabolic process, 3'-5' exonucleolytic nonsense-media
Ortholog(s) have role in cellular protein-containing complex assembly, nuclear-transcribed mRNA catabolic
Protein with a role in beta-1,6-glucan synthesis; probable N-glycosylated type II membrane protein; transcri
Protein with a potential role in beta-1,6 glucan biosynthesis; similarity to Kre6 and Skn1; possibly essential,
Putative homolog of S. cerevisiae Skn7p, which is predicted to be a response regulator protein in a phosph
bZIP transcription factor involved in cell wall damage response; represses the yeast-to-hypha transition; mu
Putative subunit D of kinetochore protein complex CBF3; regulated by Gcn4p; repressed in response to am
Protein required for assembly of the cortical actin cytoskeleton; contains three SH3 domains; transcription i
Actin binding protein with roles in growth control and morphogenesis; required for alkaline pH-induced hyph
Putative fatty acyltransferase; protein repressed during the mating process
Sphingolipid delta-8 desaturase; catalyzes desaturation at C8 in the long-chain base moiety of ceramides i
Putative GINS complex subunit; cell-cycle regulated periodic mRNA expression
Putative polysome-associated RNA binding protein; macrophage-induced gene
Alkaline-induced protein of plasma membrane; affects cell aggregation, cell wall; similar to S. cerevisiae Sl
Ortholog(s) have role in TOR signaling, actin cytoskeleton organization, actin filament bundle assembly, eis
Histidine kinase involved in a two-component signaling pathway that regulates cell wall biosynthesis; mutan
Protein similar to stomatin mechanoreception protein
Protein similar to mammalian SR-like RNA splicing factor; involved in filamentous growth and virulence; ge
Protein similar to S. cerevisiae RNA splicing factor, Slu7; induced by alpha pheromone in SpiderM medium
Protein involved in ER-to-Golgi transport; rat catheter and Spider biofilm induced
Protein similar to chromosomal ATPases; RNA abundance regulated by tyrosol and cell density; cell-cycle
Protein similar to S. cerevisiae Smc2p, which is a component of the condensin complex involved in mitotic
Protein similar to S. cerevisiae Smc3p, which is an ATPase involved in sister chromatid cohesion; likely to
Ortholog(s) have ATPase, DNA/DNA annealing activity, chromatin binding, double-stranded DNA binding,
Protein similar to S. cerevisiae Smc5p, which is involved in DNA repair; transposon mutation affects filame
Putative structural maintenance of chromosomes (SMC) protein; Hap43-induced; cell-cycle regulated perio
Putative Core Sm protein; Hap43p-induced gene; flucytosine induced
Putative core snRNP protein; induced upon adherence to polystyrene
Ortholog of S. cerevisiae Smf1; manganese transporter; Gcn4-regulated; Hap43, alkaline induced; caspofu
Putative vacuolar iron transporter; alkaline upregulated; caspofungin repressed; induced by Mnl1 under we
Cell wall biosynthesis protein; Hap43, caspofungin-repressed; Cyr1-induced in hyphal cells; reduced biofilm
Putative cell wall assembly regulatory protein; Rim101-repressed; possibly an essential gene, disruptants n

Putative dihydrouridine synthase; Hap43-induced gene; rat catheter biofilm induced; Spider biofilm induced
Putative Mg2+-dependent phosphatidate phosphatase; transcript regulated by Nrg1
Mannosyltransferase of glycosylphosphatidylinositol (GPI) biosynthesis; catalyzes mannosylation of Man3-G
SUMO, small ubiquitin-like protein; Smt3p-conjugated proteins localize to septation site and mother side of
Component of heteroheptameric complexes (Lsm1p, Lsm8p) involved in RNA processing and decay; flucyt
Functional homolog of S. cerevisiae Snf1p, which regulates sugar metabolism; constitutively expressed; Th
Protein involved in transcriptional regulation; ortholog of S. cerevisiae Snf2p, which is the catalytic subunit o
Putative subunit of the AMP-activated Snf1p kinase; ortholog of S. cerevisiae Snf4; caspofungin repressed;
SWI/SNF chromatin remodeling complex subunit involved in transcriptional regulation; mutants have defect
ESCRT III complex protein; role in proteolytic activation of Rim101 and Rim8 processing/activation; separal
Putative membrane transporter; Hap43p-induced gene; mutation confers hypersensitivity to toxic ergosterol
Putative membrane transporter; Hap43-induced; inducd by Mnl1p under weak acid stress; shows Mob2-dep
Ribosome-associated protein predicted to function in protein synthesis; 1 predicted transmembrane domain
Protein similar to RNase MRP RNA binding protein; ciclopirox olamine induced; regulated by Sef1, Sfu1, an
Protein with a predicted role in pyridoxine metabolism; stationary phase protein; regulated by Tup1, Efg1; S
Putative U6 snRNA-associated protein; transcript regulated by Mig1
Protein similar to S. cerevisiae Snq2p transporter; member of PDR subfamily of ABC family; transposon mu
Ortholog of S. cerevisiae Snt1; an NAD-independent histone deacetylase; heterozygous transposon mutatio
Protein similar to S. cerevisiae Snu114p, which is an RNA helicase involved in pre-mRNA splicing; likely to
Putative sorting nexin; induced during the mating process
Stationary phase protein; vitamin B synthesis; induced byyeast-hypha switch, 3-AT or in azole-resistant stra
Cytosolic copper- and zinc-containing superoxide dismutase; role in protection from oxidative stress; require
Mitochondrial Mn-containing superoxide dismutase; protection against oxidative stress; homotetramer activ
Cytosolic manganese-containing superoxide dismutase; protects against oxidative stress; repressed by cicl
Cu-containing superoxide dismutase; role in response to host innate immune ROS; regulated on white-opa
Cu-containing superoxide dismutase; protects against oxidative stress; induced by neutrophils, hyphal grow
Copper-containing superoxide dismutase; gene family includes SOD1, SOD4, SOD5, and SOD6; gene may
Putative protein with a predicted role in 40S ribosomal subunit biogenesis; rat catheter biofilm induced
Leucine-rich-repeat domain protein of RAM cell wall integrity signaling network; role in cell separation, azole
Subunit of the RNA polymerase II mediator complex; involved in control of cytokinesis, morphogenesis, biof
Protein kinase required for degradation of Nrg1p; mutants are sensitive to growth on hydrogen peroxide me
Cell cycle regulator; partial functional homolog of S. cerevisiae Sic1p; protein degradation regulated by SCF
Putative 6-phosphogluconolactonase; present in exponential and stationary growth phase yeast cultures; m
Enzyme involved in utilization of L-sorbose; has sorbitol dehydrogenase, fructose reductase, and sorbose re
Protein similar to Sou1; not required for utilization of L-sorbose; Spider biofilm induced
Protein involved in cell polarity, Spitzenkorper formation; required for mouse virulence; localizes to hyphal ti
Putative AdoMet-dependent methyltransferase; Hap43-induced; repressed by prostaglandins; possibly esse
Putative ATP-dependent RNA helicase; flucytosine repressed; Spider biofilm induced
Essential subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kineto
Signal peptidase complex component; role in ER protein translocation; transcript is induced upon filamento
Essential protein; similar to S. cerevisiae Spc3p, a component of the signal peptidase complex required for
Subunit of the Dam1 (DASH) complex, which acts in chromosome segregation by coupling kinetochores to
Putative component of the microtubule-nucleating Tub4p (gamma-tubulin) complex; periodic mRNA expres
Ornithine decarboxylase; enzyme of polyamine biosynthesis; mutant is viable; functionally complements pol
Putative S-adenosylmethionine decarboxylase; Hap43-induced gene; possibly adherence-induced; Spider b
Putative spermidine synthase; predicted role in pantothenate and spermidine biosynthesis; Spider biofilm re
P-type calcium-transporting ATPase, involved in control of calcium homeostasis, response to ER stress, hy
Protein similar to S. cerevisiae Spl1p, which is involved in tRNA splicing; member of pyridoxal-phosphate-de
Protein similar to phospholipase B; fungal-specific (no human or murine homolog)
DNA endonuclease; required for genetic recombination between homologous chromosomes during the para
Ortholog(s) have role in positive regulation of protein sumoylation, regulation of synaptonemal complex ass
Putative regulatory subunit of Nem1-Spo7 phosphatase holoenzyme that regulates nuclear growth by contro
Protein described as similar to S. cerevisiae sporulation protein; ortholog of S. cerevisiae Atg2, an autophag
Ortholog(s) have role in ascospore formation, ascospore wall assembly
Putative histone methyltransferase; induced by nitric oxide independent of Yhb1p; cell-cycle regulated perio
Putative GPI-anchored protein; similar but not orthologous to S. cerevisiae Spr1, a sporulation-specific exo-
Septin; similar to S. cerevisiae meiotic/sporulation septin; mutant has no obvious phenotype; two introns wit
Septin; mutant has no obvious phenotype
Peroxisomal 2,4-dienoyl-CoA reductase; stationary phase enriched protein; Spider biofilm induced
Ortholog(s) have promoter-specific chromatin binding, sequence-specific DNA binding activity
Putative DNA-binding transcription factor; predicted role in regulation of biogenesis of the cell wall; upregula
Putative transcription factor; downregulated upon adherence to polystyrene; flucytosine repressed
Protein involved in regulation of unsaturated fatty acid biosynthesis; controls the expression of the Ole1p de
Functional homolog of S. cerevisiae Spt3p; required for virulence in mouse systemic infection; homozygous

Protein similar to S. cerevisiae Spt5p transcription elongation factor; transposon mutation affects filamentou
Putative transcription elongation factor; transposon mutation affects filamentous growth; transcript induced
Putative SAGA transcriptional regulatory complex subunit; mutation confers hypersensitivity to toxic ergoste
Essential GDP-mannose pyrophosphorylase; makes GDP-mannose for protein glycosylation; functional in
Putative RNA polymerase II mediator complex subunit; early-stage flow model biofilm induced
Subunit of the RNA polymerase II mediator complex; transposon mutation affects filamentous growth; supp
Sur7 family protein with PalI-like domains; not required for stress responses; mutant is viable
Protein with a predicted role in docking and fusion of post-Golgi vesicles with the plasma membrane; filame
Signal recognition particle (SRP) receptor alpha subunit; involved in SRP-dependent protein targeting; rat c
Putative chaperone of small nucleolar ribonucleoprotein particles; macrophage/pseudohyphal-induced; rat
Putative signal recognition particle (SRP) subunit; induced in ssr1 null; Spider biofilm repressed
Two-component system response regulator; involved in stress response; Plc1-regulated; upregulated in cyr
Ortholog(s) have dehydrodolichyl diphosphate synthase activity, prenyltransferase activity, role in dolichol bi
Adenylate cyclase-associated protein; regulates adenylate cyclase activity; required for wild-type germ tube
HSP70 family chaperone; cell wall fractions; antigenic; beta-defensin peptides impport; ATPase domain bin
HSP70 family heat shock protein; mRNA in yeast and germ tubes; at yeast cell surface, not hyphae; antigen
Heat shock protein; at yeast-form cell surface, not hyphae; antigenic; Gcn4-regulated; induced by amino ac
Protein with role in resistance to host antimicrobial peptides; virulence role in murine infection; functional ho
Protein involved in ribosome biogenesis; ortholog of S. cerevisiae Ssf1; Hap43-induced; rat catheter and Sp
Protein with a role in protein translocation across membranes
Response regulator of two-component system; role in oxidative stress response, cell wall biosynthesis, viru
MAP kinase kinase kinase (MAPKKK); regulates Hog1 activation and signaling; repressed by ciclopirox ola
Putative cyclin-dependent protein kinase; with protein phosphatase Ptc2p controls hyphal elongation throug
Functional homolog of S. cerevisiae Cyc8/Ssn6; hyphal growth regulator; repressed during hyphal growth;
Ortholog of S. cerevisiae Ssn8; a component of RNA polymerase II holoenzyme; mutants are viable and ar
Plasma membrane t-SNARE; involved in fusion of secretory vesicles at the plasma membrane
Putative flavin-containing monooxygenase; F-12/CO2 early biofilm induced
Beta-glucan associated ser/thr rich cell-wall protein with a role in cell wall structure; GPI anchor; highly muta
Predicted regulator of G-protein signaling in mating pathway; null mutation causes alpha-factor hypersensiti
Protein similar to S. cerevisiae Ssu1 sulfite transport protein; Tn mutation affects filamentous growth; regula
Ortholog(s) have RNA polymerase II CTD heptapeptide repeat phosphatase activity, phosphoprotein phosp
Predicted adaptor protein involved in activation of MAP kinase-dependent signaling pathways; links respons
Amino acid sensor; required for wild-type hyphal growth on solid serum or Lees media, not under all conditi
Ortholog(s) have serine-type endopeptidase activity, role in protein autoprocessing, protein processing, res
Putative HSP70 chaperone; protein level decreases in stationary phase cultures; Spider biofilm repressed
Putative SIN3-binding protein 3 homolog; caspofungin induced; macrophage/pseudohyphal-repressed; rat
Putative transcription factor with zinc cluster DNA-binding motif; hyperactive mutation causes YOR1 overex
Putative transcription factor; involved in control of glucose-regulated gene expression; repressed by Rgt1;
Protein similar to S. cerevisiae Ste11p; mutants are sensitive to growth on H2O2 medium
Putative pheromone-processing dipeptidyl aminopeptidase; possible Kex2 substrate; transposon mutation
Protein similar to S. cerevisiae Ste18p; expressed in opaque or white MTLa/MTLa or MTLalpha/MTLalpha,
Receptor for alpha factor mating pheromone, MFalpha; required for a-type cells to respond to alpha factor,
Ortholog of S. cerevisiae Ste23 metalloprotease; role in N-terminal processing of pro-a-factor to the mature
Prenyl-dependent protease
Protein similar to S. cerevisiae Ste3p, the receptor for a-factor mating pheromone; alpha mating-type-speci
Beta subunit of heterotrimeric G protein of mating signal transduction pathway; required for mating; transcri
Protein with sterile alpha motif (SAM) and Ras-associated domain (RAD); similar to S. cerevisiae Rad50p,
Protein involved in ATP biosynthesis; repressed in hyphae; repressed by Efg1, Hap43; transcript upregulate
Protein that interacts with Cdc37 and Crk1 in two-hybrid; may be involved in Cdc37 chaperone activity; solu
Protein involved in telomere maintenance; forms a complex with Ten1p
Transcription factor; regulates SAP2, OPT1 expression and thereby protein catabolism for nitrogen source;
Amino-acid-regulated transcription factor; activates transcription of amino acid permease genes; activated
C2H2 transcription factor; induced in core caspofungin response; colony morphology-related gene regulatio
Ortholog(s) have cystathionine gamma-synthase activity and role in sulfur compound metabolic process, tra
Putative oligosaccharyltransferase complex component; flow model and rat catheter biofilm repressed
Putative phosphatidylinositol-4-kinase
Predicted subunit a of vacuolar proton-translocating ATPase V0 domain, Golgi isoform
Transcription factor TFIIB; required for transcription initiation and start site selection by RNA polymerase II;
Predicted transcription factor; induced during planktonic growth, whereas related SUA71 is downregulated
Putative TREX complex component with a predicted role in nuclear mRNA export; transcription is regulated
Zinc-finger transcription factor; regulates alpha-glucosidase exression; complements S. cerevisiae suc2 for
Putative translation initiation factor; flucytosine induced; genes encoding ribosomal subunits, translation fac
Translation initiation factor eIF2, alpha chain; genes encoding ribosomal subunits, translation factors, and t
Putative translation initiation factor; genes encoding ribosomal subunits, translation factors, and tRNA synth

Putative sulfate transporter; transcript negatively regulated by Sfu1; amphotericin B induced; F-12/CO2 and
Cell wall glycosidase; role in biofilm formation and cell separation; possibly secreted; hypoxia, hyphal induce
Translation factor eRF3; shows prion-like aggregation in some, not all, studies; partially complements S. ce
Putative ceramide hydroxylase; predicted enzyme of sphingolipid biosynthesis; regulated by Tsa1, Tsa1B u
Protein required for normal cell wall, plasma membrane, cytoskeletal organization, endocytosis; localizes to
Zn2Cys6 transcription factor involved in sterol uptake; flow model biofilm induced; Spider biofilm repressed
RNA helicase; with exonuclease Msu1p forms a two-component complex (mtEXO) responsible for mitocho
Putative survival factor; stationary phase enriched protein; fluconazole-induced; regulated by Gcn4p; repres
Subunit of the NuA4 histone acetyltransferase complex
Ortholog(s) have histone methyltransferase activity (H3-K4 specific) activity
Ortholog(s) have histone methyltransferase activity (H3-K4 specific) activity and role in histone H3-K4 meth
Ortholog(s) have histone methyltransferase activity (H3-K4 specific) activity and role in chromatin silencing
Putative protein kinase with a role in control of growth and morphogenesis, required for full virulence; muta
Protein involved in transcription regulation; ortholog of S. cerevisiae Swi1p, which is a subunit of the SWI/S
Putative component of the SBF transcription complex involved in G1/S cell-cycle progression; periodic mR
Putative component of the MBF and SBF transcription complexes involved in G1/S cell-cycle progression;
Component of the SWR1 complex, which has a role in exchanging histone variant H2AZ for histone H2A in
Ortholog(s) have role in signal transduction and plasma membrane localization
Putative endosomal SNARE; role in protein transport; rat catheter and Spider biofilm induced
Putative Golgi integral membrane protein; transcript regulated by Mig1
Protein similar to S. cerevisiae Sys3p; putative role in endosome-Golgi vesicle docking; upregulated in biofi
Zn(2)-Cys(6) transcriptional activator of drug-responsive genes (CDR1 and CDR2); binds DRE element; ge
YEATS domain-containing protein involved in transcription regulation; TFIIF and TFIID subunit; detects crot
Protein similar to S. cerevisiae Taf145p, a component of RNA polymerase II transcription factor TFIID; flucy
Putative TFIID subunit; mutation confers hypersensitivity to amphotericin B; rat catheter biofilm induced
Putative TFIID subunit; mutation confers hypersensitivity to toxic ergosterol analog
Putative TFIID and SAGA complex subunit; mutation confers hypersensitivity to amphotericin B
Transaldolase; protein present in exponential and stationary growth phase yeast cultures; oxidative stress-i
Ortholog of S. cerevisiae Tar1p; Transcript Antisense to Ribosomal RNA; encoded within the 25S rRNA ge
Putative lyso-phosphatidylcholine acyltransferase, required for normal phospholipid content of mitochondria
Essential transcription factor; induces ribosomal protein genes and the rDNA locus; acts with Cbf1 at subse
Transcription initiation factor; binds TATA box sequence, binding does not require TFIIA; caspofungin repre
Putative transcription factor/corepressor; regulation of filamentation and virulence; interacts with Tup1; regu
Putative homolog of S. cerevisiae Tco89p, which is a component of the TOR C1 complex that is involved in
Chaperonin-containing T-complex subunit, induced by alpha pheromone in SpiderM medium; stationary ph
NAD-linked glyceraldehyde-3-phosphate dehydrogenase; binds fibronectin, laminin; at cell surface; antigeni
Putative transcription factor with zinc cluster DNA-binding motif; has similarity to S. cerevisiae Tea1p; Hap4
TEA/ATTS transcription factor; white cell pheromone response, hyphal gene regulation; required for Spider
Translation elongation factor 1-alpha; at cell surface; binds human plasminogen; macrophage/pseudohyph
Translation elongation factor 1-alpha; genes encoding ribosomal subunits, translation factors, and tRNA sy
Putative translation elongation factor; genes encoding ribosomal subunits, translation factors, and tRNA sy
Ortholog(s) have protein kinase activity, protein serine/threonine kinase activity, telomeric DNA binding acti
Putative GTPase involved in mitotic exit and cytokinesis; induced under Cdc5p depletion
Protein involved in telomere maintenance; forms a complex with Stn1; transcription is regulated upon yeast
Putative protein phosphatase of the PTP family (tyrosine-specific), similar to S. cerevisiae Tep1p
Telomerase reverse transcriptase; catalytic protein subunit of telomere synthesis; essential for telomerase
Putative acyl-CoA thioesterase
Putative acyl-CoA thioesterase; Hap43-repressed; Spider biofilm induced
Protein with polyglutamate motifs and abundant Ser/Thr residues; described as a subunit of TFIIE, which is
Putative C3HC4 zinc finger transcription factor; transcript positively regulated by Tbf1; Spider biofilm induce
Putative RNA polymerase III transcription initiation factor complex (TFIIIC) subunit; induced by Mnl1 under
Protein similar to S. cerevisiae Tfg1p, which is part of transcription factor TFIIF; transposon mutation affect
Subunit of vacuolar H+-ATPase; stationary phase enriched protein; sumoylation target; Spider biofilm repre
Putative carboxypeptidase y inhibitor; transcript regulated upon yeast-hypha switch; colony morphology-rela
Has domain(s) with predicted role in lipid metabolic process
tRNA guanylyltransferase, with role in tRNA modification; catalyzes reverse (3'-5') nucleotide polymerizatio
Thiamin pyrimidine synthase; synthesis of the thiamine precursor hydroxymethylpyrimidine phosphate; sing
Putative trifunctional enzyme of thiamine biosynthesis, degradation and salvage; Spider biofilm induced
Thiamine biosynthetic enzyme precursor; repressed during the mating process; stationary phase enriched
Putative thiamin-phosphate pyrophosphorylase, hydroxyethylthiazole kinase; fungal-specific; Spider biofilm
Putative homoserine kinase; regulated by Tup1; amphotericin B repressed; regulated by Gcn2 and Gcn4; S
Putative threonine synthase; protein present in exponential and stationary growth phase yeast cultures; Gc
Putative threonyl-tRNA synthetase; transcript regulated by Mig1 and Tup1; repressed upon phagocytosis b
Translation initiation factor; upregulated in highly virulent strain compared to less virulent strain; antigenic in

Translation initiation factor eIF1a; possibly transcriptionally regulated upon hyphal formation; genes encodi
Putative translation initiation factor; genes encoding ribosomal subunits, translation factors, and tRNA synth
Putative translation initiation factor eIF3, p39 subunit; mutation confers hypersensitivity to roridin A, verruca
Putative translation initiation factor; repressed upon phagocytosis by murine macrophage; Spider biofilm re
Putative translation initiation factor eIF4G; overexpression causes hyperfilamentation; hyphal- and macroph
Putative translation initiation factor; repressed upon phagocytosis by murine macrophage; Spider biofilm re
Predicted protein of the mitochondrial intermembrane space with role in protein import into mitochondrial in
Predicted component of the TIM22 complex, involved in protein import into mitochondrial inner membrane;
Predicted mitochondrial intermembrane space protein with a role in protein import into mitochondria
Predicted component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex), involved i
Component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); for protein import in
Mitochondrial inner membrane protein; predicted role in protein import; Hap43-repressed gene; flow model
Protein involved in mitochondrial matrix protein import
Protein involved in transport across membranes; Spider biofilm repressed
Predicted component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); involved i
Predicted component of the mitochondrial TIM22 complex; involved in protein import into mitochondrial inne
Predicted mitochondrial intermembrane space protein with role in protein import into mitochondrial inner me
Predicted protein of the mitochondrial intermembrane space; rat catheter biofilm induced; Spider biofilm re
Protein with a predicted role in biogenesis of ER-derived COPII transport vesicles; mutation confers hypers
Protein similar to human CAND1 (Cullin-Associated Nedd8-Dissociated) protein involved in regulation of S
Protein interacting with Sec20p, possibly involved in retrograde transport between the Golgi and the endopl
Protein involved in TOR signaling pathway; regulates protein phosphatase 2A (PP2A) activity; regulates Ra
Putative transketolase; localizes to surface of yeast cells, not hyphae; soluble protein in hyphae; transcript
Putative syntaxin-like t-SNARE; macrophage/pseudohyphal-repressed
Member of a family of telomere-proximal genes of unknown function; hypha-induced expression; rat cathet
Member of a family of telomere-proximal genes of unknown function
Member of a family of telomere-proximal genes of unknown function; may be spliced in vivo
Member of a family of telomere-proximal genes of unknown function; may be spliced in vivo; overlaps orf19
Member of a family of telomere-proximal genes of unknown function; may be spliced in vivo
Non-telomeric member of a family of telomere-proximal genes of unknown function; predicted N-terminus i
Member of a family of telomere-proximal genes of unknown function; transcript induced in an RHE model o
Member of a family of telomere-proximal genes of unknown function; may be spliced in vivo
Member of a family of telomere-proximal genes of unknown function; may be spliced in vivo; rat catheter bi
Member of a family of telomere-proximal genes of unknown function; may be spliced in vivo
Member of a family of telomere-proximal genes of unknown function; Hap43p-repressed gene
Cell wall protein, ortholog of S. cerevisiae Tma19p (Ykl065cp)
Putative nicotinic acid transporter; detected at germ tube plasma membrane by mass spectrometry; transcr
Putative TFIIA small subunit; protein abundance decreased in CAI4 strain compared to the SC5314 strain,
Outwardly rectifying, noisily gated potassium channel; modulates sensitivity to human salivary histatin (Hst5
Putative E3 ubiquitin ligase; transcript regulated by Nrg1 and Mig1
Putative mitochondrial primary import receptor
Putative mitochondrial import receptor subunit; colony morphology-related gene regulation by Ssn6
Protein involved in mitochondrial protein import; Spider biofilm repressed
Predicted component of the TOM (translocase of outer membrane) complex, involved in protein import into
Predicted component of the TOM (translocase of outer membrane) complex involved in protein translocatio
Ortholog(s) have mitochondrion targeting sequence binding, protein transmembrane transporter activity
DNA topoisomerase I; required for wild-type growth and for wild-type mouse virulence; sensitive to campto
DNA topoisomerase II; catalyzes ATP-dependent DNA relaxation and decatenation in vitro; Y842 predicted
Protein similar to TOR family phosphatidylinositol kinases; mutation confers resistance to rapamycin; involv
Protein similar to alpha agglutinin anchor subunit; secreted; exogenously expressed protein is a substrate f
Putative fork-head transcription factor; rat catheter and Spider biofilm repressed
Subunit of protein serine/threonine phosphatase PPA2, involved in regulation of cytokinesis and morphoge
Triose-phosphate isomerase; antigenic in mouse/human; mutation affects filamentation; macrophage-repre
cAMP-dependent protein kinase catalytic subunit; Tpk2 isoform; involved in regulation of filamentation, phe
cAMP-dependent protein kinase catalytic subunit; isoform of Tpk1; involved in regulation of filamentation, p
Putative tropomyosin isoform 2; regulated by Gcn4; repressed by amino acid starvation; macrophage-induc
Putative polyamine transport protein; fungal-specific (no human or murine homolog)
Putative polyamine transporter; MFS-MDR family; induced by Sfu1, regulated upon white-opaque; decrease
Putative sperimidine transporter; fungal-specific (no human or murine homolog); Spider biofilm induced; pr
Putative polyamine transporter; mutation confers hypersensitivity to toxic ergosterol analog; hyphal induced
Trehalose-6-phosphate synthase; role in hyphal growth and virulence in mouse systemic infection; induced
Trehalose-6-phosphate (Tre6P) phosphatase; mutant heat sensitive, accumulates Tre6P, decreased mous
Predicted trehalose-phosphate synthase regulatory subunit; regulated by Efg1; regulated by Tsa1, Tsa1B u
tRNA 2'-phosphotransferase; enzyme of tRNA splicing; functionally complements viability of S. cerevisiae t

Subunit of the NuA4 histone acetyltransferase complex
Potassium transporter; mediates K+ and Cl- influx; role in sensitivity to cationic antimicrobial peptides, not b
Putative N2,N2-dimethylguanine tRNA methyltransferase; induced upon adherence to polystyrene
Ortholog(s) have S-adenosylmethionine-dependent methyltransferase activity, transferase activity, transferr
Putative tRNA methyltransferase; repressed by prostaglandins; Spider biofilm induced
Putative tRNA methyltransferase; repressed during the mating process
Phosphoribosylanthranilate isomerase; tryptophan biosynthesis; expected unifunctional, unlike trifunctional
Putative anthranilate synthase with a predicted role in tryptophan biosynthesis; regulated by Gcn2p and Gc
Putative bifunctional enzyme with predicted indole-3-glycerol-phosphate synthase and anthranilate synthas
Predicted enzyme of amino acid biosynthesis; upregulated in biofilm; regulated by Gcn2p and Gcn4p; S. ce
Predicted tryptophan synthase; identified in detergent-resistant membrane fraction (possible lipid raft comp
Putative thioredoxin peroxidase/alkyl hydroperoxide reductase; induced in low iron; regulated by Gcn4; indu
Thioredoxin reductase; regulated by Tsa1/Tsa1B, Hap43; induced by nitric oxide, peroxide; oxidative stress
Ortholog(s) have role in cellular protein-containing complex assembly, endoplasmic reticulum to Golgi vesic
Putative TRAPP complex subunit; constitutive expression independent of MTL or white-opaque status
Thioredoxin; involved in response to reactive oxygen species; biofilm, benomyl, flucytosine, peroxide, Hap4
Similar to thioredoxins; not expected to be enzymatically active because it lacks a canonical thioredoxin act
Transcription factor; regulator of yeast form adherence; required for yeast cell adherence to silicone substra
RING-finger transcription factor; regulator of yeast form adherence; required for yeast cell adherence to sili
C2H2 transcription factor; fluconazole-repressed; induced in ssr1 mutant; required for yeast cell adherence
Zn(II)2Cys6 transcription factor; regulator of yeast form adherence; required for yeast cell adherence to sili
Helix-loop-helix transcription factor; regulator of yeast form adherence; required for yeast cell adherence to
TSA/alkyl hydroperoxide peroxidase C (AhPC) family protein; similar to thiol-dependent peroxidases of oxid
Putative peroxidase; orf19.7398.1 is contig-truncated fragment of gene identical to TSA1; Tsa1p and Tsa1
Protein similar to S. cerevisiae Tsc11p which is involved in sphingolipid biosynthesis; transposon mutation
Putative GTPase-activating protein; similar to mammalian tuberin; involved in control of filamentous growth
Putative transcription initiation factor TFIID subunit; transcript is upregulated in clinical isolates from HIV+ p
Component of 20S pre-rRNA processing unit; repressed by prostaglandins
Protein with a predicted role in pre-rRNA processing; repressed by prostaglandins
Putative glutaredoxin; described as a glutathione reductase; induced by human neutrophils and benomyl tre
Alpha-tubulin; gene has intron; complements cold-sensitivity of S. cerevisiae tub1 mutant; C. albicans has s
Beta-tubulin; functional homolog of ScTub2; overproduction makes S. cerevisiae inviable; has two introns;
Putative gamma-tubulin; induced upon adherence to polystyrene; transcript regulated by Nrg1 and Mig1; pe
Translation elongation factor TU; macrophage/pseudohyphal-induced; repressed upon phagocytosis by mu
Transcriptional corepressor; represses filamentous growth; regulates switching; role in germ tube induction
Putative guanine nucleotide exchange factor; induced by Mnl1 under weak acid stress; Spider biofilm induc
Putative integral membrane protein; fluconazole-induced
bHLH transcription factor; control of glycolysis; required for biofilm formation; hyphally regulated by Cph1, C
Putative prepephenate dehydrogenase; enzyme of tyrosine biosynthesis; fungal-specific (no human or muri
Putative tRNA-Tyr synthetase; downregulated upon phagocytosis by murine macrophages; stationary phas
UDP-N-acetylglucosamine pyrophosphorylase, catalyzes biosynthesis of UDP-N-acetylglucosamine from U
Ubiquitin-activating enzyme; protein level decreases in stationary phase cultures
Ortholog(s) have SUMO activating enzyme activity, role in protein sumoylation and SUMO activating enzym
Putative ubiquitin activating protein; Hap43-repressed; induced by prostaglandins; clade-associated gene e
Putative E2 ubiquitin-conjugating enzyme
Ortholog(s) have proteasome binding, protein-macromolecule adaptor activity, ubiquitin binding, ubiquitin c
Predicted ubiquitin-conjugating enzyme that negatively regulates gluconeogenesis by mediating the glucos
Fusion of ubiquitin with the S34 protein of the small ribosomal subunit; mRNA decreases upon heat shock,
Ubiquitin precursor (polyubiquitin) contains 3 tandem repeats of the ubiquitin peptide that are processed to
Ortholog(s) have thiol-dependent deubiquitinase activity, role in negative regulation of protein autoubiquitin
Ortholog of S. cerevisiae Ubp13; putative ubiquitin carboxyl-terminal hydrolase; flow model biofilm induced;
Putative ubiquitin-specific protease of the 26S proteasome; oxidative stress-induced via Cap1p
Protein similar to S. cerevisiae Ubr1p ubiquitin-protein ligase; regulates stability of Ume6p in response to o
Upregulated by cAMP in filamentous growth; induced in high iron, decreased upon yeast-hypha switch; dow
Protein required for damage to oral epithelial cells and for normal hyphal growth and stress resistance; tran
Protein interacting with Sec20p, possibly involved in retrograde transport between the Golgi and the endopl
Putative GABA transaminase; transcription regulated by Mig1 and Tup1; stationary phase enriched protein;
Putative gamma-aminobutyrate (GABA) transaminase; macrophage-induced; overlaps orf19.854.1, which i
Predicted succinate semialdehyde dehydrogenase; predicted role in glutamate catabolism; transcription reg
Zn(II)2Cys6 transcription factor; required for utilization of gamma-aminobutyrate (GABA) as a nitrogen sour
Predicted Zn(II)2Cys6 transcription factor; has similarity to S. cerevisiae Uga3, a transcription factor involve
Zinc-finger transcription factor; similar to S. cerevisiae Uga3 which regulates gamma-aminobutyrate metab
Putative gamma-aminobutyric acid/polyamine permease; nitrogen catabolite repressed gene, induced in ab
Putative GABA-specific permease; decreased transcription is observed upon benomyl treatment or in an a

UTP-glucose-1-phosphaturidyl transferase; localizes to yeast, not hyphal cell surface; Hog1-repressed; stat
UDP-glucose:sterol glucosyltransferase; enzyme of sterol glucoside (membrane-bound lipid) biosynthesis;
SUMO deconjugation enzyme that cleaves the small ubiquitin-like modifier (SUMO) off proteins
SUMO deconjugation enzyme; removes the small ubiquitin-like modifier (SUMO) from proteins; Spider biofi
SUMO deconjugation enzyme that removes the small ubiquitin-like modifier (SUMO) from proteins
Ortholog of C. dubliniensis CD36 : Cd36_73630, C. parapsilosis CDC317 : CPAR2_805330, C. auris B844
Zn(II)2Cys6 transcription factor; has a long 5'-UTR that regulates translational efficiency and controls transi
Putative transcription factor with zinc cluster DNA-binding motif; similar to S. cerevisiae Ume6p, which is a
Zn2-Cys6 transcript factor; regulator of ergosterol biosynthetic genes and sterol uptake; binds ERG2 promo
Dihydroorotate dehydrogenase; de novo pyrimidine biosynthesis; regulated by yeast-hypha switch, Nrg1/Mi
Putative bifunctional carbamoylphosphate synthetase-aspartate transcarbamylase; flucytosine induced; ma
Orotidine-5'-phosphate decarboxylase; pyrimidine biosynthesis; gene used as genetic marker; decreased e
Dihydroorotase; protein present in exponential and stationary growth phase yeast cultures
Putative orotate phosphoribosyltransferase; protein abundance is affected by URA3 expression in the CAI-
Ortholog(s) have adenylate kinase activity, uridylate kinase activity, role in 'de novo' pyrimidine nucleobase
CTP synthase 1; flucytosine induced; protein present in exponential and stationary growth phase yeast cultu
Functional homolog of S. cerevisiae Ure2p, which is a regulator of nitrogen utilization, and which also has a
Protein similar to uridine kinase; repressed by ciclopirox olamine; Spider biofilm induced
Ortholog(s) have role in Golgi vesicle docking, SNARE complex assembly, endoplasmic reticulum to Golgi
Kinesin-associated protein; forms heterodimer with Kar3; involved in spindle formation; transcription is indu
Putative vesicular transport protein; transcript induced by filamentous growth; rat catheter biofilm repressed
Putative U3 snoRNA-associated protein; Hap43-induced; repressed in core stress response; physically inte
Small subunit (SSU) processome component; mutation confers resistance to 5-fluorocytosine (5-FC); physi
Putative U3 snoRNA-associated protein; Hap43-induced; repressed in core stress response; physically inte
Putative snoRNA-binding protein; S. cerevisiae Utp20 ortholog; likely essential for growth; repressed in core
Putative U3 snoRNP protein; Hap43-induce; physically interacts with TAP-tagged Nop1; Spider biofilm indu
Putative U3 snoRNP protein; Ssr1-induced; repressed by prostaglandins; heterozygous null mutant is resist
Putative U3 snoRNA-associated protein; Hap43-induced; physically interacts with TAP-tagged Nop1; Spide
Putative U3 snoRNA-associated protein; Hap43p-induced gene; mutation confers resistance to 5-fluorocyto
Essential nucleolar protein; involved in tRNA export from the nucleus and ribosomal small subunit biogenes
Small-subunit processome protein; Ssr1-induced; repressed by prostaglandins; physically interacts with TA
Putative GPI anchored cell wall glycosidase; role in adhesion, hyphal growth on Spider (not serum) medium
Ortholog of S. cerevisiae Vac7; integral vacuolar membrane protein involved in vacuole inheritance and mo
Protein involved in vacuolar inheritance; required for hyphal growth; contains armadillo repeats
Predicted syntaxin-like vacuolar t-SNARE, involved in vacuolar inheritance
Member of Mnn9 family of mannosyltransferases; ortholog of S. cerevisiae Van1p; fungal-specific (no huma
Putative tRNA-Val synthetase; genes encoding ribosomal subunits, translation factors, and tRNA synthetas
Putative H+/Ca2+ antiporter; Spider biofilm repressed
Subunit of the NuA4 histone acetyltransferase complex; soluble protein in hyphae; Spider biofilm repressed
Protein similar to S. cerevisiae Vid27p; transposon mutation affects filamentous growth; mutation confers h
Subunit G of the V1 peripheral membrane domain of the vacuolar H+-ATPase (V-ATPase); involved in vacu
Predicted ortholog of S. cerevisiae Tfp3/Vma11; c' subunit of the V0 subcomplex of the vacuolar ATPase;
Predicted proton-transporting ATPase; predicted role in ATP hydrolysis coupled proton transport; rat cathet
Vacuolar H(+)-ATPase; protein present in exponential and stationary growth phase yeast cultures; plasma
Ortholog(s) have unfolded protein binding activity and role in vacuolar acidification, vacuolar proton-transpo
H+ transporting ATPase E chain; transcript regulated by Mig1; caspofungin repressed; protein level decreas
Putative vacuolar H(+)-ATPase; plasma membrane localized; rat catheter biofilm repressed
Putative subunit of the V-ATPase complex, which is involved in control of vacuolar pH; highly similar to S. c
Putative vacuolar H+-ATPase subunit; regulated by Nrg1 and Mig1; transcript increases in populations of ce
Vacuolar H(+)-ATPase; transcription regulated by Nrg1, Mig1, and Tup1
Protein required for for proper vacuolar ATPase assembly and vacuolar functions
Dynamin-family GTPase-related protein; induced upon adherence to polystyrene; regulated by Gcn2p and
Protein involved in protein trafficking; putative role in vesicle-target membrane fusion; mutant lacks vacuole
Putative vacuolar protein sorting-associated protein; gene used for multilocus sequence typing
Protein involved in retrograde endosome-to-Golgi protein transport; required for normal virulence
Protein similar to S. cerevisiae Vps16p, which is involved in protein-vacuolar targeting; likely to be essential
Ortholog(s) have phosphatidylinositol-3-phosphate binding, protein carrier activity
Ortholog(s) have role in ATP export, intralumenal vesicle formation, late endosome to vacuole transport an
ESCRT III complex protein; role in multivesicular body (MVB) trafficking; required for processing of Rim8; B
Late endosomal Rab small monomeric GTPase involved in transport of endocytosed proteins to the vacuol
ESCRT-II complex protein with a role in multivesicular body (MVB) trafficking; required for processing of Ri
ESCRT I protein sorting complex protein; involved in proteolytic activation of Rim101, which regulates pH re
Protein similar to S. cerevisiae Vps24p, which is a member of the ESCRT III protein sorting complex; down
Putative ESCRT-0 complex protein with a role in multivesicular body (MVB) trafficking

ESCRT I protein sorting complex subunit; involved in Rim8 processing and proteolytic activation of Rim101
Ortholog(s) have ATP binding, phosphatidylinositol binding activity
Autophosphorylated class III phosphatidylinositol 3-kinase; required for normal vesicle transport, hyphal gro
Putative role in vacuolar sorting; downregulated in biofilm; induced upon adherence to polystyrene
ESCRT II protein sorting complex subunit; involved in Rim8 processing and proteolytic activation of Rim101
AAA-ATPase involved in transport from MVB to the vacuole and ESCRT-III complex disassembly; mutation
Protein similar to S. cerevisiae Vps41p, which is involved in vacuole organization and biogenesis; transposo
Protein with a role in vacuolar function; null mutant has defect in damaging oral epithelial and vascular endo
Protein required for hyphal growth; has similarity to S. cerevisiae Vps52p
Ortholog(s) have role in Golgi to vacuole transport, cellular sphingolipid homeostasis, retrograde transport,
Has domain(s) with predicted peptidase activity and role in proteolysis
Putative vacuolar sorting protein; downregulated upon adherence to polystyrene
GDP-mannose transporter; essential; required for glycosylation, hyphal growth; functional homolog of S. ce
Verprolin-related protein involved in actin cytoskeleton organization and polarized morphogenesis; interacts
Putative polyphosphate synthetase; downregulated in core caspofungin response; Hog1p-induced; transcri
Putative polyphosphate synthetase; decreased expression in hyphae compared to yeast-form cells; fungal-
Ortholog(s) have SNAP receptor activity and role in Golgi to vacuole transport, intra-Golgi vesicle-mediated
Protein required for hyphal growth and for wild-type cell morphology, polarized budding, endocytosis, vacuo
Zn(II)2Cys6 transcription factor; plays a role in resistance to weak organic acids; required for yeast cell adh
Putative oligosaccharyltransferase subunit; Spider biofilm repressed
White-phase yeast transcript; expression in opaques increases virulence/switching; mutant switches as WT
Putative RNA binding protein; induced during infection of murine kidney, compared to growth in vitro; has m
Transcription factor ("master switch") of white-opaque phenotypic switching; required to establish and main
Zn(II)2Cys6 transcription factor; regulator of white-opaque switching; required for maintenance of opaque s
Transcription factor; modulator of white-opaque switch; induced in opaque cells; promoter bound by Wor1;
Predicted C2H2 zinc finger protein, involved in transcriptional regulation of white-opaque phenotypic switchi
Putative tRNA-Trp synthetase; genes encoding ribosomal subunits, translation factors, tRNA synthetases a
Putative cell wall component; transcript upregulated in cyr1 mutant (yeast or hyphae); Spider and flow mode
Putative cell wall integrity and stress response protein; mRNA binds She3; Spider biofilm induced
Putative cell wall integrity and stress response subunit 4 precursor; transcription is specific to white cell type
Putative xylulokinase; Hap43-repressed; induced by prostaglandins; rat catheter biofilm repressed
Exo-1,3-beta-glucanase; 5 glycosyl hydrolase family member; affects sensitivity to chitin and glucan synthes
Putative high-affinity, high-capacity xanthine-uric acid/H+ symporter; similar to A. nidulans UapA; member o
D-xylulose reductase; immunogenic in mice; soluble protein in hyphae; induced by caspofungin, fluconazole
Ortholog(s) have protein-macromolecule adaptor activity, role in protein maturation by [4Fe-4S] cluster trans
YEATS domain-containing protein involved in transcription regulation; detects crotonylated lysine residues i
Protein similar to oxidoreductases; induced in high iron; Hap43-repressed
Predicted serine-threonine protein kinase; involved in hyphal growth regulation and biofilm formation; flow m
Putative subunit of a replication fork-pausing checkpoint complex
P-loop ATPase with similarity to human OLA1 and bacterial YchF; Spider biofilm repressed
Protein involved in response to oxidative stress, binds and stabilizes Cap1p transcription factor in response
Putative glutathione S-conjugate transporter; MRP/CFTR-subfamily, ABC type transporter; human neutroph
Putative condensin G
Plasma membrane protein similar to S. cerevisiae casein kinase I; mutation or inhibition impairs virulence a
Flavodoxin-like protein involved in oxidative stress protection and virulence; flow model, rat catheter and Sp
Putative condensin complex subunit; cell-cycle regulated periodic mRNA expression
Alkaline dihydroceramidase; involved in sphingolipid metabolism; Mob2-dependent hyphal regulation; trans
Putative type I HSP40 co-chaperone; heavy metal (cadmium) stress-induced
Putative uridine diphosphate-N-acetylglucosamine (UDP-GlcNAc) transporter; required for cell wall chitin sy
Frataxin; may be required for iron storage or delivery; role in oxidative stress resistance; transcript regulated
Nitric oxide dioxygenase; acts in nitric oxide scavenging/detoxification; role in virulence in mouse; transcript
Protein related to flavohemoglobins; not required for wild-type nitric oxide resistance; has predicted globin,
Flavohemoglobin-related protein; not required for normal NO resistance; predicted globin/FAD-binding/NAD
Putative mitochondrial carrier protein; fungal-specific (no human or murine homolog); Hap43p-repressed ge
Predicted carrier protein; exports citrate from and imports oxoglutarate into the mitochondrion; alkaline indu
Protein similar to protease of mitochondrial inner membrane; increased transcription is observed upon beno
Possible heterohexameric Gim/prefoldin protein complex subunit; role in folding alpha-tubulin, beta-tubulin,
Putative protein of the vacuolar SNARE complex; predicted role in vacuolar fusion; rat catheter biofilm repre
Yku70p-Yku80p Ku complex subunit involved in nonhomologous end joining during double-strand break rep
Putative inner mitochondrial membrane transporter; flucytosine induced; Spider biofilm repressed
Putative mitochondrial carrier protein; Gcn4-regulated; F-12/ CO2 early biofilm induced; Spider biofilm induc
Ortholog(s) have ATP-dependent peptidase activity
Putative mitochondrial ribosomal protein; induced upon adherence to polystyrene
Putative NADH dehydrogenase; macrophage-downregulated gene; induced by nitric oxide; rat catheter biof

Nucleoside diphosphate kinase (NDP kinase); homo-hexameric; soluble protein in hyphae; flucytosine indu
Protein similar to S. cerevisiae Yor1; ABC-type plasma membrane transporter involved in resistance to aur
Putative homeodomain-containing transcription factor; transcriptional repressor; periodic mRNA expression
Phosphohistidine intermediate protein in a phosphorelay signal transduction pathway; residue His69 is the
Putative aspartic-type endopeptidase with limited ability to degrade alpha pheromone; mutants show increa
Functional homolog of S. cerevisiae Ypt1p, which is an essential small Ras-type GTPase involved in protei
Protein required for resistance to toxic ergosterol analog
Rab-family GTPase involved in vacuolar trafficking, colocolizes with Vps1p and Ypt53p in late endosome
Rab-family GTPase involved in vacuolar trafficking, colocolizes with Vps1p and Ypt52p in late endosome;
Protein of YPT/RAB family; induced during the mating process
Vacuolar Rab small monomeric GTPase involved in vacuolar biogenesis; involved in filamentous growth an
Functional homolog of S. cerevisiae Yrb1p; regulates Gsp1 GTPase activity and thereby affects nucleocyto
Predicted Nudix hydrolase family member with ADP-ribose pyrophosphatase activity; role in metabolism of
Ribosome-associated protein; antigenic in mice; complements S. cerevisiae yst1 yst2 mutant; similar to lam
Protein similar to S. cerevisiae Yta6p ATPase but ortholog of S. cervisiae Sap1; transposon mutation affect
Putative mRNA cleavage and polyadenylation specificity factor; transcription is regulated upon yeast-hyphal
Protein similar to S. cerevisiae Ytm1p, which is involved in biogenesis of the large ribosomal subunit; transp
Putative ubiquitin C-terminal hydrolase; sumoylation target
Putative vacuolar cation channel shock; repressed by alpha pheromone in SpiderM medium; flow model bio
Putative dual specificity phosphatase (phosphoserine/threonine and phosphotyrosine phosphatase); require
Secreted yeast wall protein; possible role in dispersal in host; involved in adhesion and biofilm formation; pr
Zn(II)2Cys6 transcription factor; transcript regulated during hypha formation; 5'-UTR intron; mutants show d
Putative transcription factor with zinc cluster DNA-binding motif
Zn(II)2Cys6 transcription factor; required for wild-type filamentous growth; mRNA binds She3
Predicted Zn(II)2Cys6 transcription factor; similar to but not the true ortholog of S. cerevisiae Hap1; mutants
Putative Zn(II)2Cys6 transcription factor; caspofungin induced
Predicted Zn(II)2Cys6 transcription factor of unknown function; rat catheter biofilm induced
Predicted Zn(II)2Cys6 transcription factor; mutants are viable; rat catheter biofilm induced
Putative Zn(II)2Cys6 transcription factor
Putative Zn(II)2Cys6 transcription factor; heterozygous null mutant displays sensitivity to virgineone and de
Predicted Zn(II)2Cys6 transcription factor
Zn(II)2Cys6 transcription factor, required for adaptation to reactive sulfur species; regulates sulfite toleranc
Zn(II)2Cys6 transcription factor orthologous to S. cerevisiae Hap1; regulated by Sef1, Sfu1; Hap43-induced
Predicted Zn(II)2Cys6 transcription factor; mutants display increased colonization of mouse kidneys; Spider
Predicted Zn(II)2Cys6 transcription factor
Predicted Zn(II)2Cys6 transcription factor; ortholog of S. cerevisiae Gsm1; flow model biofilm induced
Predicted Zn(II)2Cys6 transcription factor; caspofungin induced; Hap43-repressed
Putative Zn(II)2Cys6 transcription factor
Zn2-Cys6 transcription factor of unknown function; induced by alpha pheromone in SpiderM medium
Putative Zn(II)2Cys6 transcription factor
Zn(II)2Cys6 transcription factor; required for yeast cell adherence to silicone substrate; Spider biofilm induc
Zn(II)2Cys6 transcription factor; mutants sensitive to caffeine, menadione, beauvericin;resistant to fenpropi
Zn(II)2Cys6 domain transcription factor; required for filamentous growth, resistance to rapamycin and flucyt
Predicted Zn(II)2Cys6 transcription factor; mutants are viable; repressed by fluphenazine; Spider biofilm ind
Zn(II)2Cys6 transcription factor of unknown function; mutant is sensitive to copper and SDS, and resistant t
Zn(II)2Cys6 transcription factor involved in regulation of biofilm formation; Hap43-repressed
Zn(II)2Cys6 transcription factor; Hap43-induced; Spider biofilm induced
Putative Zn(II)2Cys6 transcription factor
Zn(II)2Cys6 transcription factor; mutants are viable; filament induced; required for yeast cell adherence to s
Putative Zn(II)2Cys6 transcription factor
Zn(II)2Cys6 transcription factor; colony morphology-related gene regulation by Ssn6
Putative transcription factor with zinc cluster DNA-binding motif; involved in virulence
Predicted Zn(II)2Cys6 transcription factor; mutant shows reduced colony wrinkling on Spider medium and is
Predicted Zn(II)2Cys6 transcription factor; repressed by fluphenazine treatment; required for yeast cell adhe
Putative Zn(II)2Cys6 transcription factor; hypersensitive to toxic ergosterol analog ECC69 and/or ECC1384
Nonessential protein; similar to S. cerevisiae Zds1p
Zn(II)2Cys6 transcription factor; regulator of yeast form adherence; mutants display increased colonization
Zn(2)-Cys(6) transcription factor; regulated by Gcn2 and Gcn4; gene located in zinc cluster region of Chrom
Protein with putative zinc finger; regulated by Gcn4p; repressed in response to amino acid starvation (3-am
Putative zinc transporter; acts with Pra1 in sequestration of zinc from host tissues during infection; hyphal,
Zinc transporter, essential for zinc uptake and acidic conditions tolerance; transcript induced by amphoteric
Ortholog od S. cerevisiae Tis11, a mRNA-binding protein; transcription regulated by yeast-hyphal switch; flo
Ortholog of S. cerevisiae Zuo1; a cytosolic ribosome-associated chaperone; likely to be essential for growth
Glucose-6-phosphate dehydrogenase; antigenic in mice; activity induced by O2 or oxidizing agents H2O2,

growth temperatures; upregulated iby human neutrophils; protein enriched in stationary phase; Spider biofil

temic infection; localizes to hyphal septum or bud neck; Asn-rich; aberrant gel mobility; phosphorylated in v

ndothelial cell adherence and flocculence; flow model biofilm, alkaline or caspofungin induced

; Hog1, CO2-induced; chlamydospore formation repressed in C. albicans and C. dubliniensis; rat catheter

d; Spider biofilm induced

amphotericin B repressed; gene used for strain identification by multilocus sequence typing; farnesol-, Hap

uced

associated gene expression; protein levels decrease in stationary phase yeast; mutant is viable; flow model

uced; Spider biofilm induced

n domain peptide; does not bind mRNA TPase and mRNA GTase (Cet1,Cgt1); functional homolog of S. ce

tivity to cell wall stress, increased hyphal branching; essential, no mammalian homolog; Cyr1-regulated; ra

; protein only detected in stationary phase yeast-form cultures; Spider biofilm repressed

netic process

1, Tup1; Hap43-induced

ssed; 5'-UTR intron; gene used for strain identification by multilocus sequence typing; Hap43-induced; flow

erence, virulence in a mice; mutant is hyperfilamentous; rat catheter and Spider biofilm induced

ed on polystyrene adherence; farnesol-, ketoconazole-induced; no human or murine homolog; stationary p

hagocytosis, farnesol induced; Hap43, fluconazole-repressed; Gcn4-regulated; antigenic in infection; flow a

(3-AT); protein levels decrease in stationary phase yeast; flow model and Spider biofilm repressed

ted gene regulation by Ssn6p; protein newly produced during adaptation to the serum

ony morphology-related gene regulation by Ssn6; only in stationary phase cultures; rat catheter biofilm repr

d protein; soluble protein in hyphae; gene contains intron; flow model and Spider biofilm repressed

and hyphal cells; required for wild-type Cdc42 localization; unprocessed N terminus; Hap43-induced; Spide

fungin; required for the normal transcriptional response to caspofungin; required for yeast cell adherence to

uced in GCN response, unlike the S. cerevisiae ortholog; fungal-specific (no human or murine homolog); lev

t induced during GCN response, in contrast to S. cerevisiae ADE12, which is induced by Gcn4p; stationary

N response, in contrast to the S. cerevisiae ortholog; repressed by nitric oxide

man; soluble protein in hyphae; not induced during GCN response, in contrast to the S. cerevisiae ortholog

virulence in immunosuppressed mouse infection; not induced in GCN response, in contrast to S. cerevisiae

34p; required for hyphal growth and virulence; flucytosine induced; not induced in GCN response, in contra

contrast to S. cerevisiae Ade6; protein in stationary phase yeast-form cultures; flow model and rat catheter

ulated in biofilm; S. cerevisiae ortholog is Gcn4p regulated; protein enriched in stationary phase yeast-form

ice; complements S. cerevisiae adh1 adh2 adh3 mutant; fluconazole, farnesol-induced; flow model biofilm

Ssn6; indued by Mnl1 in weak acid stress; protein enriched in stationary phase yeast cultures; Spider biofilm

itric oxide independent of Yhb1; Spider biofilm induced

g MDR1; transcript is increased in populations of cells exposed to fluconazole over multiple generations; m

e infection; regulated by Nrg1, Tup1; Hap43, macrophage repressed, flow model biofilm induced; Spider b

ed as marker for cell lysis; possibly essential (UAU1 method); flow model biofilm induced; rat catheter and

ole-induced; protein level decrease in stationary phase cultures; sumoylation target; Spider biofilm repress

cation by multilocus sequence typing

arget genes; transposon mutation affects filamentous growth; Spider biofilm induced

is viable; regulated by Sef1, Sfu1, and Hap43

essential for growth, based on an insertional mutagenesis strategy

by Gcn2p and Gcn4p

phal growth, colony morphology, virulence; complements S. cerevisiae aft1 mutation; Spider biofilm induce

iofilm induced

nsport, intra-Golgi vesicle-mediated transport

ation affects endocytosis, hyphal growth, chemical and drug resistance, and sensitivity to cell wall inhibitors

cosamine (UDP-GlcNAc) biosynthesis

Efg1, Nrg1, Tup1; rat catheter biofilm repressed

onse, during cell wall regeneration, by flucytosine; regulated by Sef1, Sfu1, and Hap43; rat catheter and Sp

-induced via Cap1; rat catheter biofilm induced; flow model biofilm repressed

epressed; core stress response induced; Ssk1/Nrg1/Tup1/Ssn6/Hog1 regulated; flow model biofilm induced

acts as repressor of START; forms complex with Mcm1; mutant is sensitive to 5-fluorocytosine and lithium
epressed by elevated CO2; flow model biofilm repressed

gulated; repressed by amino acid starvation (3-AT); translation-related genes downregulated upon phagocy
induced; fluconazole-downregulated; protein abundance is affected by URA3 expression in the CAI-4 strain
que switch; rat catheter biofilm induced; rat catheter and Spider biofilm induced
ly to be essential for growth, based on an insertional mutagenesis strategy
the Man5GlcNAc2-PP-dolichol intermediate during asparagine-linked glycosylation in the ER; Spider biofilm
ik1, and sln1 homozygous null mutants
nts not obtained by UAU1 method
1, and sln1 homozygous null mutants; repressed by nitric oxide; possibly essential gene, disruptants not ob
ot elevated in chk1, nik1, and sln1 homozygous null mutants; possibly essential gene, disruptants not obtai
sln1 homozygous null mutants, but not in the chk1 null mutant; possibly an essential gene, disruptants not

mponent); predicted N-terminal acetylation; nitric oxide-repressed; plasma membrane-localized; protein dec

ion causes fluconazole resistance in WT and causes multidrug resistance in a cdr1 cdr2 double mutant; ra
protective role against oxidative damage; plasma membrane-localized;required for full virulence in a mous

r biofilm induced; flow model biofilm repressed; CAI-4 strain background effects; promoter bound Bcr1, Te
n buccal epithelial cells; putative GPI-anchor; induced by ketoconazole, low iron and at cell wall regeneratio
in mice; binds SspB adhesin of S. gordonii in mixed biofilm; induced in/required for Spider biofilm; flow mod
uring infection of human buccal epithelial cells; repressed by vaginal contact; biofilm induced; repressed du
othelium or ECM, endothelial invasiveness by endocytosis and, at high abundance, ECM-induced aggregat
erminal adhesion domain; ALS family includes cell-surface glycoproteins, some with adhesin function
le repeat regions; expression in S. cerevisiae does not confer adhesiveness; ALS family includes adhesins
dhesion to S. cerevisiae; highly variable; putative GPI-anchor; Hap43-repressed
d flow model biofilm induced

o toxic ergosterol analog; F-12/CO2 early biofilm induced
l biofilm induced; Spider biofilm induced
y murine macrophage; Hap43-induced; GlcNAc-induced protein; Spider biofilm repressed
ecific (no human or murine homolog)
me proliferation; rat catheter biofilm induced
lved in a cyanide-resistant respiratory pathway present in plants, protists, and some fungi, absent in S. cere
dospore formation repressed; rat catheter, Spider biofilm induced; regulated in Spider biofilms by Bcr1, Tec
d by prostaglandins; Hap43-repressed; Spider biofilm repressed
n, peak at cell-cycle S/G2 phase
ons; protein repressed during mating; Hog1, farnesol-induced; may be essential (UAU1 method); rat cathete
ed

in and is involved in vesicle mediated transport; induced in core caspofungin response; rat catheter biofilm
uole transport; phosphorylated protein; mutant is viable;
ylated protein; Tn mutation affects filamentous growth; Spider biofilm repressed
polarized growth through endocytic recycling of chitin synthase Chs3p
ungal-specific (no human or murine homolog)

in stationary phase yeast cultures
essed; flow model/RPMI/Spider/rat catheter biofilm induced; required for RPMI biofilm formation; Bcr1-indu
L-xylose, L-galactose; inhibited by metal ions, thiol group-specific reagents; induced on polystyrene adher
ary phase yeast-form cultures; Spider biofilm repressed

); rat catheter biofilm repressed
onfers hypersensitivity to cytochalasin D
utation affects filamentous growth; rat catheter and Spider biofilm repressed

rabitol is a marker for active infection in humans; rat catheter and Spider biofilm induced
inhibits enzyme activity; ketoconazole-induced; Hap43-repressed; flow model biofilm induced; Spider biofi
RMES); one of several C. albicans ADP-ribosylation factors; N-myristoylprotein; substrate of Nmt1; Spider
itivity to Brefeldin A; Spider biofilm repressed
biofilm repressed (see Locus History Note for Assembly 19 correction)
(3-AT), benomyl treatment; stationary phase enriched protein; repressed in alkalinizing medium; rat cathet
or ARG2, is induced upon phagocytosis by macrophage
; rat catheter and Spider biofilm induced
ed; flow model biofilm induced; Spider biofilm induced
rg6) activity and acetylglutamate-phosphate reductase (Arg5) activity; Gcn4 regulated; alkaline repressed;
n induced
sistance to caffeine; required for yeast cell adherence to silicone substrate
invasive colony growth, is unable to utilize proline as a nitrogen source; flow model biofilm induced
dose-dependent sensitivity to Brefeldin A
ntegrity and formation of biofilm; fungal-specific (no human or murine homolog); Gcn2p-, Gcn4p-regulated
ein abundance affected by URA3 expression in CAI-4 strain; Spider biofilm induced
ationary phase yeast cultures; GlcNAc-induced protein
edback-inhibited by phe if expressed in S. cerevisiae; decreased in stationary phase; flow model biofilm re
; feedback-inhibited by tyrosine if produced in S. cerevisiae Aro3p and Aro4p catalyze same reaction; prote
nt alkaline induction; protein abundance affected by URA3 expression in CAI-4 strain; Gcn4-regulated; sta
matic alcohol biosynthesis via the Ehrlich pathway; mutant is viable
egulation (alkaline induced); Hap43-induced gene
, not for endocytosis; mutation confers hypersensitivity to cytochalasin D; regulated by Gcn2 and Gcn4; Sp
sitivity to cytochalasin D; Spider biofilm repressed
ol analog, and to amphotericin B; rat catheter biofilm induced
Arp2/3 complex involved in actin-dependent processes; likely to be essential for growth, based on an inser
nic compounds; benomyl-induced; Gcn4-regulated; Hap43-repressed; mutant is viable; Spider biofilm indu
precursors
aglandins
r virulence in mice; snoRNA snR24 encoded in ASC1 intron; repressed in stationary phase; GlcNAc-induce
, peak at cell-cycle G2/M phase
growth, based on an insertional mutagenesis strategy
Mcm1 regulon; induced by alpha pheromone in SpiderM medium
by She3; required for WT virulence and filamentous growth on solid media; Ras1 repressed in yeast, Cyr1
chores to spindle microtubules
an azole-resistant strain that overexpresses MDR1; flow model biofilm induced; F-12/CO2 early biofilm indu
pH 4 vs pH 8; protein detected during exponential and stationary phases of yeast-form growth
sed by Cyr1, Ras1; colony morphology-related regulated by Ssn6; stationary phase enriched; Hap43-induce
protein; Spider biofilm induced
acid trehalase (Ath1p); Hap43p-repressed gene
-to-vacuole targeting (Cvt) pathway; Spider biofilm induced
trafficking of Lap41; Spider biofilm induced
ron; induced by nitric oxide independent of Yhb1
m induced; Spider biofilm induced
sine induced; Efg1, caspofungin repressed; may be essential; sumoylation target; stationary phase-enriche
ation to the serum; Spider biofilm repressed

ed
pider biofilm repressed
ungin repressed; macrophage/pseudohyphal-induced; detected during exponential and stationary growth p
ine induced; caspofungin repressed; macrophage/pseudohyphal-induced
uced; present in exponential and stationary growth phases; Hap43p-induced gene
nary growth phases
e yeast cultures; Spider biofilm repressed
ol, macrophage-downregulated protein abundance; protein present in exponential and stationary yeast gro
egulated by Sef1, Sfu1, and Hap43
ed
lrug target; flow model biofilm induced; Spider biofilm induced
mitochondrial function under ER stress; macrophage/pseudohyphal-repressed; alternatively spliced intron
n
on independent of MTL or white-opaque status; Spider biofilm induced
sis and in clinical isolates from HIV+ patients with oral candidiasis
-glycosylated by Pmt4; mutant is viable
essed
ed gene regulation by Ssn6p
mutant exhibits adenine auxotrophy and abnormal colony morphology
mino acid starvation (3-aminotriazole treatment); early-stage flow model biofilm formation
GlcNAc, amino acid starvation (3-aminotriazole treatment); present in exponential and stationary growth p
e to caspofungin
herence, impermeability, impenetrability, fluconazole resistance; Tup1/Tec1/Mnl1-regulated; mRNA binds S
g; required for nuclear localization of Tpk1; physically interacts with Tpk1; apoptosis-regulated
NA abundance detected in null mutant; macrophage/pseudohyphal-repressed
ses pseudohyphal and filamentous growth defects of various S. cerevisiae mutants and heat sensitivity of
odel biofilm repressed
s that control cell polarity; similar to S. cerevisiae Bem3p
mediated transport, protein geranylgeranylation, protein targeting to membrane
tion checkpoint signaling, negative regulation of exit from mitosis and Bfa1-Bub2 complex, spindle pole bo
stationary phase enriched protein; Spider biofilm repressed
a-glucan content; antigenic; virulence role in mouse systemic infection; rat catheter biofilm induced
filamentation, adhesion, and virulence; rat catheter biofilm repressed
es from HIV+ patients with oral candidiasis; Spider biofilm induced; biotin-dependent transcription regulate
dation by inducing gate opening; ortholog of S. cerevisiae Blm10; transcript regulated by Nrg1 and Mig1
yeast-form cell surface, not hyphae; alternatively spliced 5' UTR intron; Spider biofilm repressed
induced; repressed by prostaglandins; Spider biofilm induced
cell wall phosphopeptidomannan; 9-gene family member; mutants induce higher levels of inflammatory cyto
mannan, elongation of beta-mannose chains on the phosphopeptidomannan acid-labile fraction; Hap43-ind
osphopeptidomannan; 9-gene family member; regulated by Tsa1, Tsa1B; flow model biofilm induced; rat ca
amily includes Bmt1, Bmt2, Bmt3, and Bmtp with roles in mannosylation of cell wall phosphopeptidomann
including Bmt1, Bmt2, Bmt3, and Bmt4 with roles in mannosylation of cell wall phosphopeptidomannan; flo
MT3, and BMT4 with roles in beta-1,2-mannosylation of cell wall phosphopeptidomannan; downregulated in
es in beta-1,2-mannosylation of cell wall phosphopeptidomannan; transposon insertion in promoter region
4 with roles in beta-1,2-mannosylation of cell wall phosphopeptidomannan; regulated by Sef1, Sfu1, Hap4
ous growth; Hap43p-repressed gene; oral infection upregulated; mutants have reduced capacity to damag
ed localization to site of polarized growth, bud neck; localizes to Spitzenkorper of hyphae, minor localizatio
S. cerevisiae Bni4p (targeting subunit for Glc7p phosphatase, involved in bud-neck localization of chitin sy
r biofilm induced
e beige gene implicated in disease syndromes involving defective lysosomal trafficking; mutant is viable
ing hyphal development; transposon mutation affects filamentous growth
disruptants not obtained by UAU1 method
epressed; Spider and flow model biofilm induced; required for Spider biofilm formation; Bcr1-repressed in R
Rim101 pathway; macrophage and pseudohyphal-repressed; flow model biofilm induced
: B9J08_003841 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_120956

ent; flow model biofilm induced; Spider biofilm induced

involved in bud-site selection and genome integrity in S. cerevisiae; induced by alpha pheromone in Spider
uidance; required for wild-type budding pattern; induced in low iron; regulated by tyrosol and cell density
ntous growth

core stress response; repressed by prostaglandins

specifying the bud site; Spider biofilm induced

rper); localizes to polarisome
lgi to plasma membrane transport, Golgi to vacuole transport, fungal-type cell wall chitin biosynthetic proce
quitination; mutants are viable; macrophage/pseudohyphal-induced; rat catheter biofilm induced
. cerevisiae; Hap43-repressed gene; rat catheter biofilm induced
wth, adherence to buccal epithelial cells, or virulence in mouse systemic infection
lymerization

ne formation and cytosol, prospore membrane localization
patients with oral candidiasis; mutants are viable; Spider biofilm repressed
l by nitric oxide; required for flow model biofilm formation; Spider biofilm repressed

and integral component of endoplasmic reticulum membrane localization
; repressed by ciclopirox olamine; filament induced; regulated by Rfg1, Tup1; overlaps orf19.6078.1

ne to Golgi and endosome, retromer complex, retromer, cargo-selective complex localization

lation, cytoskeleton organization, mitochondrion inheritance, regulation of actin cytoskeleton organization
exadecenal to hexadecenoic acid; Spider biofilm induced
pressed; protein present in exponential and stationary growth phase yeast; Hap43-repressed; Spider biofil
phosphatidylinositol-4-phosphate binding, ubiquitin binding activity
ance of crista junctions and inner membrane architecture; Spider biofilm repressed

process and integral component of mitochondrial inner membrane localization
etic process and mitochondrion localization

NRRL Y-1498 : CANTEDRAFT_125085 and Debaryomyces hansenii CBS767 : DEHA2D09086g
neral amino acid permease Gap1; repressed in an azole-resistant strain overexpressing MDR1; Spider bio
tion, regulation of cytokinesis

ne dinucleotide binding activity

: B9J08_004945 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_133175
in dolichol-linked oligosaccharide biosynthetic process
1498 : CANTEDRAFT_112621 and Debaryomyces hansenii CBS767 : DEHA2D09812g

l morphology and invasive growth

in endocytosis, site selection
a stipitis Pignal : PICST_32745 and Candida tropicalis NEW ASSEMBLY : CTRG1_CGOB_00170
chondrion localization

ess and mitochondrion localization
tants not obtained by UAU1 method

localization

L : B9J08_003399 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_93515

zation

nscript induced by Mnl1p under weak acid stress; flow model biofilm induced; Spider biofilm induced

ot induced by Mnl1p under weak acid stress; flow model biofilm induced

ocess

nd cytoplasm; Spider biofilm induced

iosis, meiotic recombination checkpoint signaling, synaptonemal complex assembly

atio for correct folding of disulfide-bonded proteins; Spider biofilm repressed

4422 and Candida albicans WO-1 : CAWG_01254

L : B9J08_002021 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114227

ed gene regulation by Ssn6; induced by prostaglandins; flow model biofilm induced

on of PHO81; filament induced

doplasmic reticulum localization

rt; Spider biofilm induced

nding activity

ssed by nitric oxide

promoter bound by Bcr1, Efg1, Ndt80, and Rob1; orf19.3338 Bcr1-repressed in RPMI a/a biofilms

synthetases are downregulated upon phagocytosis by murine macrophage; downregulated by growth in th

osomal subunit localization

ne C. albicans fitness test

biofilm induced; rat catheter biofilm repressed

chondrion localization

ow model biofilm induced

ein serine/threonine kinase activator activity, cyclin-dependent protein serine/threonine kinase regulator act

olyadenylation, response to DNA damage checkpoint signaling and U2 snRNP, mRNA cleavage factor com

ulum membrane; predicted adhesin-like protein; mutants are viable

osynthetic process

activity, role in microtubule-based movement and microtubule associated complex localization

ort and TRAPPI protein complex, TRAPPII protein complex, TRAPPIII protein complex localization

s NRRL Y-1498 : CANTEDRAFT_96322 and Debaryomyces hansenii CBS767 : DEHA2C02310g

hase complex assembly and mitochondrion localization

anscription elongation from RNA polymerase II promoter, protein folding and prefoldin complex localization

sitive regulation of transcription by RNA polymerase II, telomere maintenance, telomere maintenance via r

ed in an ssr1 null mutant

L : B9J08_000959 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116785

and integral component of membrane localization

anscription, DNA-templated

duced

alis MYA-3404 : CTRG_04653 and Candida albicans WO-1 : CAWG_01134

III; Hap43p-repressed gene; S. cerevisiae ortholog FMP25 localizes to mitochondrion

ained by UAU1 method

sed on comparative genome analysis

lamage oral epithelial cells; Spider biofilm induced

catheter biofilm repressed

L : B9J08_003270 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115724

atabolic process, nuclear-transcribed mRNA poly(A) tail shortening, positive regulation of endodeoxyribonu

ation step, spliceosomal complex disassembly

L : B9J08_003254 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_107500

gulation of cardiolipin metabolic process and mitochondrial inner membrane, mitochondrion localization

2850, C. parapsilosis CDC317 : CPAR2_110240 and C. auris B8441 : B9J08_004952

_02920, C. parapsilosis CDC317 : CPAR2_108490 and C. auris B8441 : B9J08_000615

alization

L : B9J08_002035 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_100285

catheter biofilm induced

L : B9J08_000283, Debaryomyces hansenii CBS767 : DEHA2G16500g and Pichia stipitis Pignal : PICST_

esses MDR1

zation

d

phosphatidylinositol-4-phosphate binding activity

g, nucleosome-dependent ATPase activity, rDNA binding activity

eatment); protein present in exponential and stationary growth phase yeast cultures

tion

ne formation and protein localization to cell division site, more

ony morphology-related gene regulation by Ssn6; Spider biofilm repressed

iofilm and planktonic cells; flow model biofilm induced gene; GlcNAc-induced protein

; Spider biofilm repressed

RL Y-1498 : CANTEDRAFT_102387 and Debaryomyces hansenii CBS767 : DEHA2B06776g

mediated transport, protein secretion and Golgi membrane, cis-Golgi network, cytoplasm, organelle memb

flow model biofilm induced

RNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and mRNA processing, more
L : B9J08_004984 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_106351
mydospore formation in C. albicans and C. dubliniensis; Spider biofilm induced
otein palmitoylation, protein targeting to membrane
ne oxidoreductase)
mic reticulum, endoplasmic reticulum membrane, endoplasmic reticulum-Golgi intermediate compartment
proteasome-mediated ubiquitin-dependent protein catabolic process
nd Spider biofilm induced
ochondrion localization
er biofilm induced
d droplet organization and endoplasmic reticulum, lipid droplet localization
FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine)
_03920, C. parapsilosis CDC317 : CPAR2_107150 and C. auris B8441 : B9J08_005139
nd immune escape
organization, nuclear pore organization
L : B9J08_003358 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113999
L : B9J08_003367, Candida tenuis NRRL Y-1498 : CANTEDRAFT_113990 and Pichia stipitis Pignal : PICS
or biosynthetic process
e membrane, trans-Golgi network membrane localization
ive regulation of nucleotide metabolic process and mitochondrion localization
zation
candidiasis; Spider biofilm induced
na pheromone in SpiderM medium; Spider and early-stage flow model biofilm induced
sm localization
ction; mutants have reduced ability to damage oral epithelial cells; early-stage flow model biofilm induced
L : B9J08_000021 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114891
lgi to endoplasmic reticulum, vacuole organization
sis and lipid droplet localization
certed chromosome loss (CCL) process that leads to depolyploidization after mating
L : B9J08_002463, Debaryomyces hansenii CBS767 : DEHA2D07128g and Pichia stipitis Pignal : PICST_
al particles; rat catheter and Spider biofilm induced
_01504, Pichia stipitis Pignal : psti_CGOB_00118 and Candida tropicalis NEW ASSEMBLY : CTRG1_CG
plex; Spider biofilm repressed
s elongisporus NRLL YB-4239 : LELG_03202 and Candida metapsilosis : CMET_5254
_04600, C. parapsilosis CDC317 : CPAR2_105630 and C. auris B8441 : B9J08_004487
ndida tropicalis MYA-3404 : CTRG_04484 and Candida albicans WO-1 : CAWG_00904
r response to DNA damage stimulus, cellular response to methylmercury
anule localization
commitment complex localization

:e, cell tip, cytoplasm, fungal-type vacuole, fungal-type vacuole membrane localization
:ch; Hap43-repressed; rat catheter, Spider and flow model biofilm induced
ed in a cyr1 mutant
ı initiation from RNA polymerase III promoter and RNA polymerase III complex localization
3378 and Candida albicans WO-1 : CAWG_00876
tituent of ribosome activity
rt and TRAPPII protein complex, trans-Golgi network localization
L : B9J08_004520 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_136277
ing of nuclear-transcribed mRNA and Dcp1-Dcp2 complex, P-body, cytoplasm, cytoplasmic side of membr
L : B9J08_003698 and Candida tenuis NRRL Y-1498 : cten_CGOB_00159
ss; Hap43-, Sfu1- and Sef1-regulated; flow model biofilm induced, Spider biofilm induced
synthesis via transamidation, mitochondrial translation and glutamyl-tRNA(Gln) amidotransferase complex,
ıg, structural constituent of nuclear pore activity
L : B9J08_004575 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94695
zine treatment or in an azole-resistant strain that overexpresses CDR1 and CDR2
L : B9J08_004570 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115252
erM medium; Spider biofilm induced; Bcr1-repressed in a/a RPMI biofilms
sis; Spider biofilm induced
one catabolic process and cytoplasm, glutathione hydrolase complex, nuclear periphery localization
epressed; colony morphology-related gene regulation by Ssn6; possibly subject to Kex2 processing
ty, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor activity
ha pheromone in SpiderM medium
4 and is required in transcriptional silencing near telomeres; repressed in an azole-resistant strain overex
on transport, ubiquinol to cytochrome c and mitochondrial respiratory chain complex III localization
zation
, single-strand annealing, removal of nonhomologous ends
L : B9J08_000594, Pichia stipitis Pignal : PICST_30324 and Candida guilliermondii ATCC 6260 : PGUG_0
1 signaling, peptidyl-serine phosphorylation, protein autophosphorylation and cytoplasm localization
L : B9J08_000597 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_112420

1498 : CANTEDRAFT_91852 and Debaryomyces hansenii CBS767 : DEHA2G15356g
L : B9J08_000606, Candida tenuis NRRL Y-1498 : CANTEDRAFT_91858 and Pichia stipitis Pignal : PICST
repressed
Golgi transport vesicle, Golgi apparatus, endoplasmic reticulum localization
L : B9J08_000608 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_112428
induced
nd cytoplasm; Spider biofilm induced
gative regulation of translational initiation, stress granule assembly and P-body, cytoplasmic stress granule
ndida tropicalis MYA-3404 : CTRG_04227 and Candida albicans WO-1 : CAWG_00750
slocase complex assembly, protein targeting to mitochondrion
lation, mitochondrion inheritance, regulation of actin cytoskeleton organization, ubiquitin-dependent ERAD
dependent); induced by alpha pheromone in SpiderM medium; Spider biofilm induced
L : B9J08_003766 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_125137
chitin synthase activity during cytokinesis; Spider biofilm repressed
ne, disruptants not obtained by UAU1 method
se activity, enzyme regulator activity, phosphodiesterase decapping endonuclease activity
L : B9J08_003388 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114052
ide of mitochondrial inner membrane, mitochondrial matrix localization
4047, Debaryomyces hansenii CBS767 : DEHA2D14388g and Pichia stipitis Pignal : PICST_37629
d CCR4-NOT core complex localization
s NRRL Y-1498 : CANTEDRAFT_114040 and Pichia stipitis Pignal : PICST_51125
; possibly essential, disruptants not obtained by UAU1 method; rat catheter and Spider biofilm induced
L : B9J08_005439 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_111035
mage oral epithelial cells
_06600, C. parapsilosis CDC317 : CPAR2_208850 and C. auris B8441 : B9J08_005435
aintenance; Spider biofilm induced
L : B9J08_002282 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_136902
CBS767 : DEHA2F26620g and Pichia stipitis Pignal : PICST_62738
um-grown cells in a Cph2-dependent manner; Hap43-repressed; rat catheter, Spider and flow model biofil
ll mutation abolishes cellular ammomium permease activity; fungal-specific (no human or murine homolog
an epithelium (RHE), while expression of the C. dubliniensis ortholog is not; mutant is viable; Spider biofilm
g activity
n, transcription by RNA polymerase II, transcription initiation from RNA polymerase II promoter
nt of spindle microtubules to kinetochore, mitotic spindle assembly
abolic process
L : B9J08_001617 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_95854
nding activity
and alpha DNA polymerase:primase complex, nuclear envelope, nucleus localization
tarvation (3-AT treatment); alkaline upregulated; macrophage-induced protein
L : B9J08_003149 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_108836
esis
1498 : cten_CGOB_00237 and Debaryomyces hansenii CBS767 : DEHA2F25542g

reductase activity
ruptants not obtained by UAU1 method; Spider biofilm induced
liasis
lear periphery, nucleus localization
: B9J08_001596 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_95879
nd Spider biofilm induced; F-12/CO2 early biofilm induced
_07340, C. parapsilosis CDC317 : CPAR2_208340 and C. auris B8441 : B9J08_001600
complex-dependent catabolic process, chromatin assembly, positive regulation of ubiquitin protein ligase a
NRRL Y-1498 : CANTEDRAFT_116488 and Debaryomyces hansenii CBS767 : DEHA2F26114g
Hap43p-induced; rat catheter biofilm induced
in S. cerevisiae; Spider biofilm induced
tic and oxidative stress via Hog1; Spider biofilm induced
112, Debaryomyces hansenii CBS767 : DEHA2G14938g and Candida guilliermondii ATCC 6260 : PGUG_
: B9J08_004229 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_104385
vity, role in tRNA modification, tRNA wobble adenosine to inosine editing and tRNA-specific adenosine-34
d by UAU1 method
expression; induced by hypoxia
from the prevacuolar compartment; Spider biofilm induced
NRRL Y-1498 : cten_CGOB_00051 and Pichia stipitis Pignal : psti_CGOB_00173
07900, C. parapsilosis CDC317 : CPAR2_207070 and C. auris B8441 : B9J08_003608
tochondrial membrane, mitochondrion localization
ced
zation
: B9J08_000292 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114140
hod
repressed; induced in oralpharyngeal candidasis; flow model biofilm induced; Spider biofilm repressed
n localization
localization
tivity
itochondrial matrix localization
_08220, C. parapsilosis CDC317 : CPAR2_804440 and C. auris B8441 : B9J08_004556
nsport and Golgi transport complex localization
9W and S. pombe SPAP11E10.01; rat catheter biofilm induced
bolic process, protein dephosphorylation and extracellular region, fungal-type vacuole, fungal-type vacuole
medium
ortholog of S. cerevisiae MSL1; Hap43p-induced gene
ne; Spider biofilm induced
: B9J08_004186 and Candida tenuis NRRL Y-1498 : cten_CGOB_00267
zation
nd mitochondrion localization
01590, C. auris B8441 : B9J08_004547 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_109732
ning, postreplication repair and PAN complex localization
nduced by Mnl1p under weak acid stress

mily; Spider biofilm induced
sis
, C. parapsilosis CDC317 : CPAR2_803690 and C. auris B8441 : B9J08_004047

iofilm repressed
induced

A gene-mediated silencing and cytosol, mitochondrion, nucleolus, nucleus localization
biofilm induced

NRRL Y-1498 : cten_CGOB_00021 and Debaryomyces hansenii CBS767 : DEHA2F11088g

2_214170, C. auris B8441 : B9J08_005393 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_95066

thase at high temperature; rat catheter biofilm repressed

and nucleus localization
hansenii CBS767 : DEHA2B10516g and Pichia stipitis Pignal : PICST_30058
rRNA and LSU-rRNA), more
283, Debaryomyces hansenii CBS767 : DEHA2B10604g and Pichia stipitis Pignal : PICST_40454

in-macromolecule adaptor activity

n; possibly an essential gene, disruptants not obtained by UAU1 method; Spider biofilm induced
03450, C. auris B8441 : B9J08_002739 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_131760

r biofilm induced
ne localization

r biofilm induced

rox olamine; constitutive expression independent of MTL or white-opaque status; Spider biofilm induced

mily; Spider biofilm induced
: B9J08_004031 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_136811
RraA family; repressed by benomyl; Hap43-induced; Spider biofilm induced
: B9J08_004034 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_95780

mplex, cytoplasm, nuclear periphery localization
d in a ssr1 null mutant

phenazine treatment; possibly transcriptionally regulated by Tac1p; induced by nitric oxide; fungal-specific

, protein ubiquitination, ubiquitin-dependent endocytosis and Golgi apparatus, cytosol, plasma membrane
09830, C. parapsilosis CDC317 : CPAR2_804210 and C. auris B8441 : B9J08_004773
oral candidiasis; mutants have reduced ability to damage oral epithelial cells; transcript possibly regulated

UAU1 method
iae; mutants are viable

rowth; null mutants are viable; fungal-specific (no human or murine homolog)

comparative genome analysis

fluorouracil (5-FU); Hog1-induced; planktonic growth-induced; rat catheter and Spider biofilm repressed

alis MYA-3404 : CTRG_04072, Candida albicans WO-1 : CAWG_00348 and Candida metapsilosis : CME
epressed by prostaglandins
: B9J08_000256 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_105553
age checkpoint signaling and mitotic sister chromatid cohesion, more
ype 1 promoter sequence-specific DNA binding, more
hod
tabolic process and inositol phosphoceramide synthase complex, integral component of Golgi membrane
core stress response

luorocytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine); Hap43-induced; Spider bio
gulation of peroxisome size; Hap43-repressed gene
thod

w model, rat catheter and Spider biofilm induced
polyadenylation and mRNA cleavage and polyadenylation specificity factor complex, nucleus localization
methylthioadenosine
localization

nthetic process and integral component of endoplasmic reticulum membrane localization
on

morphology-related gene regulation by Ssn6; flow model biofilm induced; Spider biofilm induced
ally oriented; Spider biofilm repressed

ricin B, ketoconazole, and hypoxia induced; regulated by Cyr1, Ssn6; induced in oralpharyngeal candidasis
, via spliceosome

gnition and U5 snRNP localization
candidasis; 16h flow model biofilm repressed, late-stage flow model biofilm induced; rat catheter and Spide

a stipitis Pignal : PICST_29620 and Candida guilliermondii ATCC 6260 : PGUG_03306
TC; subsequently reinstated in Assembly 21 based on comparative genome analysis

6_10860, C. parapsilosis CDC317 : CPAR2_203700 and C. auris B8441 : B9J08_001575

ort, fungal-type cell wall organization, protein retention in Golgi apparatus
rine (OAS) pathway of sulfur assimilation; F-12/CO2 early biofilm induced; Spider biofilm induced

induced; Spider biofilm induced
: B9J08_000968 and Candida tenuis NRRL Y-1498 : cten_CGOB_00256
l cells; regulated by Gcn2 and Gcn4; Spider biofilm induced

athaspora passalidarum NRRL Y-27907 : SPAPADRAFT_60017 and Candida guilliermondii ATCC 6260 :

ıd neck; Spider biofilm induced

Efh1 regulated; 5'-UTR intron; induced by Mnl1 under weak acid stress; rat catheter biofilm induced

e; mainly associated with nuclear envelope and ER; flow model and Spider biofilm repressed

chondrial DNA metabolic process, response to oxidative stress

ytic nonsense-mediated decay, protein ubiquitination and cytoplasm, nucleolus, nucleus, polysome localiza

ossibly an essential gene, disruptants not obtained by UAU1 method

ne to vacuole transport, late endosome to vacuole transport via multivesicular body sorting pathway

06250, C. auris B8441 : B9J08_005263 and Debaryomyces hansenii CBS767 : DEHA2E13794g

6_72650, C. parapsilosis CDC317 : CPAR2_805190 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_

 : B9J08_002727 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116279

SpiderM medium; transcript reduced in ace2 mutant; flow model, rat catheter and Spider biofilm repressed

 : B9J08_005277, Pichia stipitis Pignal : PICST_28850 and Candida guilliermondii ATCC 6260 : PGUG_0

ı protein phosphorylation

 : B9J08_001721 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_120384

jophore assembly site localization

 : B9J08_003931 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_104365

vel decreases in stationary phase

lease activity, tRNA binding activity

ı induced

 : B9J08_003474 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115679

1498 : CANTEDRAFT_112512 and Debaryomyces hansenii CBS767 : DEHA2E16808g

 : B9J08_003468 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_91948

zation

ner membrane, mitochondrial inner membrane peptidase complex localization

ubiquitin chain polymerization, postreplication repair, protein K63-linked ubiquitination, protein polyubiquitin

x localization

 : B9J08_002515 and Candida tenuis NRRL Y-1498 : cten_CGOB_00224

1498 : cten_CGOB_00231 and Debaryomyces hansenii CBS767 : DEHA2D04928g

gression; Spider biofilm induced

stant strain that overexpresses MDR1

 : B9J08_003701 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114815

etic process

II activity, RNA polymerase III activity, RNA-directed 5'-3' RNA polymerase activity gin induced; Spider biofilm induced

OB_00101, Candida tropicalis MYA-3404 : CTRG_06172 and Candida albicans WO-1 : CAWG_02233

se assembly, positive regulation of mitochondrial translational initiation

slation factors, tRNA synthetases are downregulated upon phagocytosis by murine macrophage

1 : B9J08_002031, Candida tenuis NRRL Y-1498 : CANTEDRAFT_135403 and Pichia stipitis Pignal : PICS

tion in both C. albicans and C. dubliniensis; rat catheter biofilm repressed

nthetic process

genesis and cytoplasm, nucleus localization

lex, involved in meiotic and mitotic double-strand break repair; upregulated in a cyr1 null mutant

AR2_201430, C. auris B8441 : B9J08_000642 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_13672

rospore membrane formation, endocytosis, exocytosis, vesicle fusion, vesicle-mediated transport

10, C. parapsilosis CDC317 : CPAR2_201590 and C. auris B8441 : B9J08_002506

1 : B9J08_002511 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_107586

chondrial matrix localization

1 : B9J08_004645 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94106

tasis, cellular manganese ion homeostasis, cobalt ion transport, manganese ion transport

reased colony wrinkling in filamentous growth-inducing conditions, but does not block hyphal formation in l

all regeneration; stationary phase enriched; possibly essential (UAU1 method); F-12/CO2 early biofilm indu

18S rRNA processing; flow model biofilm repressed

ein complex assembly, protein folding, protein import into mitochondrial intermembrane space, protein refol

tosol, nucleus localization

1 : B9J08_003318 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_135418

does not block hyphal growth in liquid media; mutation confers hypersensitivity to toxic ergosterol analog; S

d by UAU1 method

pressed

u1, Hap43; flow model biofilm induced

e position uridine thiolation and mitochondrion localization

nent of membrane, mitochondrial inner membrane localization

F from Assembly 19; removed from Assembly 20; restored based on comparative genome analysis; flucyto

d; Spider biofilm repressed

on and degradation of proteasome substrates; role in fission of mitochondria and peroxisome; Spider biofil ofilm repressed

ralkylamines (e.g. tryptamine, phenylethylamine); Spider biofilm repressed

teins; un-merged from orf19.7275 in a revision of Assembly 21 based on comparative genome analysis an

pies of a linear dsDNA; rat catheter biofilm repressed

of splicing; Spider biofilm induced

, retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum and GET complex localization

o iron and cytosol localization

snoRNP required for 18S rRNA synthesis; Hap43-induced; Spider biofilm induced

evisiae; Hap43-repressed gene

ssed; Spider biofilm induced

vity, ethanolamine transmembrane transporter activity

1 : B9J08_002200 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_119026

uring growth in the mouse cecum; Spider biofilm induced

1 : B9J08_000687 and Debaryomyces hansenii CBS767 : DEHA2B02442g

1, and Hap43; Spider biofilm induced

nplex assembly, proteolysis, signal peptide processing

1 : B9J08_001290 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_135034

nd integral component of membrane, lipid droplet localization

iofilm induced

d

gosterol analog, and to amphotericin B

of isopentenyl diphosphate biosynthetic process, mevalonate pathway

r cluster assembly

localization

1 : B9J08_003344 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116162

film repressed

calis MYA-3404 : CTRG_01155, Candida albicans WO-1 : CAWG_03868 and Candida metapsilosis : CME

calis NEW ASSEMBLY : CTRG1_01156 and Candida orthopsilosis Co 90-125 : CORT_0A12230

nd during growth in the mouse cecum; induced in oralpharyngeal candidasis; Spider biofilm induced

ial large ribosomal subunit localization

4 : CTRG_04298

ase I, transcription by RNA polymerase I, transcription elongation from RNA polymerase I promoter

s hansenii CBS767 : DEHA2A01320g and Pichia stipitis Pignal : PICST_29434
om methylthioadenosine
asis, retrograde transport, endosome to Golgi and GARP complex, Golgi apparatus localization
16070, C. parapsilosis CDC317 : CPAR2_213850 and C. auris B8441 : B9J08_003194

on binding, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular o
establishment of sister chromatid cohesion, interstrand cross-link repair, mitotic sister chromatid cohesion

L : B9J08_003044 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_92202
grade transport, endosome to Golgi and endosome localization

y, actin filament organization, endocytosis and actin cortical patch localization
vity and role in regulation of transcription, DNA-templated

exponential and stationary growth phase yeast cultures; Spider biofilm induced
ndida tropicalis MYA-3404 : CTRG_01238 and Candida albicans WO-1 : CAWG_03918
ts not obtained by UAU1 method

upon hyphal formation; Spider biofilm induced

none in SpiderM medium
DNA replication initiation, meiotic cell cycle, negative regulation of pseudohyphal growth

er domain; Spider biofilm induced
essed
nsic component of mitochondrial inner membrane, mitochondrial intermembrane space localization
volved in chromosome segregation, spindle checkpoint activity and kinetochore clustering; Hap43-induced

duced; Spider biofilm induced
L : B9J08_000158 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116870
Assembly 21 based on comparative genome analysis; overlaps orf19.1490.2, which is annotated as block
spliceosome localization

L : B9J08_004860 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_128446

2_212450, C. auris B8441 : B9J08_002176 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_92365

, proteasome-mediated ubiquitin-dependent protein catabolic process

L : B9J08_001195 and Candida tenuis NRRL Y-1498 : cten_CGOB_00169

ned by UAU1 method

polyadenylation, regulation of mRNA 3'-end processing, response to DNA damage checkpoint signaling

ralpharyngeal candidasis; flow model biofilm induced; Spider biofilm induced

d; required for normal filamentous growth; mRNA binds She3 and is localized to hyphal tips

ed

zation

trand break repair

t component); repressed by nitric oxide; predicted transmembrane helix

n

none in SpiderM medium

tarvation

n

ruptants not obtained by UAU1 method

nanol

c ion binding activity and role in regulation of transcription, DNA-templated

-induced gene

facilitator superfamily (MFS); mRNA binds She3

gene regulation by Ssn6; flow model biofilm induced; Spider biofilm induced

ofilm induced

process

L : B9J08_003086 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_101113

nd Aim21-Tda2 complex, actin cortical patch localization

RI complex, UTP-C complex localization

alization

vity

alis MYA-3404 : CTRG_01348, Candida albicans WO-1 : CAWG_04043 and Candida metapsilosis : CME

cis splicing, via spliceosome, spliceosomal complex assembly

Golgi transport vesicle, endoplasmic reticulum membrane, integral component of Golgi membrane localiz

R2_212430, C. auris B8441 : B9J08_004968 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_128807

vesicle-mediated transport, intra-Golgi vesicle-mediated transport, macroautophagy

Spider biofilm induced

flow model biofilm induced

ferase activity

12150, C. auris B8441 : B9J08_004964 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_128815

thylation

etabolic process, phospholipid metabolic process and mitochondrial matrix localization

L : B9J08_004599 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_112898

L : B9J08_004373 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_109928

Golgi

cytoplasm localization

repressed gene

CBS767 : DEHA2E20636g, Pichia stipitis Pignal : PICST_66811 and Candida tropicalis MYA-3404 : CTRG

of TORC1 signaling and Lst4-Lst7 complex, cytoplasm, vacuolar membrane localization

ctin cytoskeleton organization and perinuclear endoplasmic reticulum localization

ytic nonsense-mediated decay, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay a

zation

Debaryomyces hansenii CBS767 : DEHA2D04356g and Pichia stipitis Pignal : PICST_34839

development of azole resistance; induced by Ca(2+) in a calcineurin-dependent manner; Spider biofilm in

ohydrolase activity and role in N-terminal protein amino acid modification, protein catabolic process

ylation

nduced by Mnl1 under weak acid stress

embrane localization

to aureobasidin A

NP, post-mRNA release spliceosomal complex localization

on, hyphal growth and heat stress response; fungus-specific

ilm repressed

L : B9J08_004484 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115371

at catheter and Spider biofilm induced

L : B9J08_004481 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_135843

SU-rRNA, 5.8S rRNA, LSU-rRNA) and nucleolus, preribosome localization

egative regulation of ribosomal DNA heterochromatin assembly, more

AR2_211020, C. auris B8441 : B9J08_000865 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_11614

rotein tyrosine kinase activity

s hansenii CBS767 : DEHA2F08690g and Candida guilliermondii ATCC 6260 : PGUG_01488

ound in lipid particles; hyphal-induced expression

ytoplasm, mitochondrion localization

UAU1 method

L : B9J08_003718 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115581

periphery, nucleolus, preribosome, large subunit precursor localization

an essential gene, disruptants not obtained by UAU1 method

d; Spider biofilm induced

L : B9J08_003188 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114035

L : B9J08_002949 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113479

L : B9J08_002950 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113478

Swr1 complex localization

ranslational initiation and mitochondrial small ribosomal subunit localization

on localization

L : B9J08_004606 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_134010

ganization, actin filament bundle assembly, endocytosis and actin cortical patch localization

ein newly produced during adaptation to the serum

ation complex, chromosome, centromeric region localization

dial cisterna localization

ed; Spider biofilm induced

atory element binding activity and role in negative regulation of translation, protein stabilization, ribosomal l

ibosomal subunit; the snoRNA CD39 is encoded within the MRPS35 intron
L : B9J08_005014 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113905
L : B9J08_005009 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113899
sion independent of MTL or white-opaque status; Spider biofilm induced
L : B9J08_003636 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_100922
1498 : CANTEDRAFT_117672 and Debaryomyces hansenii CBS767 : DEHA2D11154g
s NRRL Y-1498 : cten_CGOB_00075 and Debaryomyces hansenii CBS767 : DEHA2F07964g
F-1 complex, cytoplasm, nucleus localization
yl-lysine monomethylation, vesicle-mediated transport
al small subunit export from nucleus and cytosol, nucleus localization
gulated upon adherence to polystyrene
n SpiderM medium
colony wrinkling under filamentous growth-inducing conditions, but does not block true hyphal formation in
avage and tRNA-intron endonuclease complex localization
model and Spider biofilm repressed
(SSU-rRNA, 5.8S rRNA, LSU-rRNA), rRNA processing, ribosomal large subunit export from nucleus
nstated in Assembly 21 based on comparative genome analysis
ed
t and Golgi membrane localization
g; Spider biofilm induced
nsport and Golgi transport complex localization
possibly essential, disruptants not obtained by UAU1 method
e pairing at meiosis, protein sumoylation, reciprocal meiotic recombination, synaptonemal complex asseml
al candidiasis
calis MYA-3404 : CTRG_01513 and Candida albicans WO-1 : CAWG_04340
isome localization
L : B9J08_001214 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_95516
brane localization
biosynthetic process, thiamine metabolic process
L : B9J08_001215 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116074
d
L : B9J08_001221, Candida tenuis NRRL Y-1498 : CANTEDRAFT_116071 and Pichia stipitis Pignal : PICS
RRL Y-1498 : CANTEDRAFT_116070 and Debaryomyces hansenii CBS767 : DEHA2F04994g
slation and mitochondrial matrix localization
n in the C. albicans fitness test
lization
s NRRL Y-1498 : CANTEDRAFT_133951 and Debaryomyces hansenii CBS767 : DEHA2F02068g
L : B9J08_000085 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_103989
cognition, mRNA splicing, via spliceosome, positive regulation of RNA binding
ynthetic process
vity and role in tRNA N1-guanine methylation, tRNA methylation
L : B9J08_003191 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115100
embly; rat catheter, flow model and Spider biofilm induced
psilosis : CMET_3324 and Candida tropicalis NEW ASSEMBLY : CTRG1_04756
r to orf19.7550

Golgi compartments; clade-associated gene expression
and Candida orthopsilosis NEW ASSEMBLY : CORT1B05695
NA transcript (SSU-rRNA, 5.8S rRNA and LSU-rRNA), more
: B9J08_000069 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_104515
tin ring assembly and cytoplasm, nucleus localization
mal subunit precursor, interacts with U3 snoRNA in S. cerevisiae; gene has intron; Spider biofilm induced
Ssr1; Hap43-repressed; flow model biofilm repressed
_21210, C. parapsilosis CDC317 : CPAR2_406880 and C. auris B8441 : B9J08_004580
NRRL Y-1498 : CANTEDRAFT_127772 and Candida tropicalis MYA-3404 : CTRG_01766
utant
in SpiderM medium; Spider biofilm induced
_21290, C. parapsilosis CDC317 : CPAR2_406670 and C. auris B8441 : B9J08_002805
: B9J08_002803 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_130046
zation
spliceosome localization
uced via Cap1; stationary-phase enriched protein; Spider biofilm induced
: B9J08_002799 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_103408
Isw1a complex localization
MDR1; early-stage flow model biofilm induced; Spider biofilm repressed
ndida tropicalis MYA-3404 : CTRG_01739 and Candida albicans WO-1 : CAWG_05814
dium
binding and oxidoreductase activity, more
tures; required for biofilm formation; Spider biofilm repressed
methylation, meiotic cell cycle, nucleologenesis, regulation of telomere maintenance via telomerase, tRN
NRRL Y-1498 : CANTEDRAFT_112352 and Debaryomyces hansenii CBS767 : DEHA2C08008g
iosynthetic process, triglyceride metabolic process
biofilm induced; Spider biofilm repressed
d nicotinamide riboside salvage pathways; Spider biofilm induced
ane, lipid droplet localization
ome, positive regulation of mRNA splicing, via spliceosome
roxisome targeting signal; Hap43-repressed; Spider biofilm induced
lled ribosome, ribosome-associated ubiquitin-dependent protein catabolic process and RQC complex local
gnal transduction and intracellular anatomical structure localization
azine treatment; regulated by Sfu1, Nrg1, Tup1; stationary phase enriched protein; Spider biofilm induced
iofilm induced
zation
and chromosome, telomeric region, site of double-strand break localization
stipitis Pignal : psti_CGOB_00208 and Candida tropicalis NEW ASSEMBLY : CTRG1_01709
hansenii CBS767 : DEHA2F19756g and Pichia stipitis Pignal : PICST_61375

nsenii CBS767 : DEHA2C08118g, Candida metapsilosis : CMET_5047 and Pichia stipitis Pignal : psti_CG

sitive regulation of mitochondrial translation and Cbp3p-Cbp6 complex, mitochondrial ribosome localization

nucleotide binding activity

s NRRL Y-1498 : CANTEDRAFT_109454 and Debaryomyces hansenii CBS767 : DEHA2C10076g

hetic process from peptidyl-histidine and cytoplasm, endosome localization

repressed

polar cellular bud site selection, regulation of COPII vesicle coating

CAWG_05895

repressed

lasmic reticulum organization and endoplasmic reticulum tubular network membrane organization, more

lus localization

atheter biofilm repressed; mRNA binds She3

3rg1, Rob1 and induced by Efg1, Ndt80; Spider biofilm induced

s NRRL Y-1498 : cten_CGOB_00049 and Candida tropicalis MYA-3404 : CTRG_01823

nduced

ndida tropicalis MYA-3404 : CTRG_01829 and Candida albicans WO-1 : CAWG_05920

ndida tropicalis MYA-3404 : CTRG_01825 and Candida albicans WO-1 : CAWG_05921

biofilm induced

ndida tropicalis MYA-3404 : CTRG_01836 and Candida albicans WO-1 : CAWG_01505

d DNA binding activity

L : B9J08_005066 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113677

L : B9J08_004017 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_104937

OB_00044, Candida orthopsilosis Co 90-125 : CORT_0C06265 and Candida tropicalis MYA-3404 : CTRG_

iosynthetic process, metabolic process

a stop codon in the region corresponding to the Ywp1p signal peptide; disruption causes no apparent phen

mutant; induced by nitric oxide independent of Yhb1p

x binding, chromatin binding activity

gulated by Sef1, Sfu1, and Hap43

L : B9J08_004792 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_108823

ed by Mnl1 under weak acid stress

activity

reinstated in Assembly 21 based on comparative genome

nic reticulum membrane localization

l starvation (3-aminotriazole treatment); Spider biofilm induced

al gene, disruptants not obtained by UAU1 method; flow model biofilm induced; Spider biofilm induced

0089, Debaryomyces hansenii CBS767 : DEHA2B13508g and Pichia stipitis Pignal : PICST_59544

clinical development of fluconazole resistance

ofilm induced

Spider biofilm induced

site, cytoplasm, division septum localization

ndida tropicalis MYA-3404 : CTRG_01968 and Candida albicans WO-1 : CAWG_05983

processing, more
1, Brg1, Rob1
perfamily (MFS)
eticulum membrane localization
ed by fluphenazine treatment or in an azole-resistant strain that overexpresses CDR1; Spider biofilm induce
s NRRL Y-1498 : cten_CGOB_00249 and Debaryomyces hansenii CBS767 : DEHA2B01980g
s hansenii CBS767 : DEHA2B02002g and Pichia stipitis Pignal : PICST_31649
L : B9J08_003033 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116822
L : B9J08_003025 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116829
e translesion synthesis and mitochondrion, zeta DNA polymerase complex localization
ansport, mitochondrial transport
L : B9J08_005288 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116273
sporter activity and role in cellular copper ion homeostasis, copper ion transmembrane transport, phosphat
Spider biofilm induced
sporter activity, role in NAD transmembrane transport, mitochondrial pyruvate transmembrane transport an
ded protein binding activity and role in protein retention in ER lumen, ubiquitin-dependent ERAD pathway
wobble uridine modification and Nbp35-Cfd1 ATPase complex, cytoplasm localization
port, retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum, vesicle fusion
ganization, endocytosis; flow model biofilm induced; Spider biofilm repressed
Debaryomyces hansenii CBS767 : DEHA2B13310g and Candida metapsilosis : CMET_5731
in SpiderM medium
RRL Y-1498 : CANTEDRAFT_114646 and Debaryomyces hansenii CBS767 : DEHA2B05654g
on independent of MTL or white-opaque status
dent of MTL or white-opaque status; Hap43-repressed
w model, rat catheter, Spider biofilm induced
ellular spore, ubiquitin-dependent ERAD pathway and extrinsic component of membrane, nucleus localizat
NA wobble uridine modification
tapsilosis : CMET_2070 and Pichia stipitis Pignal : PICST_31669
nthesis from pantothenate; rat catheter biofilm repressed
elated expression; Spider biofilm repressed
30, C. parapsilosis CDC317 : CPAR2_407430 and C. auris B8441 : B9J08_003802
ulation of transcription from RNA polymerase II promoter by pheromones, protein folding and cytoplasm loc
alis MYA-3404 : CTRG_02088, Candida albicans WO-1 : CAWG_06084 and Candida metapsilosis : CME
Spider biofilm repressed
andidiasis; Spider biofilm induced
ld-type outer spore wall formation in S. cerevisiae; possibly an essential gene (UAU1 method); Hap43p-rep

ic process, one-carbon metabolic process
S. cerevisiae Mig2p
n high-resolution tiling arrays; Spider biofilm induced
ilm repressed
ion
f transcription by RNA polymerase I, positive regulation of translational fidelity, protein phosphorylation
calis MYA-3404 : CTRG_02045, Candida albicans WO-1 : CAWG_06134 and Candida metapsilosis : CME
sis; Spider biofilm induced
UAU1 method
regulated by fluphenazine treatment or in an azole-resistant strain that overexpresses CDR1 and CDR2
1 : B9J08_001500 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116924
r biofilm repressed
Spider biofilm repressed
n tiling arrays; Spider biofilm repressed
ulation by Ssn6; overlaps orf19.5472; Spider biofilm repressed
st identical to orf19.6113, orf19.4055, orf19.5370
e for first transesterification step
candidiasis and in clinical isolates from HIV+ patients with oral candidiasis; Spider biofilm repressed
al candidiasis; regulated by Ssn6
1 : B9J08_005021 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_130872
Pignal : PICST_29581, Candida tropicalis MYA-3404 : CTRG_06175 and Candida albicans WO-1 : CAWG
mbly and mitochondrial matrix, mitochondrion localization
e; clade-associated gene expression
olog)
ndida tropicalis MYA-3404 : CTRG_06188 and Candida albicans WO-1 : CAWG_02379
rial large ribosomal subunit localization
ation
70, C. parapsilosis CDC317 : CPAR2_503390 and C. auris B8441 : B9J08_003812
NA binds She3 and is localized to hyphal tips
ne treatment
drial inner membrane, mitochondrial intermembrane space localization
ex assembly, vacuolar acidification and RAVE complex, cytoplasm, extrinsic component of membrane loca
RNA catabolic process, deadenylation-dependent decay, protein localization
otin behavior, and cytokinesis in S. cerevisiae; possibly an essential gene, disruptants not obtained by UAU
70, C. parapsilosis CDC317 : CPAR2_102260 and C. auris B8441 : B9J08_002841
1 : B9J08_002362 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_103482

ida tropicalis NEW ASSEMBLY : CTRG1_04030 and Candida tropicalis MYA-3404 : CTRG_04030

ofilm induced

film formation, respiration and virulence

_80910, C. parapsilosis CDC317 : CPAR2_102230 and C. auris B8441 : B9J08_002616

. albicans and C. dubliniensis; Hog1-repressed; Spider biofilm induced

alis MYA-3404 : CTRG_02575 and Candida albicans WO-1 : CAWG_02441

055, Spathaspora passalidarum NRRL Y-27907 : spas_CGOB_00040 and Candida albicans WO-1 : CAW

324, Debaryomyces hansenii CBS767 : DEHA2G01980g and Pichia stipitis Pignal : PICST_45936

1 : B9J08_002621 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116326

dium ions and hydrogen peroxide; Hap43-induced; Spider biofilm induced

al inner membrane localization

090, C. parapsilosis CDC317 : CPAR2_101950 and C. auris B8441 : B9J08_002355

s hansenii CBS767 : DEHA2A09042g and Pichia stipitis Pignal : PICST_42519

esion, hyphal growth and biofilm formation

1 : B9J08_003308 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_101483

Spider biofilm induced

cal patch localization

ation

ed; regulated by Nrg1, Tup1, Upc2; induced by prostaglandins; flow model biofilm induced; rat catheter and

erase I and polymerase II transcript metabolism; Hap43-induced gene

bohydrate metabolic process

1 : B9J08_001004 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_93693

1 : B9J08_001892 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115755

1 : B9J08_001894 and Candida tenuis NRRL Y-1498 : cten_CGOB_00261

e vesicle-mediated transport, Golgi to ER transport; flow model biofilm repressed

ed in an ssr1 null mutant

nplex assembly and mitochondrial intermembrane space localization

nily domain; Hap43-repressed gene

e growth in S. cerevisiae; induced by alpha pheromone in SpiderM medium

zation

sitol-3-phosphate binding, sphingolipid binding activity

lis NEW ASSEMBLY : CTRG1_02378 and Candida tropicalis MYA-3404 : CTRG_02378

peptide processing and mitochondrial inner membrane localization

erevisiae; Hap43-induced gene; Spider biofilm induced

ed transport, intracellular protein transport and COPII vesicle coat localization

1 : B9J08_000205 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114065

der biofilm repressed
OB_00188, Candida orthopsilosis Co 90-125 : CORT_0C04470 and Candida orthopsilosis NEW ASSEMBI
, disruptants not obtained by UAU1 method
1 : B9J08_002633 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_127317
ed gene
-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) and 90S preribosome, nucleol
s
and chromosome, centromeric region, site of double-strand break localization
c oxide
e and mitochondrial function under ER stress
alization
ed; Spider biofilm repressed
smic reticulum membrane localization
in serine/threonine kinase activity
lex localization
Pignal : psti_CGOB_00155 and Candida tropicalis MYA-3404 : CTRG_02557
Hap43-repressed; Spider biofilm induced
s NRRL Y-1498 : CANTEDRAFT_118463 and Pichia stipitis Pignal : PICST_32241
a stipitis Pignal : PICST_32242 and Candida tropicalis NEW ASSEMBLY : CTRG1_02580
lc48p
1 : B9J08_001199, Candida tenuis NRRL Y-1498 : CANTEDRAFT_133198 and Candida albicans WO-1 : C
orus NRLL YB-4239 : LELG_02117 and Debaryomyces hansenii CBS767 : DEHA2G01012g
s NRRL Y-1498 : cten_CGOB_00165 and Debaryomyces hansenii CBS767 : DEHA2G00990g
nplex, TRAPPII protein complex, TRAPPIII protein complex localization
ganization, histone acetylation, transcription by RNA polymerase II
nization, regulation of phospholipid translocation and plasma membrane localization
ptants not obtained by UAU1 method
10, C. parapsilosis CDC317 : CPAR2_103210 and C. auris B8441 : B9J08_001101
1 : B9J08_001100 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_112860
ter transfer and mitochondrial matrix localization
_83160, C. parapsilosis CDC317 : CPAR2_101820 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_11
sma membrane
parnafungin and cordycepin in the C. albicans fitness test
ressed
ctivity, role in peptidyl-glutamine methylation, regulation of translation and eRF1 methyltransferase complex

ining U2, U5, and U6 snRNAs; Spider biofilm induced
s NRRL Y-1498 : CANTEDRAFT_98613 and Debaryomyces hansenii CBS767 : DEHA2D07282g
nd Hap43

hology-related gene regulation by Ssn6p
T I complex, endosome localization

expresses CDR1 and CDR2; transcript possibly regulated by Tac1
rce; part of 4-aminobutyrate and glutamate degradation pathways; rat catheter biofilm induced

540, C. parapsilosis CDC317 : CPAR2_404520 and C. auris B8441 : B9J08_002269
1 : B9J08_002270, Debaryomyces hansenii CBS767 : DEHA2B13794g and Pichia stipitis Pignal : PICST_3
onent of mitochondrial inner membrane, mitochondrion, nucleus localization

rion morphogenesis, negative regulation of proteolysis, protein folding
A, histone deacetylation, negative regulation of transcription by RNA polymerase II and HDA1 complex, cy
response to starvation, sphingolipid metabolic process

sed on comparative genome analysis
iofilm induced; Spider biofilm induced
alysis

onent of mitochondrial inner membrane localization
itotic spindle organization, response to osmotic stress and protein phosphatase type 2A complex localizati
rdycepin in the C. albicans fitness test

869, Debaryomyces hansenii CBS767 : DEHA2F18260g and Pichia stipitis Pignal : psti_CGOB_00119
scription by RNA polymerase II and transcription factor TFIID complex localization

nner membrane electron transport chain; Hap43-repressed gene

s NRRL Y-1498 : CANTEDRAFT_98617 and Debaryomyces hansenii CBS767 : DEHA2D07392g
sed on comparative genome analysis

1498 : cten_CGOB_00085 and Debaryomyces hansenii CBS767 : DEHA2B08404g
sterification step, snoRNA splicing and U2-type catalytic step 1 spliceosome localization
lic process and endoplasmic reticulum, fungal-type vacuole, fungal-type vacuole membrane localization
s NRRL Y-1498 : CANTEDRAFT_137075 and Debaryomyces hansenii CBS767 : DEHA2F11462g
r and Spider biofilm induced

biofilm induced
tment or in an azole-resistant strain that overexpresses MDR1; Spider biofilm induced

1 : B9J08_005507 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_133308

4380, C. auris B8441 : B9J08_005504 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_101635

mponent of fungal-type vacuolar membrane localization

induced

1 : B9J08_003958 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115339
1 : B9J08_003750 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115338
10, C. parapsilosis CDC317 : CPAR2_404550 and C. auris B8441 : B9J08_003753

ent) activity
1 : B9J08_001731 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_136475
Golgi transport vesicle, integral component of Golgi membrane, integral component of endoplasmic reticu
nduced

pider biofilm repressed
rat catheter and Spider biofilm induced
embly and cytosol, nucleus localization
human or murine homolog)
90, C. parapsilosis CDC317 : CPAR2_405620 and C. auris B8441 : B9J08_004462
zole-resistant strains that overexpress CDR1 and CDR2 or MDR1
doreductase activity, zinc ion binding activity
under filamentous growth-inducing conditions, but does not block true hyphal formation in liquid media
din complex localization
RNA (m2G10) methyltransferase complex localization
der biofilm repressed
tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA and LSU-rRNA), more
um
thetic process, phosphatidylethanolamine biosynthetic process
: B9J08_004442 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115544
er biofilm induced
n family; virulence-group-correlated expression; Spider biofilm induced
: B9J08_000903 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116052
2709, Debaryomyces hansenii CBS767 : DEHA2E00110g and Pichia stipitis Pignal : PICST_30109
ination, ubiquitin-dependent ERAD pathway and endoplasmic reticulum membrane localization
psilosis : CMET_5772 and Candida tropicalis NEW ASSEMBLY : CTRG1_CGOB_00191
n pantothenate, coenzyme A biosynthetic process and CoA-synthesizing protein complex, cytoplasm, nucl
A polymerase II and DUBm complex, SAGA complex localization
avage and mitochondrial outer membrane, tRNA-intron endonuclease complex localization
nucleotide binding activity
negative regulation of gluconeogenesis, proteasome-mediated ubiquitin-dependent protein catabolic proces
ansferase activity, role in rRNA base methylation and nucleolus localization
lic process, nonsense-mediated decay, regulation of mRNA stability, stress granule assembly
tif; rat catheter and Spider biofilm induced
s); ortholog of S. cerevisiae MUD1
: B9J08_002007 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_96983
s activity
ation, positive regulation of mitochondrial translation, protein insertion into mitochondrial inner membrane fi
nscription by RNA polymerase II, regulation of fungal-type cell wall organization and nucleolus localization
zation
: B9J08_000040 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94473
stress
use serine or threonine as a sole nitrogen source; Spider biofilm repressed
_86190, C. parapsilosis CDC317 : CPAR2_404740 and C. auris B8441 : B9J08_000043
, positive regulation of transcription by RNA polymerase II and core mediator complex localization
rRNA and LSU-rRNA), more

mitochondrion, nucleus localization

rotein N-linked glycosylation and oligosaccharyltransferase complex localization

: B9J08_002385 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_100862

: B9J08_002384 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_112184

icles; regulated by Sef1, Sfu1, and Hap43; Spider biofilm induced

cell division site, septin ring assembly and cellular bud neck, cellular bud neck septin ring localization

DNA replication, double-strand break repair via break-induced replication

Candida tropicalis MYA-3404 : CTRG_05698

ida tropicalis NEW ASSEMBLY : CTRG1_05695 and Candida tropicalis MYA-3404 : CTRG_05695

-repressed; mutants display a strong defect in flow model biofilm formation; Spider biofilm induced

not obtained by UAU1 method

l molecule activity

activity, ubiquitin conjugating enzyme binding, ubiquitin-like protein binding activity

43-repressed; Spider biofilm repressed

clade-associated gene expression

on particle, endoplasmic reticulum targeting localization

and fungal-type vacuole, fungal-type vacuole membrane localization

: B9J08_004750 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113621

anization and P-body, cytoplasmic stress granule, perinuclear region of cytoplasm localization

network to specify asymmetric spindle pole body inheritance; Hap43-induced gene

e formation in both C. albicans and C. dubliniensis

ndoplasmic reticulum to Golgi vesicle-mediated transport

sicles; contributes to clathrin-coated vesicle formation and endocytosis; flow model biofilm repressed

1 method

zation

se activity, tRNA 2'-O-methyltransferase activity

lization

e phosphatase activity

uring chlamydospore formation in both C. albicans and C. dubliniensis

t transesterification step

rocess, purine ribonucleoside salvage

ler biofilm induced

: B9J08_001750 and Debaryomyces hansenii CBS767 : DEHA2F07084g
_87480, C. parapsilosis CDC317 : CPAR2_808240 and C. auris B8441 : B9J08_001753
pider biofilm induced
ng under filamentous growth-inducing conditions, but does not block true hyphal formation in liquid media
10, C. parapsilosis CDC317 : CPAR2_808090 and C. auris B8441 : B9J08_004134
d
Hap43p-repressed gene
ssed
biofilm repressed
ns; Spider biofilm repressed
strand break repair, reciprocal meiotic recombination and checkpoint clamp complex, nucleus localization
: B9J08_003539 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94507
ss via the multivesicular body sorting pathway
lated gene regulation by Ssn6; induced in cyr1 mutant; Spider biofilm induced
and cytoplasm, prospore membrane localization
2_402170, C. auris B8441 : B9J08_003513 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_137348
: B9J08_003511 and Candida tenuis NRRL Y-1498 : cten_CGOB_00197
4 specific) and histone demethylase activity (H3-monomethyl-K4 specific), more
reductase activity and acting on paired donors, more
lyubiquitination, protein ubiquitination
ity and role in ATP synthesis coupled proton transport, cristae formation, protein-containing complex asse
tone biosynthetic process
atalytic activity, septin cytoskeleton organization
NF family of DNA-dependent ATPases; Spider biofilm induced
ytoplasm localization
yubiquitination, ubiquitin-dependent ERAD pathway, ubiquitin-dependent protein catabolic process
ctivity and role in dephosphorylation
zation
nsporter activity, nucleoside transmembrane transporter activity
odderomyces elongisporus NRLL YB-4239 : LELG_04263 and Debaryomyces hansenii CBS767 : DEHA2
diated endocytosis, response to pheromone and actin cortical patch, cytosol, endosome, plasma membra

ylcarbamoyladenosine modification, tRNA threonylcarbamoyladenosine modification
itochondrion, magnesium ion transport and mitochondrial inner membrane localization
L : B9J08_001954 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_119698

n SpiderM medium and during oralpharyngeal candidasis; Spider biofilm induced
RNA cytidylyltransferase activity, tRNA adenylyltransferase activity, tRNA binding activity

ulated during planktonic growth
A polymerase II, tRNA wobble uridine modification and elongator holoenzyme complex localization

model biofilm induced; rat catheter biofilm repressed
30, C. parapsilosis CDC317 : CPAR2_401340 and C. auris B8441 : B9J08_002665

al candidiasis; Spider biofilm induced
ap43p

uced

spliceosome localization

L : B9J08_000767 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94704
er biofilms by Bcr1, Tec1, Ndt80, Brg1
ndida tropicalis MYA-3404 : CTRG_00187 and Candida albicans WO-1 : CAWG_03642

r response to methylmercury and SCF ubiquitin ligase complex localization
ion; S. cerevisiae ortholog has a role in invasive and pseudohyphal growth
tivity
onoubiquitination, protein polyubiquitination, ubiquitin-dependent endocytosis and ubiquitin ligase complex l
ngin and cordycepin in the C. albicans fitness test; possibly an essential gene, disruptants not obtained by U

l, extrinsic component of membrane localization

nance, transcription-coupled nucleotide-excision repair, ubiquitin-dependent protein catabolic process and

d

thetic process, cytokinesis, fungal-type cell wall organization and ribose phosphate diphosphokinase comp

kground; protein present in exponential and stationary growth phase yeast cultures; rat catheter biofilm rep
ofilm induced
ne, disruptants not obtained by UAU1 method

L method

L : B9J08_002205 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_103033
uced
olic process
UAU1 method; Spider biofilm repressed
processing, more
osynthesis; regulated by Tsa1p, Tsa1Bp under H2O2 stress conditions

42050, C. parapsilosis CDC317 : CPAR2_403320 and C. auris B8441 : B9J08_001404

a stipitis Pignal : PICST_74821 and Candida tropicalis NEW ASSEMBLY : CTRG1_00174
a stipitis Pignal : PICST_52615 and Candida tropicalis MYA-3404 : CTRG_00173
ed
predicted Kex2p substrate

s hansenii CBS767 : DEHA2G17754g and Pichia stipitis Pignal : PICST_31424

d colony wrinkling but does not block true hyphal growth; induced by nitric oxide independent of Yhb1p

arnafungin and cordycepin in the C. albicans fitness test

transport and integral component of endoplasmic reticulum membrane localization

perfamily; Hap43-induced gene; alkaline upregulated by Rim101; possibly an essential gene, disruptants no

ilm induced

ylase activity (H3-K36 specific), histone demethylase activity (H3-K9 specific), sequence-specific DNA bindi

s NRRL Y-1498 : CANTEDRAFT_113280 and Lodderomyces elongisporus NRLL YB-4239 : LELG_04166

F-1 complex, chromatin, chromosome, centromeric region, nucleus localization

ce of elevated CO2

lida tropicalis NEW ASSEMBLY : CTRG1_00248 and Spathaspora passalidarum NRRL Y-27907 : SPAPA

repair, reciprocal meiotic recombination and Rad17 RFC-like complex localization

ctor 2 complex assembly, positive regulation of translational initiation

pressed

n DNA binding activity, role in reciprocal meiotic recombination and MutSgamma complex, nuclear chromo

in tRNA; repressed in core stress response

ortholog of S. cerevisiae Ear1; transcript regulated by iron; Ssr1-represssed; Spider biofilm induced

iofilm induced

II activity, RNA polymerase III activity, RNA-directed 5'-3' RNA polymerase activity, zinc ion binding activity

ved in cellular protein catabolic process and fungal-type vacuole lumen localization

preinitiation complex assembly, transcription initiation from RNA polymerase II promoter

idylserine flippase activity

iod

wobble nucleosides in tRNA; Spider biofilm induced

sembly and U2 snRNP, U2-type prespliceosome localization

Plc1-regulated; possibly an essential gene, disruptants not obtained by UAU1 method

tease, integrase; downstream of RHD2, similar to the Gag region encoding nucleocapsid-like protein; rat ca

action between organisms, cellular response to DNA damage stimulus

_00040

L : B9J08_004708 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94387

, Pichia stipitis Pignal : PICST_32156 and Candida guilliermondii ATCC 6260 : PGUG_04611

zation

candidiasis; Spider biofilm induced

s hansenii CBS767 : DEHA2A08250g and Pichia stipitis Pignal : PICST_29838 facilitator superfamily (MFS)

NA N1-guanine methylation and cytoplasm, mitochondrial matrix localization

f 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA and LSU-rRNA), more

nal termination, translational termination and mitochondrial inner membrane, mitochondrion localization

athaspora passalidarum NRRL Y-27907 : SPAPADRAFT_64619 and Candida tropicalis MYA-3404 : CTR

ly

kling under filamentous growth-inducing conditions, but does not block true hyphal formation in liquid medi

cytoplasm to vacuole transport by the Cvt pathway, early endosome to Golgi transport, macroautophagy

activity and role in mRNA export from nucleus in response to heat stress, nuclear pore organization

s NRRL Y-1498 : CANTEDRAFT_93767 and Debaryomyces hansenii CBS767 : DEHA2G16984g

L : B9J08_000308, Debaryomyces hansenii CBS767 : DEHA2G16962g and Pichia stipitis Pignal : PICST_

, sterol regulatory element binding protein cleavage and Dsc E3 ubiquitin ligase complex, clathrin-coated v

rane, translocation and signal recognition particle, endoplasmic reticulum targeting localization

detected by mass spec in stationary phase cultures

elated genes in the RB2 repeat sequence

Pignal : PICST_68242, Candida tropicalis MYA-3404 : CTRG_00303 and Candida albicans WO-1 : CAWG

ngin induced

y

drial inner membrane, integral component of mitochondrial membrane localization

pressor protein 4 domain; induced by alpha pheromone in SpiderM medium

L : B9J08_005206 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114940

repair and endoplasmic reticulum localization

calis MYA-3404 : CTRG_05742 and Candida albicans WO-1 : CAWG_03407

site, and is membrane-bound; Spider biofilm induced

uperfamily (MFS)

L : B9J08_000295 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_102588

ed

L : B9J08_004187 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_105448

al protein targeting to membrane, translocation

responses to nutrient stress; Spider biofilm induced

; possibly an essential gene, disruptants not obtained by UAU1 method; Hap43p-induced gene

sing, negative regulation of telomere maintenance via telomerase and nucleolus, nucleoplasm localization

n induced

L : B9J08_001760 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_137302

hr 4; clade-associated gene expression

s NRRL Y-1498 : CANTEDRAFT_105331 and Debaryomyces hansenii CBS767 : DEHA2E03454g

mpound biosynthetic process, one-carbon metabolic process, purine nucleobase biosynthetic process and

protein catabolic process, traversing start control point of mitotic cell cycle and GID complex localization

plasmic reticulum tubular network maintenance and endoplasmic reticulum tubular network organization, m

d tRNA (m7G46) methyltransferase complex localization

zation

:a junction localization
tor superfamily (MFS); induced by alpha pheromone in Spider medium

5-FC), 5-fluorouracil (5-FU); repressed in core stress response; repressed by prostaglandins; Hap43-induce

iculum localization

ndida tropicalis MYA-3404 : CTRG_04054 and Candida albicans WO-1 : CAWG_03295
biosynthetic process and Golgi apparatus, integral component of membrane, mitochondrial outer membran
process, chromatin assembly, protein ubiquitination and anaphase-promoting complex localization
d tubercidin (7-deazaadenosine)

p43-induced gene
970, C. parapsilosis CDC317 : CPAR2_500860 and C. auris B8441 : B9J08_003204
of S. cerevisiae MAK11

phosphatidylinositol-4-phosphate binding, phosphatidylinositol-5-phosphate binding activity
n Group I intron splicing, mitochondrial mRNA processing, positive regulation of mitochondrial translation
calization

her biofilm induced; rat catheter and Spider biofilm induced; F-12/CO2 early biofilm induced

gulated; Spider biofilm induced
_45200, C. parapsilosis CDC317 : CPAR2_500480 and C. auris B8441 : B9J08_005034

1 : B9J08_005037 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_103249
C. albicans fitness test; Spider biofilm repressed
nide isomerase activity and role in histidine biosynthetic process
LSU-rRNA) and nucleolus localization
sion; induced by alpha pheromone in SpiderM medium; Hap43-induced; Spider biofilm repressed
gulation of transcription from RNA polymerase II promoter in response to oxidative stress and Lid2 comple
port, intra-Golgi vesicle-mediated transport, macroautophagy, regulation of GTPase activity

30, C. parapsilosis CDC317 : CPAR2_500650 and C. auris B8441 : B9J08_005169
se complex, extrinsic component of mitochondrial inner membrane, mitochondrial matrix localization

some system, positive regulation of transcription elongation from RNA polymerase II promoter, tubulin com
d nucleus localization
h is a putative phosphopantothenoylcysteine decarboxylase

e in cellular response to phosphate starvation, nucleoside triphosphate metabolic process
r response to DNA damage stimulus, error-free translesion synthesis, error-prone translesion synthesis
1 : B9J08_003351 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_105024

rRNA genes by RNA polymerase I in S. cerevisiae; possibly an essential gene, disruptants not obtained by
sion, mitochondrion inheritance, mitochondrion localization, nuclear migration along microtubule
uperfamily; induced by alpha pheromone in SpiderM medium
, reciprocal meiotic recombination and condensed nuclear chromosome localization
sm localization

al : psti_CGOB_00141 and Candida metapsilosis : CMET_534
t; Hap43p-induced gene
s NRRL Y-1498 : CANTEDRAFT_116046 and Pichia stipitis Pignal : PICST_28890
ity, guanosine-diphosphatase activity and nucleoside-diphosphatase activity, more

L : B9J08_000913 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_126814

Pignal : PICST_43336, Candida tropicalis MYA-3404 : CTRG_04038 and Candida albicans WO-1 : CAWG

to vacuole and fungal-type vacuole, plasma membrane localization

cript is upregulated in an RHE model of oral candidiasis

L : B9J08_004783 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_119393

letely synthesized proteins and mitochondrial inner membrane localization

nbrane transporter activity and role in carbohydrate transport, pyrimidine nucleotide-sugar transmembrane

nd positive regulation of cellular response to phosphate starvation, more

nd Golgi apparatus, TRAPPII protein complex localization

r biofilm induced

-induced gene

ndida tropicalis MYA-3404 : CTRG_03792 and Candida albicans WO-1 : CAWG_03165

L : B9J08_001807 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_97195

um membrane, extrinsic component of membrane localization

dent protein catabolic process and cytoplasm, nucleus localization

ss-induced via Cap1; rat catheter biofilm repressed

m RNA polymerase II promoter

ential gene, disruptants not obtained by UAU1 method

; Spider biofilm repressed; sumoylation regulated by Hsp90p

ression, protein initiator methionine removal involved in protein maturation

ess, pyrimidine-containing compound salvage and cytoplasm, nucleus localization

treatment or in an azole-resistant strain that overexpresses CDR1 and CDR2; induced by nitric oxide; rat

s hansenii CBS767 : DEHA2B15730g and Candida tropicalis MYA-3404 : CTRG_03755

EW ASSEMBLY : CTRG1_03758 and Spathaspora passalidarum NRRL Y-27907 : spas_CGOB_00037

lymerase III complex localization

lpha pheromone in SpiderM medium

ter and Spider biofilm induced

biofilm induced; Spider biofilm induced

ryomyces hansenii CBS767 : DEHA2G16104g and Pichia stipitis Pignal : psti_CGOB_00212

095 and Candida albicans WO-1 : CAWG_04820

, cellular manganese ion homeostasis; Spider biofilm repressed

elomere and SAS acetyltransferase complex localization

m HIV+ patients with oral candidiasis; Spider biofilm repressed

ignal and attaches GPI to proteins in the ER; Spider biofilm repressed

process, protein ubiquitination and anaphase-promoting complex, nuclear periphery localization

sed

sed on comparative genome analysis

zation

induced

e in NLS-bearing protein import into nucleus, proteasome localization, protein import into nucleus, protein ta

1 : B9J08_004528 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_109949

ntial, disruptants not obtained by UAU1 method; Spider biofilm repressed

lex localization

osynthetic process, cytokinesis, fungal-type cell wall organization

rial recombination, apoptosis and maintenance of polyploidy; Spider biofilm repressed

of pol I to the promoter; Hap43-induced gene

calization

separation during anaphase; Spider biofilm repressed

pressed; flow model biofilm induced

1 : B9J08_001314 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_98299

1 : B9J08_000441 and Candida tenuis NRRL Y-1498 : cten_CGOB_00233

s NRRL Y-1498 : CANTEDRAFT_107934 and Pichia stipitis Pignal : PICST_63283

d merged with orf19.2224, based on comparative genome analysis; flow model biofilm repressed

sferase activity

sential gene, disruptants not obtained by UAU1 method

1 : B9J08_002049 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_93989

lation of cell aging, telomere maintenance, telomere maintenance via recombination and EKC/KEOPS con

s, formin-nucleated actin cable assembly, regulation of GTPase activity, regulation of protein localization

inhibition by 1-methyl-D,L-tryptophan increases hyphal growth; expressed in yeast and hyphae; rat cathete

zation

calization

stone lysine methylation, telomere maintenance

s NRRL Y-1498 : cten_CGOB_00020 and Debaryomyces hansenii CBS767 : DEHA2F24310g

zation

n RHE model; regulated by Nrg1, Tup1

303850, C. auris B8441 : B9J08_000423 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114159

on

and endoplasmic reticulum palmitoyltransferase complex, extrinsic component of endoplasmic reticulum m

1 : B9J08_005315 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_135271

nt in exponential and stationary phase yeast cultures; Hap43-induced; Spider biofilm repressed

calis MYA-3404 : CTRG_05379, Candida albicans WO-1 : CAWG_04514 and Candida metapsilosis : CME

ne biosynthetic process and mitochondrial inner membrane, mitochondrion localization

e metabolic process and cytoplasm localization

ant strain overexpressing CDR1 and CDR2; induced by benomyl treatment

c reticulum, peroxisomal membrane, peroxisome localization

biofilm induced

tion

1 : B9J08_002922 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115294

ine synthesis and cytoplasm, nucleus localization
L : B9J08_001459 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_135125
L : B9J08_001456 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_135127
nding activity

, in shmoo formation and nuclear migration in the pre-zygote of S. cerevisiae; Hap43-repressed
; Spider biofilm induced
dephosphorylation and endoplasmic reticulum localization
ome and U2-type prespliceosome localization
idine synthase activity and role in riboflavin biosynthetic process, tRNA pseudouridine synthesis
ressed by nitric oxide; virulence-group-correlated expression; Spider biofilm induced

ndida tropicalis MYA-3404 : CTRG_05315 and Candida albicans WO-1 : CAWG_04584
ymerase III assembly, formation of translation preinitiation complex and cytoplasm localization

oup required for cytochrome c oxidase activity; Spider biofilm repressed
ulation of cleistothecium development and positive regulation of conidium formation, more
L : B9J08_001942 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94797

ells exposed to fluconazole over multiple generations; overexpression increases resistance to farnesol and
eatment); rat catheter biofilm repressed
ome activity and role in 2-oxoglutarate metabolic process, tricarboxylic acid cycle
L : B9J08_002552 and Debaryomyces hansenii CBS767 : DEHA2F14278g

adenosine polyphosphates; Spider biofilm induced

n induced

asmic reticulum, fungal-type vacuole membrane localization

cribed mRNA catabolic process, no-go decay

morphology-related gene regulation by Ssn6p; induced during cell wall regeneration; possibly essential

of Gpa1 in S. cerevisiae; regulated by Gcn4; repressed in response to amino acid starvation (3AT); rat cath
L : B9J08_004350 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115972

t protein catabolic process, regulation of nitrogen utilization and GID complex localization
n and cordycepin in the C. albicans fitness test
hment of mitochondrion localization, nuclear-transcribed mRNA catabolic process, deadenylation-depende

sis; flow model biofilm induced

sed on comparative genome analysis
ondrially-encoded genes; Hap43-induced
anscription by RNA polymerase II

and CIA complex, cytosol, nucleus localization
anization and extrinsic component of mitochondrial inner membrane localization

nscription by RNA polymerase II, silent mating-type cassette heterochromatin assembly
s hansenii CBS767 : DEHA2G06908g and Candida guilliermondii ATCC 6260 : PGUG_02858
omplex, U6 snRNP, nucleolus, nucleus localization
n methylthioadenosine
to vacuole transport via multivesicular body sorting pathway, protein targeting to vacuole and cytoplasm, la

sion, regulated by Cyr1, Ras1, Efg1; rat catheter biofilm repressed

chain complex I assembly and membrane localization
L : B9J08_002489 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_133407

P complex localization
ndida tropicalis MYA-3404 : CTRG_05968 and Candida albicans WO-1 : CAWG_04684
L : B9J08_002492 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_92321
; Spider biofilm induced; rat catheter biofilm repressed

J5 tri-snRNP complex, U5 snRNP, post-mRNA release spliceosomal complex, spliceosomal complex local
ation
otein localization to endoplasmic reticulum exit site

pider biofilm induced; flow model biofilm repressed

bly and cellular bud neck contractile ring, incipient cellular bud site, myosin II complex localization

zation

superfamily (MFS)
hotericin B induced; colony morphology regulated by Ssn6; reduced oral epithelial cell damage by mutant; S
uently reinstated in Assembly 21 based on comparative genome analysis
nduced
sed on comparative genome analysis
atients with oral candidiasis

of protein localization to endoplasmic reticulum membrane, ubiquitin-dependent ERAD pathway
ve genome analysis; F-12/CO2 early biofilm induced
ocess, peptidyl-diphthamide biosynthetic process from peptidyl-histidine

tidyl-histidine

andida tropicalis NEW ASSEMBLY : CTRG1_05538 and Spathaspora passalidarum NRRL Y-27907 : SPA
epressed; Spider biofilm repressed

a stipitis Pignal : PICST_32162 and Candida tropicalis NEW ASSEMBLY : CTRG1_03193
omplex assembly, chromatin organization, histone acetylation, transcription by RNA polymerase II
(thiamine diphosphate); active as a homodimer
s hansenii CBS767 : DEHA2G07766g and Pichia stipitis Pignal : psti_CGOB_00176

Pignal : PICST_32155, Candida tropicalis MYA-3404 : CTRG_03184 and Candida albicans WO-1 : CAWG

e in S. cerevisiae; Spider biofilm induced

nbrane; repressed by alpha pheromone in SpiderM medium

ced
e-resistant strain that overexpresses CDR1 and CDR2; transcription is repressed in response to alpha phe
ne, trans-Golgi network localization
alization

ı localization
ɔd; Hap43-repressed; sumoylation target; Spider biofilm repressed
L : B9J08_004358 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116966
ced

in-disulfide reductase activity and role in protein folding
10, C. parapsilosis CDC317 : CPAR2_100920 and C. auris B8441 : B9J08_004360
es; Hap43p-repressed gene

of autophagy of mitochondrion

by nitric oxide independent of Yhb1; repressed in ssr1 null; ketoconazole, hypoxia induced; Spider biofilm i

/tosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine)
L : B9J08_004395 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_96367

inner membrane from matrix, protein insertion into mitochondrial membrane
ingle-stranded RNA binding activity

RL Y-1498 : CANTEDRAFT_113855 and Debaryomyces hansenii CBS767 : DEHA2G20240g
ım organization, glutaminyl-tRNAGln biosynthesis via transamidation
 and nucleus localization
380, C. parapsilosis CDC317 : CPAR2_101110 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_1232
ıc6 complex, nucleus localization
eter and Spider biofilm induced

ndosome to Golgi
-proteins; flow model biofilm induced
tation, nuclear migration and dynactin complex localization

alization
flow model biofilm indced

ric oxide independent of Yhb1; Spider biofilm induced
ced
 transcription by RNA polymerase III, transcription initiation from RNA polymerase III promoter
localization
om Assembly 20; subsequently reinstated in Assembly 21 based on comparative genome analysis
, protein O-linked mannosylation; Spider biofilm repressed

_54670, C. parapsilosis CDC317 : CPAR2_502560 and C. auris B8441 : B9J08_004333

sis strategy
ty, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor activity
ıe monomethylation, peptidyl-lysine trimethylation and nucleolus localization
ı both C. albicans and C. dubliniensis; flow model biofilm induced
o the endoplasmic reticulum

 decreases in stationary phase cultures; Hap43-repressed; Spider biofilm repressed
L : B9J08_003974 and Candida tenuis NRRL Y-1498 : cten_CGOB_00242
zation
amage; mutants show increased virulence
s hansenii CBS767 : DEHA2D13992g and Pichia stipitis Pignal : PICST_40400
 subunit biogenesis and cytosol localization
NA replication, synthesis of RNA primer
d cytosol localization

d gene expression
in oralpharyngeal candidasis; Spider biofilm induced
ogenesis; Spider biofilm repressed
L : B9J08_002731 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94402
320, C. parapsilosis CDC317 : CPAR2_603375 and C. auris B8441 : B9J08_005197

ilenced chromosomal regions; affects transcriptional elongation; Hap43-repressed; Spider biofilm represse
ing; Hap43-repressed

60200, C. parapsilosis CDC317 : CPAR2_603320 and C. auris B8441 : B9J08_002166

mplex localization
intron; repressed by chlamydospore formation in C. albicans and C. dubliniensis; rat catheter, Spider and
iation, retrograde protein transport, ER to cytosol, ubiquitin-dependent ERAD pathway
olved in protein targeting to mitochondrion, protein stabilization and mitochondrial matrix localization
uptants not obtained by UAU1 method

ation and mitochondrion localization
L : B9J08_000521 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114325
ients with oral candidiasis
process and mitochondrial inner membrane, mitochondrion localization

alysis
snRNP, U2-type prespliceosome, U4/U6 x U5 tri-snRNP complex, U5 snRNP, post-mRNA release splicec
ne inhibitor activity
zation
e body duplication and nuclear envelope, nuclear pore, nuclear pore transmembrane ring, spindle pole boc
s NRRL Y-1498 : CANTEDRAFT_108530 and Debaryomyces hansenii CBS767 : DEHA2F15532g

Arp2/3 complex-mediated actin nucleation and actin cortical patch, cytoplasm localization
L : B9J08_001867 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115034
L : B9J08_001866 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_135512
n from RNA polymerase II promoter; flow model biofilm induced

L : B9J08_001862, Candida tenuis NRRL Y-1498 : CANTEDRAFT_115038 and Pichia stipitis Pignal : PICS
ubiquitin-proteasome system and cytosol localization

ons; repressed during infection of macrophages; Spider biofilm induced; flow model biofilm repressed
L : B9J08_003439 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_125757

ressed; induced by prostaglandins
egulated by Sef1, Sfu1, and Hap43; Spider biofilm repressed; rat catheter biofilm induced

603060, C. auris B8441 : B9J08_003420 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113703

complex IV)

L : B9J08_001119 and Candida tenuis NRRL Y-1498 : cten_CGOB_00054
CTRG_02973 and Candida albicans WO-1 : CAWG_05252

role in C-terminal protein methylation and integral component of membrane localization
L : B9J08_005399 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94450
_61340, C. parapsilosis CDC317 : CPAR2_602790 and C. auris B8441 : B9J08_005400
tive regulation of meiotic nuclear division and positive regulation of stress-activated MAPK cascade, more
n

s NRRL Y-1498 : cten_CGOB_00240 and Pichia stipitis Pignal : psti_CGOB_00191
nthesis; rat catheter biofilm induced
, mRNA destabilization, negative regulation of gene expression
ubiquitin-dependent ERAD pathway and endoplasmic reticulum, glycosylphosphatidylinositol-mannosyltrar
facilitator superfamily (MFS); Hap43p-repressed gene
nfolded protein, ubiquitin-dependent ERAD pathway and endoplasmic reticulum lumen localization
facilitator superfamily (MFS); induced by nitric oxide
utant exhibits no obvious defects
NA catabolic process, mitochondrial DNA replication, mitochondrial genome maintenance and mitochondric
.840, C. parapsilosis CDC317 : CPAR2_602630 and C. auris B8441 : B9J08_005378
x localization
nduced by nitric oxide, oxidative stress, alpha pheromone; fungal-specific; Hap43-repressed; Spider biofilm
sitivity to parnafungin and cordycepin in the C. albicans fitness test
, Debaryomyces hansenii CBS767 : DEHA2F11858g and Pichia stipitis Pignal : PICST_60705
1 : B9J08_005503 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_112751
iofilm repressed
nance of polarized growth sites; Hog1p-repressed
ditions; induced by Mnl1p under weak acid stress; Spider biofilm induced
1 : B9J08_003070 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114419
obtained by UAU1 method
sruptants not obtained by UAU1 method
s55/Vps68 complex, fungal-type vacuole membrane localization
oralpharyngeal candidasis
nedium
verexpresses CDR1 and CDR2
null mutant; Spider biofilm induced
modified tRNA; predicted Kex2p substrate; Spider biofilm induced
ne
fluconazole resistance; repressed by nitric oxide, 17-beta-estradiol, ethynyl estradiol
nthesis; Spider biofilm induced
zation
ne presence of elevated CO2
n
nduced
merase II promoter by pheromones and CHRAC localization
cecum
lex III assembly, positive regulation of mitochondrial translation
on particle, endoplasmic reticulum targeting localization
onse; oxidative stress-induced via Cap1; Spider biofilm repressed
1 : B9J08_001639 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115220
1 : B9J08_001638 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113271

L : B9J08_001637 and Candida tenuis NRRL Y-1498 : cten_CGOB_00252
1 regulated; Rgt1-repressed; protein present in exponential and stationary growth phase yeast; rat catheter

uced
erfamily (MFS)
ctivity
c reticulum and SNARE complex, integral component of cytoplasmic side of endoplasmic reticulum membr
by Cph1p, Efg1p, Cph2p; low-level expression; alkaline upregulated; fungal-specific (no human or murine h
iated transport

ndida tropicalis MYA-3404 : CTRG_05769 and Candida albicans WO-1 : CAWG_05077

ister chromatid segregation and chromosome, telomeric region, nuclear envelope localization

80, C. parapsilosis CDC317 : CPAR2_602080 and C. auris B8441 : B9J08_004864
ice; Spider biofilm induced
vth; repressed in core stress response

dephosphorylation and PAS complex, extrinsic component of membrane, fungal-type vacuole membrane, r
liasis

Candida tropicalis NEW ASSEMBLY : CTRG1_02719 and Candida tropicalis MYA-3404 : CTRG_02719
60, C. parapsilosis CDC317 : CPAR2_600230 and C. auris B8441 : B9J08_002518
sporting ATPase activity, rotational mechanism activity and role in ATP synthesis coupled proton transport

positive regulation of ubiquitin-dependent endocytosis, regulation of intracellular transport
L : B9J08_000407 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_92714

s hansenii CBS767 : DEHA2A06270g and Pichia stipitis Pignal : PICST_31363
in ergosterol metabolic process; early stage flow model biofilm induced; Spider biofilm induced
el biofilm induced; Spider biofilm induced
Pignal : PICST_32045 and Candida guilliermondii ATCC 6260 : PGUG_00070

azole-resistant strain that overexpresses MDR1; flow model biofilm induced; rat catheter biofilm repressed
621
CST_32878 and Candida guilliermondii ATCC 6260 : PGUG_03423
duced
of ASH1 mRNA; Hap43-induced gene
hod
chromatid cohesion, mitotic spindle assembly checkpoint signaling

genome maintenance, positive regulation of rRNA processing, rRNA metabolic process and mitochondrion

method
iated transport
d merged with orf19.1020 based on comparative genome analysis
perfamily (MFS); ketoconazole or caspofungin repressed; Spider biofilm induced
rase I transcription and nucleolus, rDNA heterochromatin localization
ttenuated virulence
L : B9J08_003898 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115908

zation
ryomyces hansenii CBS767 : DEHA2E19888g and Candida tropicalis NEW ASSEMBLY : CTRG1_02732

dent protein catabolic process and SCF ubiquitin ligase complex localization

ced; rat catheter and Spider biofilm induced

2 snRNP, U2-type spliceosomal complex localization

ization

s; Hog1p-induced; clade-associated gene expression

y FGR6-related genes in the RB2 repeat sequence; rat catheter biofilm repressed

ndida tropicalis MYA-3404 : CTRG_02747 and Candida albicans WO-1 : CAWG_04972

protein maturation

tivity and L-glutamate transmembrane transporter activity, more

ein localization to kinetochore, sister chromatid biorientation

s NRRL Y-1498 : CANTEDRAFT_121753 and Debaryomyces hansenii CBS767 : DEHA2E19712g

induced

Pignal : PICST_30726 and Candida guilliermondii ATCC 6260 : PGUG_04023

mitochondrial intermembrane space, mitochondrial respiratory chain complex IV localization

ERAD pathway, ubiquitin-dependent protein catabolic process, vesicle organization

ation of retrograde vesicle-mediated transport, Golgi to ER, ribophagy

calis MYA-3404 : CTRG_02757 and Candida albicans WO-1 : CAWG_04949

s NRRL Y-1498 : CANTEDRAFT_119969 and Debaryomyces hansenii CBS767 : DEHA2A05896g

charide donor for N-linked glycosylation of proteins; rat catheter biofilm repressed

ansport, transmembrane transport and membrane localization

alysis

l

tion in S. cerevisiae; possibly an essential gene, disruptants not obtained by UAU1 method

1 : B9J08_003161 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_92162

NA processing and cytoplasm localization

ylation, wobble position ribose methylation and cytoplasm, endosome localization

ed by Sef1p-, Sfu1p-, and Hap43p

pressed

tide metabolic process and mitochondrial inner membrane, mitochondrial matrix localization

uptants not obtained by UAU1 method

_70350, C. parapsilosis CDC317 : CPAR2_300160 and C. auris B8441 : B9J08_000897

al secretion signal; rat catheter and Spider biofilm repressed

aintenance, telomere maintenance via telomerase

formation; not the true Avt1 ortholog of S. cerevisiae

n and cordycepin in C. albicans fitness test; Spider biofilm repressed

2_300640, C. auris B8441 : B9J08_002252 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_124433

de export across plasma membrane, fluoride transmembrane transport and plasma membrane localization

g activity

, nucleus localization
ive stress-induced via Cap1; induced by Mnl1 under weak acid stress; macrophage-repressed; rat catheter
cted role in biotin biosynthesis and respiratory growth; Spider biofilm repressed
d cellular bud neck, cellular bud neck contractile ring localization
2_805430, C. auris B8441 : B9J08_000227 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_96597

2_805360, C. auris B8441 : B9J08_000224 and Candida tenuis NRRL Y-1498 : cten_CGOB_00114
ilm growth; Spider biofilm repressed
0410 and Candida albicans WO-1 : CAWG_05407
x binding, transcription coregulator activity, triplex DNA binding activity

1 : B9J08_001159, Debaryomyces hansenii CBS767 : DEHA2F22946g and Pichia stipitis Pignal : PICST_4
n elongation from RNA polymerase II promoter and cytoplasm, nucleus localization
050, C. parapsilosis CDC317 : CPAR2_301100 and C. auris B8441 : B9J08_001157
al candidiasis; regulated by Sef1, Sfu1, and Hap43
1 method

AR2_703230, C. auris B8441 : B9J08_003284 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_11782
uced by nitric oxide; Spider biofilm induced
d cordycepin in the C. albicans fitness test
otein targeting to vacuole, retrograde transport, endosome to Golgi and cytoplasm, endosome, nucleus loca

repressed

1 : B9J08_005266 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94947
uced

dative stress-induced via Cap1
1498 : cten_CGOB_00183 and Debaryomyces hansenii CBS767 : DEHA2F22462g

s hansenii CBS767 : DEHA2F22220g and Pichia stipitis Pignal : PICST_32459
zation
LSU-rRNA) and nucleus, preribosome, small subunit precursor localization

y FGR6-related genes in the RB2 repeat sequence

nomyl treatment or in azole-resistant strain that overexpresses MDR1; Spider biofilm induced
1 : B9J08_000715 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_105022
er biofilm induced
sphatidylglycerol binding activity
, acting on acid anhydrides, in phosphorus-containing anhydrides, m7G(5')pppN diphosphatase activity

r periphery localization

omplex assembly, mitochondrion organization and mitochondrion localization
isiae; Spider biofilm induced
xidoreductase); Hap43-induced gene; Spider biofilm induced
1 : B9J08_002141 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116256
sis; Hap43-induced gene; Spider biofilm induced; F-12/CO2 early biofilm induced
nization, nucleolar large rRNA transcription by RNA polymerase I
21; Ssn6 colony morphology-related regulation; induced by NO; Hap43-repressed; rat catheter and flow mo
n

lization

1 : B9J08_004871 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114098
S); repressed in core caspofungin response; induced in oralpharyngeal candidasis; Spider biofilm induced

dubliniensis

ded proteins from the matrix into the inner membrane; Spider biofilm repressed

translation and integral component of mitochondrial inner membrane, mitochondrial inner membrane loca

downregulaated in stationary phase yeast cultures; Hap43-repressed; flow model biofilm induced; Spider b

mitochondrial intermembrane space localization

nt signaling; Hap43-repressed; induced by ketoconazole, hypoxia, during growth in the mouse cecum; Spi

bond formation within the ER; Spider biofilm induced

erna, SNARE complex localization

ved in mitophagy; mutants are defective in mitochondrial function and virulence; regulated by Sef1p, Sfu1p,

pole localization

tion

ed

: B9J08_001563 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_102923

; induced by Mnl1 under weak acid stress; possibly essential gene, disruptants not obtained by UAU1 met

tance; induced by Mnl1 under weak acid stress

of TORC1 signaling and Lst4-Lst7 complex, cytoplasm, vacuolar membrane localization

catheter and Spider biofilm repressed

ive regulation of transcription by RNA polymerase II, more

ial large ribosomal subunit localization

stance

lis NEW ASSEMBLY : CTRG1_05049 and Spathaspora passalidarum NRRL Y-27907 : SPAPADRAFT_6

calization

NRRL Y-1498 : CANTEDRAFT_135055 and Debaryomyces hansenii CBS767 : DEHA2E07678g

psilosis : CMET_5893 and Candida orthopsilosis Co 90-125 : CORT_0C00820

psilosis : CMET_5895 and Candida orthopsilosis Co 90-125 : CORT_0C00800

p43; rat catheter biofilm induced

cytosol, nucleus, tRNA (m7G46) methyltransferase complex localization

r biofilm induced

codes nucleocapsid-like protein, reverse transcriptase, protease, and integrase

ndida tropicalis MYA-3404 : CTRG_05087 and Candida albicans WO-1 : CAWG_00654

, negative regulation of programmed cell death, positive regulation of response to oxidative stress, protein

NRRL Y-1498 : CANTEDRAFT_115664 and Debaryomyces hansenii CBS767 : DEHA2B05940g

72270, C. parapsilosis CDC317 : CPAR2_702850 and C. auris B8441 : B9J08_001027

: B9J08_001028 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_125842

liasis

: B9J08_001030 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_92002

ed as single polyprotein with Gag, reverse transcriptase, protease, and integrase; rat catheter biofilm repre

translated as single polyprotein that includes Gag, reverse transcriptase, protease, and integrase; rat cat

n

phagy, re-entry into mitotic cell cycle after pheromone arrest and Golgi trans cisterna, endoplasmic reticulu

Kennedy pathway of phosphatidylcholine and phosphatidylethanolamine biosynthesis ependent ERAD pathway

ctivity

biogenesis and cytoplasm localization

_72620, C. parapsilosis CDC317 : CPAR2_704190 and C. auris B8441 : B9J08_000738

zation

hyphal growth, and virulence

Cyr1; induced by amino acid starvation; macrophage-induced protein, macrophage-repressed; Spider biof

catheter biofilm induced

egions

ndida tropicalis MYA-3404 : CTRG_05211 and Candida albicans WO-1 : CAWG_05649

alis MYA-3404 : CTRG_05209 and Candida albicans WO-1 : CAWG_05654

vation of fructose-1,6-bisphosphatase; Hap43-repressed gene

L : B9J08_002713 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113193

eter biofilm repressed

ne space localization

ced gene; Spider biofilm induced

ulated by yeast-hyphal switch; filament induced; regulated by Nrg1, Tup1, Mob2, Hap43; mRNA binds She3

in SpiderM medium

erexpressing MDR1; Spider biofilm induced

olysaccharide exporter superfamily; Spider biofilm induced

L : B9J08_002111 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114480

sparaginyl-tRNA aminoacylation and mitochondrion localization

n

L : B9J08_003875 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_104803

CBS767 : DEHA2A05456g and Pichia stipitis Pignal : PICST_30999

plasmic reticulum

EW ASSEMBLY : CTRG1_05165 and Candida tropicalis MYA-3404 : CTRG_05165

omplex, cytoplasm localization

theter biofilm induced

to parnafungin in the C. albicans fitness test; Spider biofilm induced

d transcription is observed upon fluphenazine treatment; induced upon adherence to polystyrene

ent protein catabolism via the multivesicular body sorting pathway; Spider biofilm induced

L : B9J08_000280 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_112965

L : B9J08_000277 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_119320

ession leads to defects in respiratory growth, activation of autophagy, attenuated virulence

alis MYA-3404 : CTRG_05152 and Candida albicans WO-1 : CAWG_05735

rexpresses MDR1; induced by Mnl1 under weak acid stress; rat catheter and Spider biofilm induced

L : B9J08_004922 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_92070

ene

etyl-serine (OAS) pathway of sulfur assimilation; upregulated in biofilm; protein level decreases in stationar
pressed
al isolates from HIV+ patients with oral candidiasis; Spider biofilm repressed
equency; macrophage-induced
er biofilm repressed
script; transcript repressed by MTLa1-MTLalpha2; regulated by hemoglobin-responsive Hbr1 via MTL gene
uman CDK2; lacks glycine loop motif; conserved lysine (K36) not required for activity; possibly essential ge
pider biofilm repressed
nduced gene; Spider biofilm repressed
3 predicted N-glycosylation sites; phagocytosis by macrophages induces transcript; rat catheter, Spider ar
d; colony morphology-related regulation by Ssn6; Hap43-repressed; rat catheter and Spider biofilm induce
essed gene
r in oxidative stress; complements S. cerevisiae yap1 mutant; oralpharyngeal candidasis-, human neutrop
ion by Ssn6; alkaline induced; protein decreased in stationary phase; sumoylation target; flow model biofilm
alog, to amphotericin B; exponential and stationary phase yeast; flow model biofilm induced; rat catheter, S
on and telomere protection; mutation causes marginal increase in caspofungin sensitivity
; insertion mutation near 3' end of gene increases caspofungin sensitivity; pheromone/hyphal induced; flow
ave reduced CFU in mice, hyphal defect in C. elegans infection; Spider biofilm induced
, fluconazole, carbon source, pH, Rim101, Ssn6, Hog1, Hap43, Sfu1, Sef1, farnesol, core stress response
ndria; induced in macrophages; Hog1-repressed; stationary phase enriched; farnesol-upregulated in biofilm
t genes; mutant displays increased filamentous/invasive growth; flucytosine repressed; rat catheter biofilm
rvation-response, respiratory, glycolytic genes; does not bind to centromeres as does S. cerevisiae Cbf1;
associated; required for wild-type hyphal growth and transcriptional regulation of cell-wall-associated genes
t induced by corticosterone; contains a possible NAD/FAD binding region; regulated by Nrg1, Tup1; Spider
; repressed by NO, alkaline pH; colony morphology-related regulation by Ssn6; regulated by Sef1, Sfu1, H
p); induced by iron starvation, ciclopirox olamine; caspofungin repressed; not required for virulence in mou
nt of galvanotropism; transcript regulated by Nrg1 and Mig1; flow model biofilm repressed
Cdc28p-Ccn1p initiates Cdc11p S394 phosphorylation on hyphal induction; expression in S. cerevisiae inhi
e interaction; oxygen-induced activity; regulated by Sef1, Sfu1, and Hap43; Spider biofilm induced; rat cath
cells, but higher amounts in stationary phase; GlcNAc-induced protein
ures; Spider biofilm repressed
GlcNAc-induced protein; Spider biofilm repressed
cultures; sumoylation target
ssential; expression in S. cerevisiae inhibits Ras2-mediated pathways; CCT8 and TRP1 overlap; Spider bio
cyr1 homozygous mutant (hyphal or yeast-form cells) and in ras1 homozygous mutant (yeast-form cells)
invasion in mouse infection; forms ring at sites of cell division and filaments in mature chlamydospore; Sp
e, but not kidney colonization, immunogenicity; hyphal and cell-cycle-regulated phosphorylation; rat cathete
spore; filamentous growth induced; regulated by Nrg1, Tup1, tyrosol and cell density; rat catheter biofilm r
specificity phosphatase and cell-cycle regulator; suppresses S. cerevisiae cdc15-lyt1, dbf2-2, and (partially
le body
d; repressed by phagocytosis/farnesol; hyphal growth role; stationary phase enriched; flow model biofilm in
d Mcm1 regulon; mRNA expression peaks at cell-cycle G2/M phase; mRNA binds She3 and is localized to
pression blocks hyphal growth and causes avirulence in a mouse model of systemic infection; antigenic du
uring the cell cycle; phosphorylated mostly by Swe1 and phosphorylation is regulated by Hsl1; 5'-UTR intro
zole resistance; macrophage/pseudohyphal-repressed; virulence-group-correlated expression; gene has in
r biofilm induced

er14; functional homolog of S. cerevisiae Cdc37p; likely to be essential for growth; regulated by Gcn2p and

ansposon mutation affects filamentous growth

causes hyperfilamentation; Sol1 is a substrate of SCF-Cdc4; Spider biofilm induced

misexpression blocks hyphal growth, causes avirulence in mouse IV infection; shows actin-dependent loca

-dependent; Cdc42p is GGTase I substrate

ion. peak at cell-cycle M/G1 phase; regulated by tyrosol, cell density, Plc1; repressed by alpha pheromone

osol and cell density; merged with orf19.201 in Assembly 20; unmerged from orf19.201 in a revision of Ass

acid starvation (3-AT); macrophage/pseudohyphal-repressed; protein levels decrease in stationary phase

Cdc35-dependent filamentation; virulence-group-correlated expression; likely essential (UAU1 method); Sp

resistance; mutants show attenuated virulence in mouse model; induced by Mnl1p under weak acid stress

rowth and premature cell death

xpression, peak at cell-cycle M/G1 phase; Hap43-induced

n; periodic mRNA expression, peak at cell-cycle M/G1 phase

proofreading motifs; likely essential for growth; interacts with benzoxaborole antifungals; present in expone

:

ent; cell-cycle regulated periodic mRNA expression; S. cerevisiae ortholog is not cell-cycle regulated

vth; Spider biofilm repressed

aque switch; rat catheter, Spider and flow model biofilm induced

scriptionally induced by Mnl1 under weak acid stress

-estradiol, progesterone, corticosteroid, or cholesterol; Spider biofilm induced

biofilm induced

; overexpressed in azole-resistant isolates; repressed in young biofilms

n; expressed in opaque-phase cells; induced by macrophage interaction; fluconazole-repressed; Spider bio

repressed; fluconazole resistance not affected by mutation or correlated with expression; rat catheter and

n on surface of yeast, not hyphae; polystyrene adherence induced; higher protein amount in stationary phas

st20-Hst7-Cek1-Cph1 MAPK pathway regulates mating, and invasive hyphal growth under some condition

egulates mating; ortholog of S. cerevisiae Fus3; induced by Cph1, pheromone; transposon mutation affects

essential for growth, based on an insertional mutagenesis strategy

onal homolog of S. cerevisiae Cet1; Cet1 and Cgt1 form a 2:1 complex; flow model biofilm induced

zation

); transcription is negatively regulated by Sfu1p, copper, amphotericin B, caspofungin; induced by ciclopiro

cell tips during hyphal morphogenesis; regulated by Cdc42p

ine/ciclopirox olamine, flucytosine, fluconazole, Spider/flow model/rat catheter biofilm induced; caspofungin

ony morphology-related gene regulation by Ssn6; Hap43-repressed; Sef1-regulated

ed; Tbf1, Hap43 induced

al transition or in planktonic growth; physically interacts with Msi3p; similar to rat anti-aging gene, SMP30,

ain peptide; Cet1p and Cgt1p form a 2:1 complex; functional homolog of S. cerevisiae Ceg1p

aque switch; filament induced; Tn mutation affects filamentation; flow model biofilm induced; Spider biofilm

; flow model and rat catheter biofilm repressed

at vaginal infection; phagocytosis rate increased; Spider biofilm induced; required for RPMI biofilm; Bcr1-ind

l density

tous growth; regulated by Nrg1, Tup1

icin B repressed; Hap43p-induced gene

ced; Spider biofilm induced

enzymatically activated by proteolytic processing; complements defects of S. cerevisiae chs1 or chs2; Spid

dimorphic transition; Chs1 and Chs2, but not Chs3, are inhibited by the protoberberine HWY-289; flow mod

d at yeast-hyphal transition; Chs1 and Chs2, but not Chs3, are inhibited by the protoberberine HWY-289; S

nt resistant to Calcofluor white; prenylation and 2 transmembrane segments predicted; functional homolog

ilm repressed

itin synthase; Cyr1-regulated in hyphae; possibly essential, disruptants not obtained by UAU1 method; flow

ae Chs7p, which effects ER export of Chs3p; induced cyr1 mutant hyphae and ras1 yeast-form cells; Spide

; mRNA present in yeast and hyphae; induced during cell wall regeneration; flow model biofilm repressed

cosylation motifs of Chs2p and Chs3p; alkaline downregulated; expression not detected in yeast-form or hy

onazole, Cyr1, Efg1, pH-regulated; mRNA binds She3 and is localized to yeast-form buds and hyphal tips;

annosylation; putative signal peptide; hyphal-repressed; farnesol upregulated in biofilm; regulated by Efg1

tant sporulation defect; homozygous null mutation causes no obvious defects; transcription decreases upon

ha switch, oxidative stress (via Cap1), or macrophage interaction; stationary phase enriched protein; Spide

R2; Hap43-repressed; flow model biofilm induced st, not hyphal growth conditions; present in exponential and stationary phase; Spider biofilm repressed; rat

ith respect to fluconazole resistance; synthetically lethal with CKA2; flucytosine induced

tivity; synthetically lethal with CKA1; attenuated virulence in a mouse oropharyngeal candidiasis but not in

caspofungin and hydrogen peroxide medium

caspofungin

kinase activator activity, protein-containing complex binding, ubiquitin binding, zinc ion binding activity

mouse systemic infection; role in chlamydospore formation; functional homolog of S. cerevisiae Cla4p; mu

itotic exit; role in cell polarization; interacts with catalytic subunit Cdk1; Spider biofilm repressed

ytokinesis; Fkh2-represed; flow model biofilm repressed; farnesol-upregulated in biofilm; reduced total RN

sis; rat cathetr and Spider biofilm repressed

. cerevisiae; other biofilm induced; Spider biofilm induced

transition; mutation confers hypersensitivity to cytochalasin D and high concentrations of tunicamycin; gene

g; biochemically purified Ca2+/CaM-dependent kinase is soluble, cytosolic, monomeric, and serine-autoph

e virulence, resistance to high pH, Na(+), Li(+), Mn(2+), and fluconazole tolerance; micafungin is fungicida

d-type resistance to fluconazole or to SDS; micafungin is fungicidal to null mutant

nic infection; not transcriptionally regulated by NaCl; fungal-specific (no human or murine homolog)

t alleles for high/low-affinity isoforms; S or G at residue 328 affects specificity; Spider, flow model biofilm in

s, but higher amounts in stationary phase

blishment of cell polarity and filamentous growth of a population of unicellular organisms, more

1; Hap43-induced; Spider biofilm repressed

phages; possibly an essential gene, disruptants not obtained by UAU1 method

hage; Hap43p-repressed gene

ion (3-AT), Hap43; induced upon adherence to polystyrene; Spider biofilm repressed

lar oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen activity

ocess; Hap43-repressed gene; rat catheter biofilm induced

epressed; early-stage flow model biofilm induced; Spider biofilm repressed

uced

ophage-induced protein; repressed by nitric oxide; 5'-UTR intron; Hap43-repressed

hal-induced; repressed by nitric oxide; intron in 5'-UTR; Hap43p-dependent repression in low iron medium

film induced

es; rat catheter biofilm induced; Spider biofilm induced

th Ess1, Czf1; required with Efg1 for host cytokine response; regulates galactose metabolism genes; rat ca

nes; probably homodimeric, phosphorylated; required for colonization of the mouse GI tract; rat catheter a

tes mating, represses yeast-hyphal switch; required for virulence in mice; yeast-enriched; induced by alpha

ary phase yeast cultures; predicted mitochondrial localization; overlaps orf19.1551

stress-induced; heterozygous null mutant displays sensitivity to virgineone; rat catheter biofilm induced

n neutrophils; regulated by Gcn2 and Gcn4; putative N-glycosylation

nyl or caspofungin induced; Hap43-repressed; Spider biofilm induced

: B9J08_002680 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_107256

ersensitivity to amphotericin B; Spider biofilm repressed

: B9J08_001485 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_125790

vity, oxidoreductase activity and acting on paired donors, more

ion of G2/M transition of mitotic cell cycle, regulation of nucleocytoplasmic transport

W ASSEMBLY : CTRG1_01053 and Candida tropicalis MYA-3404 : CTRG_01053

1b complex localization

nduced in core caspofungin response; Spider biofilm induced

079, Pichia stipitis Pignal : psti_CGOB_00127 and Candida tropicalis MYA-3404 : CTRG_05490

n repressed

and Cul3-RING ubiquitin ligase complex localization

e

film induced
dent DNA biosynthetic process
siae MRPL9
alis MYA-3404 : CTRG_01022 and Candida albicans WO-1 : CAWG_01412
ty and role in farnesyl diphosphate biosynthetic process, mevalonate pathway, ubiquinone biosynthetic pro
crophages; expression upregulated during growth in the mouse cecum; Spider biofilm induced
resence of elevated CO2
ocess and endoplasmic reticulum lumen, glucosidase II complex localization
1498 : CANTEDRAFT_116265 and Debaryomyces hansenii CBS767 : DEHA2E17380g
y acid metabolic process and mitochondrion localization
e in histone demethylation, positive regulation of transcription elongation from RNA polymerase II promote
: B9J08_001023 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115661
g activity and role in negative regulation of protein phosphorylation
omplex localization
ent of cell polarity, protein palmitoylation, regulation of exocytosis, vacuole fusion, non-autophagic
: B9J08_003483 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_132053
RL Y-1498 : CANTEDRAFT_109948 and Debaryomyces hansenii CBS767 : DEHA2E17182g
s activity
mic reticulum, signal peptidase complex localization
ndida tropicalis MYA-3404 : CTRG_00984 and Candida albicans WO-1 : CAWG_01455
spliceosome, nucleus localization
: B9J08_002999 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_131795
sis strategy
: B9J08_002641 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_137093
calization
ethod
mponent of fungal-type vacuolar membrane localization
1 method
or murine homolog)
ericin B
region, fungal-type vacuole lumen localization
facilitator superfamily (MFS)
plex disassembly, autophagy, vacuole fusion, non-autophagic, vesicle fusion with Golgi apparatus
ion
zation
a stipitis Pignal : PICST_68531 and Candida tropicalis NEW ASSEMBLY : CTRG1_00947
ofilm induced
uman Pig-H, which is also involved in GPI assembly; Spider biofilm induced
entation, cellular response to oxidative stress
: B9J08_003507 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_94578
-dependent protein catabolic process
ed from orf19.2553 in a revision of Assembly 21
ssembly 20; unmerged from orf19.2552 in a revision of Assembly 21
osomal tri-snRNP complex assembly and U6 snRNP localization

ds in S. cerevisiae; Spider biofilm induced

trinsic component of membrane localization

ng over; Spider biofilm induced

cess, rescue of stalled ribosome, ribosome-associated ubiquitin-dependent protein catabolic process

idiasis; Hap43-repressed; GlcNAc-induced protein; Spider biofilm induced; biotin-dependent transcription r

ription regulated by biotin availability and Vhr1p

se I, transcription by RNA polymerase I, transcription initiation from RNA polymerase I promoter

ed

hod

L : B9J08_002705 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113198

nine; Spider biofilm induced

ate

ome segregation, regulation of phosphoprotein phosphatase activity

plex, cytoplasm localization

L : B9J08_004168 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113969

f 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA and LSU-rRNA), more

alization

exon ligation, generation of catalytic spliceosome for second transesterification step, snRNA metabolic pro

e oxidoreductase)

ucleus, nuclear pore organization, protein import into nucleus, protein localization to nuclear inner membra

i compartments; rat catheter biofilm repressed

L : B9J08_004087 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_129982

ation, post-chaperonin tubulin folding pathway, protein folding and cytoplasm localization

ylation, regulation of mitotic chromosome condensation and SUMO activating enzyme complex, cytosol, nu

d

ypha switch; Spider biofilm repressed

lymerase III complex localization

and the cytoplasm-to-vacuole targeting (Cvt) pathway; Spider biofilm induced

ranslational initiation and mitochondrial small ribosomal subunit localization

L : B9J08_000343 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_104949

family which includes PMT1, PMT2, PMT4, PMT5, and PMT6; peloto ortholog; Hap43-repressed gene

s NRRL Y-1498 : CANTEDRAFT_109615 and Debaryomyces hansenii CBS767 : DEHA2A12650g

-repressed; Spider biofilm induced

s55/Vps68 complex, late endosome localization

cess

TPase activity, positive regulation of helicase activity, rRNA processing

n

CDR1 and CDR2; possibly regulated by Tac1; induced by Mnl1 in weak acid stress; flow model biofilm inc

ent-inducing conditions, does not block true hypha formation in liquid media; rat catheter and Spider biofilm

nily, major facilitator superfamily (MFS); biotin-dependent transcription regulated by Vhr1p; amphotericin B
tomical structure localization
a stipitis Pignal : PICST_43964 and Spathaspora passalidarum NRRL Y-27907 : spas_CGOB_00057
o mitochondria
ses are downregulated upon phagocytosis by murine macrophage
rRNA and LSU-rRNA), more
cyclic beta-amino acid icofungipen/PLD-118/BAY-10-8888 and mupirocin
onent of endoplasmic reticulum membrane localization
phosphatase, GMP binding, double-stranded DNA binding, guanosine binding and mismatched DNA bindin
nelanogaster, human, and mouse
1 under weak acid stress
ndida tropicalis MYA-3404 : CTRG_00749 and Candida albicans WO-1 : CAWG_01683
ltures
of mitotic metaphase/anaphase transition and anaphase-promoting complex localization
conservation among several Candida species
phosphatase, GMP binding, double-stranded DNA binding, guanosine binding and mismatched DNA bindin
esicle coat localization
membrane localization
membrane localization
ndida tropicalis MYA-3404 : CTRG_00731 and Candida albicans WO-1 : CAWG_01703
oonents PRP4 and PRP3 in S. cerevisiae; mutants are viable
human or murine homolog)
ssed gene
ransferase activity, protein-lysine N-methyltransferase activity
s NRRL Y-1498 : CANTEDRAFT_112323 and Debaryomyces hansenii CBS767 : DEHA2F19184g
s misfolded mitochondrial proteins
mitochondria
ral component of membrane, nuclear envelope localization
protein targeting to vacuole and vesicle docking; flow model biofilm induced
otein catabolic process and protein localization to meiotic spindle pole body, more
der biofilm induced
ir binding activity
ot obtained by UAU1 method; Spider biofilm repressed
hrough
IA (m1A) methyltransferase complex localization
salvage pathway, NAD biosynthetic process, nicotinamide riboside metabolic process
of the small ribosomal subunit
ulates genes of N-acetylglucosamine (GlcNAc) catabolism; required for GlcNAc-induced hyphal growth
to endoplasmic reticulum membrane; regulated by Sef1p-, Sfu1p-, and Hap43p
I general transcription initiation factor activity and role in nucleolar large rRNA transcription by RNA polym
: B9J08_005479 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_96118
: B9J08_005543 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_91782

mutants are viable

tin organization, histone acetylation, transcription by RNA polymerase II

L : B9J08_002565 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_102086

rocess

oxyribonuclease activity, single-stranded DNA 5'-3' exodeoxyribonuclease activity

zation

L : B9J08_004836 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_110235

during autophagic body breakdown in the vacuole; possibly an essential gene, disruptants not obtained by U

facilitator superfamily (MFS)

bly involved the beta-tubulin folding; Spider biofilm repressed

e

superfamily (MFS)

L : B9J08_001978 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_114703

1498 : CANTEDRAFT_98619 and Debaryomyces hansenii CBS767 : DEHA2G22594g

lm repressed

e biosynthetic process and mitochondrion localization

s NRRL Y-1498 : CANTEDRAFT_113094 and Debaryomyces hansenii CBS767 : DEHA2G22374g

ndida tropicalis MYA-3404 : CTRG_00536 and Candida albicans WO-1 : CAWG_01831

opment

o DNA damage stimulus and cytoplasm, nucleus localization

L : B9J08_000376 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_117008

hyphal growth, and virulence

ortholog required for cell viability; Spider biofilm induced

zation

sed transcription is observed upon fluphenazine treatment or in an azole-resistant strain that overexpresse

ate; possibly an essential gene, disruptants not obtained by UAU1 method

P-1 adaptor complex, Golgi apparatus, endosome localization

s hansenii CBS767 : DEHA2F16940g and Candida tropicalis MYA-3404 : CTRG_00570

n, sterol regulatory element binding protein cleavage

nitochondrial inner membrane, mitochondrion localization

al epithelial cells; Spider and flow model biofilm induced

lymerase III complex localization

ants not obtained by UAU1 method

sed nuclear chromosome localization

L : B9J08_005117 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_104939

ing arrays; flow model biofilm induced; Spider biofilm repressed

o Golgi transport vesicle, endoplasmic reticulum membrane, integral component of Golgi membrane localiz

e

L : B9J08_001700 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_133521

10, C. parapsilosis CDC317 : CPAR2_205310 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_11237 d upon hyphal formation

network localization
of transcription, transcription elongation from RNA polymerase II promoter
nsenii CBS767 : DEHA2G10538g and Pichia stipitis Pignal : psti_CGOB_00130
activity

L : B9J08_000664, Debaryomyces hansenii CBS767 : DEHA2G10648g and Pichia stipitis Pignal : PICST_3

cess
nduced

ced by alpha pheromone in SpiderM medium; regulated by Sef1, Sfu1, and Hap43
on upregulated during growth in the mouse cecum
s hansenii CBS767 : DEHA2G10846g and Pichia stipitis Pignal : PICST_32988
orphology-related gene regulation by Ssn6; Spider biofilm induced
al cells; rat catheter biofilm repressed

g frame
L : B9J08_000806 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_136864
n both C. albicans and C. dubliniensis
s hansenii CBS767 : DEHA2G10736g and Pichia stipitis Pignal : PICST_32993
_31830, C. parapsilosis CDC317 : CPAR2_204870 and C. auris B8441 : B9J08_000809
y FGR6-related genes in the RB2 repeat sequence
L : B9J08_003984 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115848

piderM medium; Spider biofilm induced; Bcr1-repressed in RPMI a/a biofilms

embly 20; restored based on transcription data

160, C. parapsilosis CDC317 : CPAR2_203070 and C. auris B8441 : B9J08_004564
ed

s granule, polysome localization
process

erfamily (MFS); Gcn4p-regulated; flucytosine induced; ketoconazole-repressed; oxidative stress-induced vi

tronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), ribosomal small subunit biogenesis
03260, C. auris B8441 : B9J08_004567 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116778

L : B9J08_001041 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115156

btained by UAU1 method

s NRRL Y-1498 : CANTEDRAFT_121459 and Debaryomyces hansenii CBS767 : DEHA2E03938g
L : B9J08_000471 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113831

zation

olarity, small GTPase mediated signal transduction
L : B9J08_003982 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_115846
low model biofilm repressed

nsed nuclear chromosome localization
thod

xide
L : B9J08_000571 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_106599
lgi to endoplasmic reticulum, vesicle-mediated transport
L : B9J08_000567 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_93887

hypoxia induced

NP, post-mRNA release spliceosomal complex, spliceosomal complex localization
verexpresses CDR1 and CDR2
ne3; transposon mutation affects filamentous growth

and cytoplasm, endosome localization
onent of endoplasmic reticulum membrane, signal recognition particle receptor complex localization
r assembly
L : B9J08_000885 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_116124
L : B9J08_000884, Debaryomyces hansenii CBS767 : DEHA2C15840g and Pichia stipitis Pignal : PICST_
nduced
9 and Candida tropicalis NEW ASSEMBLY : CTRG1_CGOB_00075
LSU-rRNA), maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
zation

iofilm induced
ak acid stress; transcript detected in high-resolution tiling arrays
L : B9J08_002086 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_134293
50, C. parapsilosis CDC317 : CPAR2_702070 and C. auris B8441 : B9J08_002833
lm induced

Hap43-repressed gene
onential and stationary growth phase yeast cultures

L : B9J08_000104 and Candida tenuis NRRL Y-1498 : cten_CGOB_00253
omplex assembly and integral component of mitochondrial membrane, mitochondrial inner membrane loca
tein methylation, cellular protein-containing complex assembly, regulation of autophagy
L : B9J08_003843 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_92567
subfamily of ABC family; similar to S. cerevisiae Bpt1p

iofilm induced
L : B9J08_000583 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_113827
not obtained by UAU1 method
tein; antigenic during human oral infection; Hap43p-repressed gene
oxide; Spider biofilm induced
ation
ein targeting to membrane, translocation
sses MDR1
zation

son mutation affects filamentous growth

L : B9J08_000124 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_132607

n

bunit biogenesis

RRL Y-1498 : CANTEDRAFT_117073 and Debaryomyces hansenii CBS767 : DEHA2A11462g

otic spindle elongation, protein sumoylation, regulation of mitotic chromosome condensation

some, large subunit precursor localization

: B9J08_004911 and Candida tenuis NRRL Y-1498 : cten_CGOB_00133

C-palmitoyltransferase complex localization

ranscription factor catabolic process, ubiquitin-dependent protein catabolic process

n of mRNA 3'-end processing, sno(s)RNA 3'-end processing, termination of RNA polymerase II transcriptio

ced

endent decapping of nuclear-transcribed mRNA, nuclear-transcribed mRNA catabolic process, deadenylat

A (m1A) methyltransferase complex localization

itive regulation of clathrin-dependent endocytosis, protein secretion and actin cortical patch, nucleus localiz

verexpression induces apoptotic-like cell death; absent from hyphal cells; induced by Rgt1; rat catheter an

n4p-regulated

ndida tropicalis MYA-3404 : CTRG_05947 and Candida albicans WO-1 : CAWG_02181

pithelium, while expression of the C. dubliniensis ortholog is not upregulated; mutants are viable; rat cathete

ndida tropicalis MYA-3404 : CTRG_05938 and Candida albicans WO-1 : CAWG_02183

onazole treatment; overexpression does not affect drug or oxidative stress sensitivity; stationary phase en

ox olamine; positively regulated by Sfu1; Hog1, fluconazole-repressed; Hap43-induced; Spider biofilm indu

FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine); induced by nitric oxide

calization

duced

yl-lysine monomethylation

der biofilm repressed

facilitator superfamily (MFS); Spider biofilm induced

rmation and U4/U6 x U5 tri-snRNP complex localization

regation, gene silencing by RNA, histone deacetylation, negative regulation of transcription by RNA polyme

ity

azole resistance; Spider biofilm induced

RRL Y-1498 : CANTEDRAFT_112677 and Debaryomyces hansenii CBS767 : DEHA2E02420g

ant; contains a 5' UTR intron

lrial inner membrane, mitochondrion localization

ranslocation, phospholipid transport, positive regulation of phosphatidylcholine biosynthetic process

_34830, C. parapsilosis CDC317 : CPAR2_701110 and C. auris B8441 : B9J08_000560

otein present in exponential and stationary growth phase yeast cultures; Spider biofilm repressed

itator superfamily (MFS)

for cleavage leading to mature 18S rRNA; Spider biofilm induced

transferase activity

stress response; Spider biofilm induced

sed during chlamydospore formation in C. albicans and C. dubliniensis; rat catheter biofilm repressed
: B9J08_005167 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_95984
l candidiasis; alkaline upregulated by Rim101; rat catheter, Spider and flow model biofilm induced
5, C. parapsilosis CDC317 : CPAR2_200810 and C. auris B8441 : B9J08_002747
se, retrograde protein transport, ER to cytosol, ubiquitin-dependent ERAD pathway, ubiquitin-dependent g
: B9J08_002757 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_112338
40, C. parapsilosis CDC317 : CPAR2_200670 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_117734
id raft component); predicted N-terminal acetylation; repressed by nitric oxide
d break repair via sister chromatid exchange and Ada2/Gcn5/Ada3 transcription activator complex localiza
Spider biofilm induced
yphal growth, intra-Golgi vesicle-mediated transport, regulation of GTPase activity
ndida tropicalis MYA-3404 : CTRG_05848 and Candida albicans WO-1 : CAWG_02290
ransport protein particle (TRAPP) complex of the cis-Golgi; Spider biofilm induced
peptide-serine-N-acetyltransferase activity
induced
t obtained by UAU1 method; rat catheter and Spider biofilm induced
TPase activity and spliceosomal complex localization
mologous recombination-mediated repair and telomere homeostasis;
LSU-rRNA), rRNA processing and nucleolus, small-subunit processome localization
_35340, C. parapsilosis CDC317 : CPAR2_200350 and C. auris B8441 : B9J08_001244
nponent of fungal-type vacuolar membrane localization
: B9J08_001247 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_136418
; Hap43-repressed gene
and integral component of mitochondrial membrane, mitochondrial inner membrane, mitochondrion localiz
process, protein ubiquitination and anaphase-promoting complex localization
oA carboxylase and pyruvate carboxylase; transcription regulated by biotin availability and Vhr1p
calization
transmembrane transport and membrane localization
NA damage, mRNA 3'-end processing, negative regulation of transposition, RNA-mediated and site of dou
gation, protein localization to nucleolar rDNA repeats
6_35524, C. parapsilosis CDC317 : CPAR2_200040 and C. auris B8441 : B9J08_001263
localization
rfamily (MFS)
al epithelial cells
tein response, regulation of retrograde protein transport, ER to cytosol, ubiquitin-dependent ERAD pathwa
espliceosome, U4/U6 x U5 tri-snRNP complex, U5 snRNP, commitment complex, cytosol, nucleus localiz
gulated; complements copper sensitivity of an S. cerevisiae cup1 mutant; regulated by Sef1, Sfu1, and Ha
on in hyphae compared to yeast; expression regulated during planktonic growth; flow model biofilm induc
ase domain; similar to Csf4p and to antigenic A. fumigatus Aspf9; predicted Kex2p substrate; caspofungin-
during cell wall regeneration; flow model biofilm induced
ent independently of Cph1 and Efg1; functionally complements pheromone hypersensitivity of S. cerevisia
inant-negative inhibition of pheromone response
antifungal drug leptomycin B; partially suppresses signal transduction defects of S. cerevisiae ste20 muta
eter and Spider biofilm repressed
roteins; copper-induced; Tbf1-activated; suppresses Cu sensitivity of S. cerevisiae cup1 mutant; flow mod
; not required for mouse virulence; repressed by low iron; regulates Ca++ influx during alkaline pH respon
t pH 8; required for yeast cell adherence to silicone substrate; Spider biofilm induced
ed, alkaline induced by Rim101; Efg1-, Cph1, Hap43-regulated; required for WT RPMI biofilm formation;
media at 37 deg; induced by ketoconazole, nitric oxide, Hap43; required for normal RPMI biofilm formation
evisiae Cdc25p; commonly called Cdc25; transposon mutation affects filamentous growth

nucleosomes bind 1 centromere, each has 1 Cse4 molecule during most of cell cycle, 2 molecules in anap
wth phase, benomyl, macrophage interaction; azole resistance associated; Spider biofilm induced; rat cath
zed to ER; required for wild-type amino-acid responsive hyphal growth and for mouse systemic virulence; re
affects filamentous growth; Spider biofilm induced
during chlamydospore development in both species; localized to chlamydospore cell wall
amydospore development in both species; localized to chlamydospore cell wall; Hap43-repressed; Spider
nding, N-glycosylation sites; expressed in yeast and hyphae; hyphal downregulated; stationary-phase enric
entous growth; can suppress S. cerevisiae rok1 mutant inviability; Spider biofilm induced; mutants for abnor
model; Cst20p-Hst7p-Cek1p-Cph1p MAPK pathway regulates some hyphal growth; involved in Cdc42p gro
opaque mating or white biofilm formation in response to mating pheromone; induced in response to phero
ion in 1-hybrid assay in S. cerevisiae; protein levels increase under weak acid stress; nonessential
e; repressed by Efg1; member of a family of telomere-proximal genes; Tbf1-induced
elomere-proximal genes; transcript upregulated in RHE model of oral candidiasis
E model of oral candidiasis; member of a family of telomere-proximal genes; Efg1, Hap43-repressed
ssay in S. cerevisiae
y nitric oxide; induced by Mnl1 under weak acid stress; repressed upon adherence to polystyrene; Hap43-r
. cerevisiae Stb4
Cta8p levels are modulated by growth temperature to regulate basal expression of genes involved in protei
ivates transcription in 1-hybrid assay in S. cerevisiae
atty acid degradation; induced by oleate; null mutant displays carbon source utilization defects and slightly
d by alpha pheromone in SpiderM medium
process; flow model biofilm induced
nder weak acid stress; early-stage flow model biofilm induced
or virulence in mice; induced in macrophage; macrophage/pseudohyphal-repressed after 16 hr; rat catheter
uced by macrophage engulfment, hyphal growth, starvation, nonfermentable carbon sources; rat catheter,
ap43p-induced gene
a Rim101; 17-beta-estradiol repressed; complements S. cerevisiae ctr1 ctr3 copper transport mutant; flow
l gene expression; rat catheter and flow model biofilm induced
epressed
n of metallothionein genes; Hap43-repressed; Spider biofilm induced
etion, filamentous growth; caspofungin repressed
essed; ketoconazole-induced; Plc1-regulated; colony morphology-related Ssn6 regulation; Spider, flow mo
glucan; rat catheter biofilm repressed
disruptants not obtained by UAU1 method; flow model and rat catheter biofilm repressed
a fluconazole-resistant isolate; clade-associated gene expression; Hap43p-induced gene
ion of mating projections and same-sex mating; mutant has cell wall defects; transcription increased at sta
e regulation by Ssn6; Hap43-repressed; pider biofilm induced
orphology-related gene regulation by Ssn6; mutants are viable
e repressed; repressed by nitric oxide; Hap43-dependent repression in low iron; regulated by Sef1, Sfu1
e adherence, interaction with macrophage; N-glycosylation, 2 heme-binding motifs; rat catheter, Spider bio
rophage-induced protein; downregulated upon treatment of biofilm with farnesol; present in exponential and
e in stationary phase cultures; predicted endoplasmic reticulum (ER) localization
and mating; mutant hyphal growth defect rescued by exogenous cAMP; downstream of Ras1p and CO2 si
1; possibly adherence-induced; Hog1 regulated; reduced levels in stationary phase yeast cells; Spider and
d; alkaline induced; macrophage/pseudohyphal-induced; present in exponential and stationary growth phas
ed by UAU1 method; Hap43-repressed; Spider biofilm repressed
uses dominant-negative inhibition of pheromone response; required for yeast cell adherence to silicone; Sp
d-type hyphal growth and virulence in mouse systemic infection; gene and protein are GlcNAc-induced; Spi
spindle microtubules
chores to spindle microtubules
spindle microtubules
spindle microtubules
log; fluconazole-induced; induced during chlamydospore formation in C. albicans and C. dubliniensis
essed; protein enriched in stationary phase yeast cultures; flow model biofilm induced; rat catheter and Sp

urce regulation requires Gat1; possibly essential gene (by UAU1 method); Hap43-repressed
dation genes; required for yeast cell adherence to silicone substrate; Spider biofilm induced
chores to spindle microtubules
nduced in core stress response; Hog1 regulated; clade-associated expression; Hap43-repressed
septum formation, exit from mitosis, and normal hyphal morphogenesis; virulence-group-correlated expres
pment; cell-cycle regulated periodic mRNA expression; S. cerevisiae ortholog is not cell-cycle regulated
onse
ofilm induced
and role in mRNA export from nucleus, poly(A)+ mRNA export from nucleus, tRNA export from nucleus, tr
stress-repressed via Cap1p; flucytosine repressed; likely to be essential for growth, based on insertional m
repressed
ated periodic mRNA expression
as a DOCKER domain; similar to adjacent DCK2 and to S. cerevisiae Ylr422wp; regulated by Nrg1; Spider
p under weak acid stress
activity
stellii Dcr1p, which is not conserved in S. cerevisiae
al growth; upregulated in cyr1 mutant (yeast or hyphal form); Hap43-induced
Tup1
zole or in azole-resistant strain; Hog1, farnesol, alkaline repressed; stationary phase enriched; Spider, flow
re downregulated upon phagocytosis by murine macrophage; protein enriched in stationary phase yeast c
ced by fluconazole, high cell density; Efg1/hyphal regulated; role in adhesion, hyphal growth on solid media
pseudohyphal growth
; required for host tissue invasion during infection; flow model biofilm induced
VP1 induction in alkaline pH; GPI modification predicted; dfg5 dcw1 double mutant is inviable; caspofungin
ylated; Spider biofilm induced
e; binds NADPH; target of drugs that selectively inhibit the fungal enzyme rather than the human enzyme
rotein N-linked glycosylation and endoplasmic reticulum membrane localization
to be essential for growth based on insertional mutagenesis strategy; F-12/CO2 early biofilm induced
TAP-tagged Nop1; heterozygous null mutant exhibits resistance to parnafungin; Hap43-induced gene; Spic
on phagocytosis by macrophage; Gcn4-regulated; upregulated by Rim101 at pH 8; rat catheter and Spider
regulated by Nrg1, Mig1, and Tup1; role in chlamydospore formation; Spider biofilm induced
dherence to polystyrene
y Ssn6; Hap43-repressed; rat catheter biofilm induced; Spider biofilm repressed
hondrial inner membrane, mitochondrion localization
reaks and pairing between homologous chromosomes
der hydroxyurea treatment
oral candidiasis; transcript regulated by Nrg1, Mig1, and Tup1
vels; may promote efficient NHEJ in postdiauxic/stationary phase; Spider biofilm repressed
d ubiquitinated intermediates; oxidative stress-induced via Cap1; mutants are viable
ar to S. cerevisiae Dog1, Dog2, Hor1, Rhr2; regulated by Nrg1, Tup1; Spider biofilm repressed
cells; repressed upon high-level peroxide; Hap43p-induced; rat catheter biofilm induced
induced
stress; Spider biofilm induced
l for viability; rat catheter biofilm induced
nvasive growth on SD and YPD media; Spider biofilm repressed
rat catheter biofilm repressed

film repressed

is; downregulation correlates with clinical development of fluconazole resistance

ssed by 17-beta-estradiol, ethynyl estradiol; Spider biofilm induced
are downregulated upon phagocytosis by murine macrophage; protein enriched in stationary phase yeast c
crophages; flow model biofilm induced
rat catheter and Spider biofilm induced

FU), tubercidin (7-deazaadenosine); Tbf1-induced; repressed in core stress response
1 phase; Ace2p-induced; required for virulence in a mouse model of infection
ulum
-leucine catabolic process, D-tyrosine catabolic process, tRNA metabolic process

cell-cycle checkpoint; induced under Cdc5p depletion
spindle microtubules
egulated by Nrg1/Hap43; required for virulence; promotes mouse kidney and brain colonization; rat cathete
molog); not required for virulence in a mouse intravenous model

tants not obtained by UAU1 method

s; 17-beta-estradiol, ethynyl estradiol, macrophage induced; decreased in stationary phase yeast; rat cathe
spindle positioning, nuclear migration, hyphal growth; regulated by Mig1, Hap43; flow model and rat cathet

rowth defects of S. cerevisiae flo8 or flo11 mutant; biofilm induced; required for biofilm formation; Bcr1-rep
ponse; induced by oxidative, weak acid stress, NO, benomyl, GlcNAc; Cap1, Mnl1 induced; Hap43-repress
ss-induced via Cap1p
1, Nrg1, Tup1, Cph1, Efg1, Hog1, farnesol, phagocytosis; fluconazole-induced; rat catheter and Spider bio
ilamentous growth; expression is regulated upon white-opaque switching
induced by heavy metal (cadmium) stress; Hog1p regulated
sis
ed; Spider biofilm induced; rat catheter biofilm repressed
s; Gcn4-regulated; Tbf1-activated; Hap43-repressed; Spider, flow, F-12/CO2 model biofilm induced
2_103190, C. auris B8441 : B9J08_000758 and Debaryomyces hansenii CBS767 : DEHA2G08448g
im101; repressed by caspofungin and in azole-resistant strain overexpressing MDR1; flow model, rat cath

ortholog of S. cerevisiae Ecm29; transposon mutation affects filamentous growth; flow model biofilm repres
zation
d endocytosis; mutant infection is immunoprotective in murine model; fluconazole-induced; caspofungin re
gulated; Hog1, Rim101-repressed; colony morphology-related regulated by Ssn6; induced by ketoconazole
ne, disruptants not obtained by UAU1 method
ce; predicted Kex2p substrate; has HKEXRF motif
r ras1 mutant (yeast or hyphal cells); Tn mutation affects filamentous growth; stationary phase enriched; S
, disruptants not obtained by UAU1 method; Spider biofilm induced
hyphal growth

phal-induced; antigenic in mouse; farnesol-downregulated; snoRNA snR18 is encoded within the EFB1 int
wth, cell-wall gene regulation; roles in adhesion, virulence; Cph1 and Efg1 have role in host cytokine respo
us growth, phenotypic switch; EFG1 and EFH1 genetically interact; expression interferes with mouse intes
human/mouse; lacks site for regulatory phosphorylation by eEF2 kinase; GCN-regulated; higher protein a
udohyphal-induced; equal level of protein in exponential and stationary growth phase yeast cultures; Spider
udohyphal-induced; protein level decrease in stationary phase cultures; GlcNAc-induced protein; Spider bi

pheromone in SpiderM medium; Spider biofilm induced; promoter bound by Ndt80
s downregulated by phagocytosis by macrophage; alternatively spliced intron in 5' UTR; protein levels dec
in catabolism; rat catheter biofilm induced

y, growth; expressed in hyphal, pseudohyphal, and yeast form; Hap43-induced; Spider and flow model bio
ider biofilm induced

ıg the mating process

cles; functions in ER to Golgi transport; induced by alpha pheromone in SpiderM medium

-level peroxide stress; induced in oral candidiasis clinical isolates; possibly essential gene; rat catheter and
uced; osmotic stress-induced; overlaps orf19.5170.1, which is annotated as a blocked reading frame; Spid

ole repressed; repressed by alpha pheromone in SpiderM medium; flow model biofilm induced; rat catheter
ly of cell wall polysaccharides; major cell-surface antigen; binds host plasmin/plasminogen; immunoprotect
4 snoRNAs; transposon mutation affects filamentous growth; repressed by prostaglandins; Spider biofilm in
5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine); Hap43-induced; Spider biofilm induced
liasis

uorocytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine); hyphal, macrophage repress
er biofilm induced
otides from ribosomes; Hap43p-induced gene
antifungal drug target; NADH reducing cofactor but S. cerevisiae Erg1 uses NADPH; flow model biofilm ind
nce associated with azole resistance; fluconazole or ketoconazole induced; macrophage-downregulated pr
antifungals; may contribute to drug resistance; azole or flow model biofilm induced; drug treated biofilm indu
te biosynthetic process, mevalonate pathway, isopentenyl diphosphate biosynthetic process, mevalonate p
affects filamentation; amphotericin B, caspofungin repressed; exponential, stationary growth phase expres
ensitive to multiple drugs; ketoconazole-induced; flow model and Spider biofilm repressed
rity to S. cerevisiae Erg20p; likely to be essential for growth, based on an insertional mutagenesis strategy
nine; rat catheter and Spider biofilm repressed
milarity to S. cerevisiae Erg25; fluconazole-induced; induced in azole-resistant strain; rat catheter and Spid
ricin B, caspofungin repressed; possibly essential gene, disruptants not obtained by UAU1 method; Spider
termediate in ergosterol biosynthesis; amphotericin B, caspofungin repressed; Spider biofilm repressed
); possible drug target, essential for viability; functional homolog of S. cerevisiae Erg27p
cess and endoplasmic reticulum membrane localization
azole resistance and defects in hyphal growth and virulence; Efg1p-repressed; fluconazole-induced
caspofungin repressed; rat catheter biofilm repressed
ol biosynthesis, catalyze formation of the C-22(23) double bond in the sterol side chain; transposon mutatio
onfers nystatin resistance; Hap43, GlcNAc-, fluconazole-induced; upregulated in azole-resistant strain; Spi
in sterol biosynthesis; fluconazole-induced; possibly essential, disruptants not obtained by UAU1 method; r
ript regulated by Nrg1; possible drug target; not conserved in H. sapiens
essential for growth; regulated by fluconazole, lovastatin; amphotericin B, caspofungin repressed; Spider b
e-induced; induced by Mnl1 under weak acid stress; Spider biofilm induced

chondrial intermembrane space
essed

us growth; Spider biofilm repressed

amentation; rat catheter biofilm repressed
hase; mutation confers increased sensitivity to nocodazole; periodic mRNA expression, peak at cell-cycle S
ole linker between WW and isomerase domains, unlike human homolog; functional homolog of S. cerevisia
omain
processivity; not required for catalytic activity in vitro; related to mammalian Tpp1p
ures; rat catheter biofilm repressed
ubstrate; induced during cell wall regeneration; possibly an essential gene, disruptants not obtained by UAU

he hyphal tip
he hyphal tip
; Spider biofilm induced

dent of Yhb1

uolar morphology and acidification; not required for wild-type virulence in mouse systemic infection or for a
tion
ranes
ofungin induced; Plc1-regulated; colony morphology-related gene regulation by Ssn6; Spider biofilm induce
uration of 18S rRNA; Spider biofilm induced

se cells; null mutant shows no pheromone response in opaque cells; overexpression causes enhanced phe
aspofungin repressed; macrophage/pseudohyphal-induced; flow model and Spider biofilm repressed
al infection models; regulated by Efg1; fluconazole-induced; amphotericin B repressed; flow model and Sp
La opaque cells
y Nrg1, Rfg1, Tup1, Tec1, Efg1, Ntd80, Rob1, Brg1; induced in oralpharyngeal candidasis; Spider biofilm i
t-hypha switch; induced by Efg1, Gcn4, Hog1, fluconazole; phagocytosis-repressed; flow model biofilm indu
tosis; effects switch from glycolysis to gluconeogenesis in macrophage; rat flow model biofilm induced; ove
associated with resistance to flucytosine (5-FC) in a clinical isolate; hyphal downregulated; gene has intror
lamentation; partially rescues S. cerevisiae pdr1 pdr3 fluconazole sensitivity; rat catheter biofilm induced/S
cerevisiae pdr1 pdr3; Hap43-induced; required for yeast cell adherence to silicone substrate; flow model bi
al isolates; transposon mutation affects filamentation; farnesol-upregulated in biofilm
Fcy2; mutation confers resistance to 5-fluorocytosine (5-FC); flow model biofilm induced
er, than to purine-cytosine permeases
ytosine permeases; transcription is regulated by Nrg1; Spider biofilm induced
epressed; repressed by Efg1 in yeast, not hyphal conditions; stationary phase enriched; rat catheter and S
hyphal growth conditions; induced by Mnl1 under weak acid stress; Spider biofilm repressed
ants not obtained by UAU1 method; Spider and flow model biofilm induced
d
lated; repressed by nitric oxide; clade-associated gene expression; Hap43p-repressed gene
ated; reports differ if functional homolog of ScFet3; rat catheter and Spider biofilm induced
nt S. cerevisiae fet3 iron-related phenotypes; rat catheter and Spider biofilm induced
y Rim101; repressed in fluconazole-resistant isolate; Sfu1, Hog1 repressed; complements S. cerevisiae fet
utant growth under low-iron; iron-repressed; regulated by Tup1, Rim101; flow model biofilm induced; Spide
der biofilm induced
ansposon mutation affects filamentous growth
roteins; lacks an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
on mutation affects filamentous growth; caspofungin induced; mutation causes marginal increase in caspof
ownregulated
siae; transposon mutation affects filamentous growth; Hap43p-repressed gene
gulated upon white-opaque switching
cerevisiae ortholog; role in, and regulated by, filamentation, Hap43p; almost identical to orf19.5797
Hap43-repressed; flow model biofilm induced; Tn mutation affects filamentous growth;
roteins; lacks an ortholog in S. cerevisiae; transposon mutation affects filamentous growth
erence to silicone substrate; Spider biofilm induced
sential gene, disruptants not obtained by UAU1 method
ofilm repressed
filamentous growth; lacks an ortholog in S. cerevisiae
s filamentous growth; Hap43p-repressed gene
fects filamentous growth; macrophage-induced gene; Hap43p-repressed gene
repressed
nl1 under weak acid stress
repressed
ssed gene
2 repeat sequence; transposon mutation affects filamentous growth
2 repeat sequence; transposon mutation affects filamentous growth
y regulates rRNA and ribosomal protein gene transcription
ript is opaque-specific and a-specific; activated by Cph1 or alpha pheromone
aration, and for virulence in cell culture; mutant lacks true hyphae, is constitutively pseudohyphal; upregulat
nacrophage-induced; mutant defective in filamentous growth; Spider biofilm induced
hal gene expression; required for virulence in mouse systemic infection; binds Efg1p; binds Mss11p via Lis
sensitivity to toxic ergosterol analog; decreased transcription is observed upon fluphenazine treatment

nily) of transporters; involved in histatin 5 efflux; fungal-specific (no human/murine homolog)

f fluconazole resistance; Spider biofilm repressed

alog, to amphotericin B; alkaline repressed; repressed by alpha pheromone in SpiderM medium; rat cathet

human or murine homolog)

ite-opaque switch, by DNA methylation; transcriptional activation by oleate requires Ctf1; rat catheter and S

duced

ne

nal predicted; Tup1, Rim101, Ssn6, Hog1, caspofungin repressed; ciclopirox olamine induced; rat catheter

U1 method

irox olamine, and upregulated by interaction with macrophage; un-merged from orf19.6139 in a revision of

e conditions or interaction with macrophage; Spider biofilm induced

-repressed; ciclopirox-, hypoxia-, Hap43-induced; colony morphology-related regulation by Ssn6; Spider an

nce of human neutrophils; possibly adherence-induced; regulated by Sef1, Sfu1, and Hap43

ated; repressed by nitric oxide; Spider biofilm induced; rat catheter biofilm repressed

utrophils

by macrophages; possibly essential gene, disruptants not obtained by UAU1 method; protein present in ex

in exponential and stationary growth phase yeast cultures; Spider biofilm repressed

ed by Sfu1p, amphotericin B, caspofungin; induced by alkaline pH, ciclopirox olamine; regulated by Sef1p,

n, ciclopirox, Hog1p, Sef1p, Sfu1p, and Hap43p regulated; complements S. cerevisiae ftr1 iron transport; H

ne, amphotericin B, caspofungin; complements S. cerevisiae ftr1 iron transport defect; Hap43-repressed; S

r in stationary phase; rat catheter biofilm repressed

protein present in exponential and stationary growth phase

units, translation factors, and tRNA synthetases are downregulated upon phagocytosis by murine macropl

e/threonine protein kinase; induced by Mnl1 under weak acid stress; rat catheter and Spider biofilm induced

with flucytosine resistance in clade I clinical isolates; flucytosine, macrophage-induced protein; levels decr

omozygous for the MTLa locus; alpha factor induced

ressed; transcript induced by Mnl1 under weak acid stress; regulated by Nrg1, Tup1; Spider and flow mode

uced by Mnl1 under weak acid stress; stationary phase enriched protein; rat catheter biofilm repressed

se enriched protein; GlcNAc-induced protein; farnesol, hypoxia-repressed in biofilm; rat catheter and Spide

lcNAc-, fluconazole- and ketoconazole-induced; stationary phase enriched protein; rat catheter and flow m

to toxic ergosterol analog; overlaps orf19.3673; Spider biofilm induced

lved in regulation of galactose utilization genes; caspofungin repressed; Spider biofilm repressed

le; macrophage/pseudohyphal-repressed

urce; alkaline, GlcNAc, phagocytosis induced; WT virulence in mice; Spider and flow model biofilm induced

dine induction; regulated by Nrg1, Tup1; colony morphology-related gene regulation by Ssn6; Spider and fl

egulated by Hap43, Gcn2 and Gcn4; colony morphology-related gene regulation by Ssnp

7-deazaadenosine); macrophage/pseudohyphal-induced; Spider biofilm repressed

nd utilization of isoleucine, tyrosine and tryptophan N sources; required for virulence in a mouse systemic i

Spider biofilm repressed

ohydrates, pH, galactose; promotes biofilm matrix formation; flow model biofilm induced; Bcr1 repressed i

by UAU1 method; promotes biofilm matrix formation; Spider biofilm induced; Bcr1-induced in RPMI a/a bi

acrophage

ial for growth, based on an insertional mutagenesis strategy; Spider biofilm repressed

etases are downregulated upon phagocytosis by murine macrophage

oding translation factors are repressed by phagocytosis by murine macrophages

MN) cells

al complementation of an S. cerevisiae abf2 mutation suggest role in mt genome replication, maintenance;

nse, in contrast to S. cerevisiae homolog; similar to S. cerevisiae Gcn2p

MN) cells

by amino acid starvation, not by serum; human whole blood and PMN induced; required for biofilm format

rsensitivity to 5-fluorouracil (5-FU)
n contrast to intron in S. cerevisiae GCR3 gene
2, Cd, or presence of human neutrophils; possibly adherence-induced; Spider and F-12/CO2 biofilm induc
ed
by Rim101 at acid pH; transcript induced in elevated CO2; stationary phase enriched protein

nary phase enriched protein; flow model biofilm induced; Spider biofilm repressed
e hyphal induction, cell wall, and cell surface charge; not required for HeLa cell adherence; functional hom
g1, Tup1; rat catheter biofilm repressed
/CO2 early biofilm induced
oglutarate; fungal-specific; regulated by Nrg1p, Mig1p, Tup1p, and Gcn4p; stationary phase enriched; Spide
at pH 8; GlcNAc, ciclopirox, ketoconazole induced; exp and stationary phase protein; Spider biofilm repress

homeostasis

y UDP-GlcNAc, FMDP, N-acyl peptide, kanosamine-6-P; functional homolog of S. cerevisiae Gfa1p; Cagr

tance to nikkomycin Z
ene and macrophage-induced protein
lication checkpoint; ortholog of S. cerevisiae Mrc1p, an S-phase checkpoint protein; Hap43p-induced gene
S395; necessary for septin ring within germ tube but not for septin band at mother cell junction; physically

st-hypha switch; null exhibits sensitivity to sorbitol, 5-fluorocytosine, and cold temperatures; Spider biofilm r
Rim101-repressed; virulence-group-correlated expression
lium; Hap43-repressed; Spider biofilm induced
ungin, macrophage/pseudohyphal-repressed; flow model biofilm induced; Spider biofilm induced
ene, disruptants not obtained by UAU1 method; Hap43p-repressed gene
Ssn6; stationary phase enriched protein
iron; alternatively spliced intron in 5' UTR

atheter biofilm repressed
ypha-induced; Spider biofilm induced
nduced in core stress response; colony morphology-related gene regulation by Ssn6; GlcNAc-induced prote

ed
s transcription of Mep2 ammonium permease; regulated by Gcn2 and Gcn4; mRNA binds She3; Spider bi
re downregulated upon phagocytosis by murine macrophage; protein present in exponential and stationary
ressed
ate via S-lactoyl-glutathione and cytoplasm localization
rt, retrograde Golgi to ER vesicle-mediated transport; Spider biofilm repressed
verexpression correlates with multidrug resistance in a cap1 mutant, farnesol induced; stationary phase en

d; hypoxia, oxidative stress via Cap1, Hap43 induced; stationary-phase enriched; rat catheter, Spider biofil
acrophage/pseudohyphal-induced; the GLY1 locus has an RFLP and is triploid in strain SGY269; flow mode
absence of GlcNAc supplementation; required for persistent infection and wild-type virulence in mouse sys
mice; dual localization to cytosol and peroxisomes depends on alternative splicing; rat catheter and Spide
, Tup1, Gcn2, Gcn4, and alkaline regulated by Rim101; repressed during chlamydospore formation; rat cat

der some conditions, and virulence; relocalizes from the cytoplasm to the mitochondrion during oxidative or
region localization
se signaling; reports differ on role in cAMP-PKA pathway, MAP kinase cascade; Gpr1 C terminus binds G
under H2O2 stress conditions; Sflow model and Spider biofilm induced
by Ssn6, Nrg1, Efg1; induced by cell wall regeneration, macrophage/pseudohyphal growth, core stress res
onazole-induced; localizes to cell surface of hyphae, not yeast; stationary phase enriched protein; Spider b

S. cerevisiae Gpi13p, which acts in GPI anchor biosynthesis; Hap43p-induced gene
PI), the first intermediate in GPI anchor synthesis; complements S. cerevisiae gpi19 mutant; flow model bi
iosynthesis
osphodiesterase/nucleotide pyrophosphatase domain; similar to S. cerevisiae Gpi7p
eins; likely to be essential for growth, based on an insertional mutagenesis strategy
onazole, or amino acid starvation (3-AT) induced, farnesol-repressed; Hap43, flow model biofilm induced; S
y high levels of peroxide stress, farnesol; flow model biofilm induced; rat catheter and Spider biofilm repres

aling pathway that regulates beta-glucan masking and immune evasion; binds Gpa2; regulates HWP1 and
f an S. cerevisiae uga4 put4 gap1 triple mutant; complements growth of an S. cerevisiae spe1 mutant unde
or interaction with macrophage; regulated by Efg1; caspofungin repressed; Spider biofilm induced
o oxidation in response to H2O2; planktonic growth-induced
epressed; repressed by low iron; possibly involved in osmotic stress response; stationary phase enriched p
arnesol, macrophage interaction and by Mnl1 under weak acid stress; stationary-phase enriched protein; S
nine auxotroph; Spider biofilm induced; promoter bound by Bcr1, Tec1, Efg1, Ndt80 and Brg1
gulation associated with azole resistance; induced in core stress response or by oxidative stress via Cap1,
n negative control of pseudohyphal growth; regulates stability of Ume6p in response to CO2
re downregulated upon phagocytosis by murine macrophage; stationary phase enriched protein
tion (3-aminotriazole treatment)
16 predicted membrane-spanning regions; mRNA abundance declines after yeast-to-hypha transition; Spic
biofilm induced
y yeast-to-hypha transition; young biofilm repressed, induced by biofilm drug exposure; Bcr1-repressed in
by Nrg1; very low gene expression in yeast-form and hyphal cells
ge/pseudohyphal-induced; transcript not regulated by white-opaque, yeast-hypha switching; GlcNAc-induc
ted upon white-opaque switching; increased transcription is observed upon benomyl treatment
tiple generations; regulated by Nrg1, Tup1; induced by nitric oxide; stationary phase enriched; Spider biofilr
peroxide-induced; induced by alpha pheromone in SpiderM medium; Spider biofilm induced
Efg1-regulated; strong oxidative stress induced; colony morphology-related regulation by Ssn6; stationary
gulated in clinical isolates from HIV+ patients with oral candidiasis; (see Locus History Note for Assembly
aque switching; induced in the presence of human neutrophils; oxidative stress-induced via Cap1p; regula
duced by nitric oxide; Spider biofilm induced
lic process, protein glutathionylation and endoplasmic reticulum localization
edium; Spider biofilm induced
sine induced; macrophage-downregulated protein abundance; protein level decreases in stationary phase
stationary phase cultures; Hap43p-induced gene
gup1 mutant under salt stress; required for normal ergosterol distribution, hyphal growth, biofilm formation
ed in a cyr1 homozygous null mutant than in wild type
t concentrations, fluid-phase endocytosis, actin cytoskeleton polarization and vacuole biogenesis; rat cathe
l by Nrg1, Mig1, and Tup1
y and altered sensitivity to fluconazole, LiCl, and copper; Spider biofilm induced
atypical splicing at C terminus under ER stress; induced during mating and by caspofungin; mRNA binds S
duced upon phagocytosis by macrophage; Hap43-repressed; rat catheter biofilm repressed
e role in sulfur recycling; ortholog of S. cerevisiae Met22; predicted Kex2 substrate; F-12/CO2 biofilm induc
e role in sulfur recycling; Hap43-repressed; F-12/CO2 biofilm induced
l; similar to S. cerevisiae Hal9, a putative transcription factor involved in salt tolerance
n2p and Gcn4p
es Hap43 and probably Hap2 and Hap3; possibly essential, disruptants not obtained by UAU1 method; Cap
on; opaque specific, alkaline, ciclopirox olamine induced; regulated by Sef1, Sfu1, Hap43; Bcr1-regulated ir
induced in high iron; repressed in low iron; Sef1, Sfu1, and Hap43 regulated; rat catheter and Spider biofil
Mnl1 under weak acid stress; Spider biofilm induced
ponse; similar to bZIP transcription factor AP-1; repressed by Sfu1; ciclopirox olamine induced; rat cathete
regulates genes involved in respiratory growth; functional homolog of S. cerevisiae Hap5p; Cap1p-depend
RNA helicase family that is involved in biogenesis of the ribosome, particularly the small (40S) subunit; casp
mutations cause constitutive pseudohyphal growth, white to opaque switch, caspofungin sensitivity; rat cat
esis; mutations cause constitutive pseudohyphal growth, caspofungin sensitivity; rat catheter and Spider bic
aque switching, may affect survival in host; activator of MTLalpha1 and MTLalpha2; transcript activated by
tants not obtained by UAU1 method; flow model and rat catheter biofilm induced
ponse to amino acid starvation (3-aminotriazole treatment); mutants are viable

pressed
itch frequency but not opaque-to-white switch; greater expression in white cells than opaque cells; inhibitec
/ Ssn6; Hap43-repressed; Spider biofilm induced
p43, macrophage-repressed; farnesol-induced; possibly essential; flow model biofilm induced; rat catheter
ated transcript; Yfh1-induced; Hap43-repressed; rat catheter biofilm repressed
ed by a yfh1 null mutation; Spider biofilm repressed
; Spider biofilm repressed
duced in high iron, CO2; alkaline repressed; regulated by Sef1, Sfu1, and Hap43; rat catheter and Spider b
lence; Spider biofilm repressed
culture medium; required for full virulence; may have role in carbon or nitrogen scavenging; possibly an es
fects filamentous growth
silon); phosphorylated protein; mutants have a growth defect
cytosine induced
Hgc1 maintains Cdc11 S394 phosphorylation during hyphal growth; required for virulence in mice; regulate
for growth; protein newly produced during adaptation to the serum; rat catheter and Spider biofilm induced
motic stress, at low glucose in rich media, during cell wall regeneration; 12 membrane spans; Hap43p-induc
rowth; detected at germ tube plasma membrane by mass spectrometry; Snf3p-induced; 12 probable trans
ransmembrane; gene has intron; oxidative stress-induced via Cap1p; expressed in rich medium, 2% gluco
ne-spanning segments; expressed in rich medium with 2% glucose; rat catheter and flow model biofilm ind
comprises 20 members; 12 probable membrane-spanning segments; gene has intron; expressed in rich me
ments; induced at low (0.2%, compared to 2%) glucose in rich media; Spider biofilm induced
comprises 20 members; 12 probable membrane-spanning segments; expressed in rich medium with 2% gl
N terminus; expressed in rich medium; Hap43, phagocytosis, rat catheter, Spider and flow model biofilm in
ne-spanning segments; expressed in rich medium with 2% glucose; rat catheter and Spider biofilm induced
comprises 20 members; 12 probable membrane-spanning segments; regulated by Nrg1
comprises 20 members; 12 probable membrane-spanning segments, extended C terminus; expressed in ri
family; extended C terminus; high-glucose repressed; macrophage induced; flow model biofilm repressed
comprises 20 members; 12 probable membrane-spanning segments, extended N terminus; expressed in ri
azole, oralpharyngeal candidasis induced; flow model biofilm induced; Spider biofilm induced
ber C. albicans glucose transporter family; 12 TM regions predicted; flow model biofilm induced; Spider bio
transporter family; 12 probable membrane-spanning segments; gene has intron; expressed in rich mediun
comprises 20 members; 12 probable membrane-spanning segments; induced at low (0.2%, compared to 2
essed; farnesol regulated; colony morphology-related gene regulation by Ssn6; Hap43-induced; rat cathete
essed; colony morphology-related gene regulation by Ssn6; Hap43-induced; rat catheter and Spider biofilm
ced mRNA abundance in fkh2 mutant; farnesol regulated; Spider biofilm induced; rat catheter biofilm repres
nd Spider biofilm repressed
pider biofilm induced
n regulation of white-opaque switching frequency
Rim101; regulated by Gcn2, Gcn4; strain CA9 is a his1 mutant; flow model biofilm induced; Spider biofilm r
erevisiae his3-1 mutation; hyphal-induced expression; regulated by Gcn2p and Gcn4p; fungal-specific (no h
ydrolase, phosphoribosyl-ATP diphosphatase, and histidinol dehydrogenase activities; required for wild-typ
nary growth phase yeast cultures
ption induced by histidine starvation; regulated by Gcn2p and Gcn4p; higher protein level in stationary phas
el biofilm induced; Spider biofilm induced
in response to lovastatin and fluconazole
hi1; rat catheter biofilm repressed
cts as repressor of START; activates pseudohyphal growth when expressed in S. cerevisiae; repressed in
p90 compromise; acts downstream of Pcl1; Spider biofilm induced
sidues; involved in nuclear export of Npl3p; Spider biofilm repressed
1; induced by low iron; upregulated by Rim101 at pH 8; Hap43-induced; Spider and flow model biofilm indu
ny morphology-related gene regulation by Ssn6; clade-associated gene expression
ethod; Spider biofilm induced; transcription regulated by biotin and Vhr1p
heckpoint; mutant is viable
phosphorylated in response to H2O2 or NaCl; acts as repressor of START; mutant induces protective mous
omone in SpiderM medium; possibly an essential gene, disruptants not obtained by UAU1 method

nd Spider biofilm induced
ut not in mammals; ketoconazole-repressed; protein present in exponential and stationary growth phase yea
d Gcn4; early-stage flow model biofilm induced
macrophage-induced protein; protein level decreases in stationary phase cultures; flow model biofilm repres
ession in white cells than in opaque cells
function together as a complex involved in regulation of white-opaque switching, filamentous growth and v
mpared to opaque cells; has conserved deacetylation motif
acid metabolic process, cellular detoxification of nitrogen compound, protein acetylation
er biofilm induced
n in the CAI4 strain background; protein level decreases in stationary phase; Spider biofilm induced
e control; induced by hydroxyurea; Spider biofilm induced
tein; rat catheter and Spider biofilm repressed
spindle microtubules; expression regulated during planktonic growth
d hyphal cells via regulation of Swe1p and Cdc28p; required for full virulence and kidney colonization in mo
alization
uanidine-insensitive; heat shock/stress induced; repressed in farnesol-treated biofilm; sumoylation target;
and CDR2 overexpression, or ssn6 or ssk1 null mutation; overexpression increases resistance to farnesol
or ras1 mutant; stationary phase enriched protein; detected in some, not all, biofilm extracts; Spider biofil
heter biofilm induced
dmium) stress-induced; sumoylation target; protein present in exponential and stationary phase cells; Hap4
e-induced; surface localized in yeast and hyphae; antigenic in host; farnesol-downregulated in biofilm; Spide
dmium) stress-induced; stationary phase enriched protein; rat catheter and Spider biofilm induced
esis; activated by heat shock, stress; localizes to surface of hyphae, not yeast cells; mediates echinocandi
ydroxyurea and high-levels of hydrogen peroxide; Hap43p-induced; ectopic expression blocks genotoxin-in
mone transporter); required for mating of MTLa cells; a-type specific, not regulated during white-opaque or
k1p; wild-type virulence in mouse systemic infection; functional homolog of S. cerevisiae Ste7p; mutants ar
ucosylceramide biosynthesis, which is important for virulence
ulated by tyrosol and cell density; Hap43-induced gene; Spider biofilm repressed
nduced
and cell density; Spider biofilm repressed
conazole induced; Efg1 regulated; slow growth, increased white-to opaque switch in ectopic expression str
enriched protein; Spider biofilm repressed
rane transport, UDP-glucose transmembrane transport
a side of conjugation tube; virulence complicated by URA3 effects; Bcr1-repressed in RPMI a/a biofilms; S
n some media; expressed in hyphae; mutant delayed in virulence; regulated by Efg1, Tup1; similar to Hwp1
nd mouse virulence; GlcNAc-induced transcript; induced by alpha pheromone in SpiderM medium
gene regulation by Ssn6; present in exponential and stationary growth phase; flow model biofilm induced;
logy-related gene regulation by Ssn6; possibly essential gene
nogenesis; role in cell separation, azole sensitivity; required for hyphal growth
by neutrophils, azoles; regulated by Rfg1, Efg1, Nrg1, Tup1, Cyr1, Bcr1, Hap43; Spider and flow model bio
ation
L or white-opaque status
cle regulated periodic mRNA expression
cn4p
tivity to tunicamycin; transposon mutation affects filamentous growth
crophage; farnesol regulated; Pex5-dependent peroxisomal localization; stationary phase enriched; rat cath
crease in stationary phase cultures
resent in exponential and stationary growth phases; Spider biofilm repressed
netic process
ed; Spider biofilm repressed
ential and stationary phase yeast; Hap43-repressed; Spider biofilm repressed by Bcr1, Tec1, Ndt80, Rob1,
pression (not CDR1 or CDR2) in fluconazole-resistant clinical isolates; farnesol regulated; possibly essenti

1, fluconazole; rat catheter biofilm induced
-repressed gene
plastic substrate; mutants are viable; Hap43-repressed gene
UAU1 method
repressed gene; Spider biofilm induced
that overexpresses MDR1
otants not obtained by UAU1 method
es rRNA and ribosomal protein gene transcription; Spider biofilm induced
orf19.2177
by oxidative stress via Cap1, osmotic stress via Hog1; protein present in exponential and stationary phase
vith CDR1 and CDR2 overexpression or fluphenazine; putative drug-responsive regulatory site; Hap43p-re
media at 37; oralpharyngeal candidasis induced ; Spider biofilm induced; regulated in Spider biofilms by T
ed
D-118/BAY-10-8888 and mupirocin; protein present in exponential and stationary growth phase yeast cultu
tein present in yeast exponential and stationary phase cultures; early-stage flow model biofilm induced
tionary phase enriched protein
and stationary growth phase; Sef1, Sfu1p, Hap43-regulated; farnesol-repressed; flow model biofilm induce
macrophage-repressed protein; protein present in exponential and stationary phase; flow model and Spide
in present in exponential and stationary growth phase yeast; Spider biofilm repressed
and mizoribine monophosphate; antigenic during infection; repressed in core stress response; snoRNA sn
ssed
nitochondria
nitochondria
d
required for ingression of the plasma membrane into the bud neck during cytokinesis; contains a C2 mem
ream inositol/choline regulatory element; glycosylation predicted; rat catheter, flow model induced; Spider
lcholine and phosphatidylinositol biosynthesis, fatty acid beta-oxidation, and peroxisome biogenesis
atidylcholine and phosphatidylinositol biosynthesis, fatty acid beta-oxidation, and peroxisome biogenesis; g
evels; affects hyphal growth, virulence, cell integrity; interacts with Irs4p
and mouse cecal colonization and systemic virulence; similar to S. cerevisiae Bud4; Hap43-induced gene
for synthesis of 1,2,3,4,5,6-hexakisphosphate; Spider biofilm induced
yphal growth
uptants not obtained by UAU1 method
tein present in exponential and stationary phase yeast; possibly essential (UAU1 method); sumoylation tar
ol-P)2-ceramide, M(IP)2C, from MIPC; required for wild-type membrane localization of Cdr1; Spider biofilm
sociation with Bni1/Bnr1, Iqg1 degradation, and ring disassembly; mutation causes cytokinetic defects; rat c
tive form; Spider biofilm induced; flow model biofilm repressed
ersensitive to caspofungin; Spider biofilm induced
4; suppresses S. cerevisiae aft1 mutant low-iron growth defect; hyphal-induced; reports differ about iron re
nd agar-embedded filamentous growth; antigenic in human infection; similar to S. cerevisiae Irs4p
Hap43; Spider biofilm induced
theter and Spider biofilm induced
ngolipids to produce ceramide; mutant is viable
alization to plasma membrane, regulation of phosphatidylinositol dephosphorylation
biofilm induced; rat catheter and Spider biofilm induced
ormation; Hap43-induced gene; repressed by high-level peroxide stress
lm induced
n; fluconazole, caspofungin repressed; possibly essential (UAU1 method); flow model, rat catheter and Sp
ves the ubiquitin-like protein tag Rub1p off the cullin (Cdc53p) molecule
R-associated degradation of misfolded proteins, and also has a role in karyogamy; has J domain and 4 tet
asma membrane; Spider biofilm induced

UAU1 method; rat catheter and Spider biofilm induced

stress response; Hap43-induced gene

in present in exponential and stationary growth phase yeast cultures; flow model and Spider biofilm repress

mutants are viable; null has high-frequency white-opaque switching phenotype

; role in karyogamy; opaque-specific, a-specific; induced by alpha factor

actor

k, hyphal tip; wild-type localization requires actin and microtubule cytoskeleton; induced by alpha factor

during mating pheromone response in S. cerevisiae; induced by alpha pheromone in SpiderM medium

ly decreased filamentation ratio; not required for buccal epithelial cell adherence or virulence in mice

h/mating of S. cerevisiae kem1 mutant; required for SD or Spider medium biofilm formation

owth and wild-type virulence in mice; required for maturation of candidalysin Ece1p

anscript induced in an RHE model of oral candidiasis; stationary phase enriched protein; Hap43-repressed;

ressed

role in cell separation, azole sensitivity; required for hyphal growth; constitutive expression is MTL, white-o

ulation; mutants are hypersensitive to caspofungin

in SpiderM medium; periodic mRNA expression, peak at cell-cycle G2/M phase

nt hyphal regulation; regulated by Nrg1, Tup1; oralpharyngeal candidasis induced; Spider biofilm induced;

(ASC and KIS domain); interacts with Snf4p; mutants are hypersensitive to caspofungin and hydrogen pe

on with Snf1p complex is regulated by carbon source, decreased on ethanol; N-terminal myristoylation; Ho

thway, phosphorylates Rpc53p to regulate ribosome and tRNA biosynthesis; Spider and flow model biofilm

r growth, based on an insertional mutagenesis strategy

killer toxin sensitivity; caspofungin induced; Spider/rat catheter/flow model biofilm induced; Bcr1-repressed

utation confers hypersensitivity to amphotericin B

mouse IV model; partially complements S. cerevisiae kre5 mutant defects; flow biofilm repressed, Bcr1-re

ion; alkaline induced by Rim101, on cell wall regeneration; Spider biofilm induced; Bcr1-repressed in RPM

ization of galactose and for growth on glucose; similar to S. cerevisiae Kre9p and Knh1p; O-glycosylated b

MDR1; F-12/CO2 early biofilm induced

riched protein; Spider biofilm repressed

hypersensitivity to amphotericin B

of wobble nucleosides in tRNAs; rat catheter and Spider biofilm induced

killer toxin; predicted Kex2p substrate; Hap43p-induced gene

fic (no human or murine homolog); possibly an essential gene, disruptants not obtained by UAU1 method

Bcr1-repressed in RPMI a/a biofilms

rs for glucosylsphingolipids; caspofungin induced

correlated expression; induced by alpha pheromone in SpiderM medium; Hap43-induced; Spider and flow

in macrophage response; flow model biofilm induced

wth phase yeast cultures; Spider biofilm repressed

FC), 5-fluorouracil (5-FU); macrophage-induced; Spider biofilm induced

tion target; Spider biofilm repressed

luced

by human whole blood or PMNs; regulated by Sef1, Sfu1, and Hap43; rat catheter biofilm induced, Spider

vel decreases in stationary phase; GlcNAc-induced protein; flow model biofilm repressed

line induced; induced by Mnl1 under weak acid stress; required for yeast cell adherence to silicone substra

or PMNs; macrophage/pseudohyphal-repressed after 16h; Spider biofilm repressed

lls; regulated by Gcn2 and Gcn4; stationary phase enriched protein; Spider biofilm induced

leavage, tRNA 3'-trailer cleavage, endonucleolytic, tRNA folding, tRNA processing and nucleolus, nucleopl

ned by UAU1 method; flow model biofilm repressed

sses S. cerevisiae ime1-1 mutant IME2 transcription defect; required for wild-type filamentous growth and v

o carbon source and during infection; may have a role in nutrition and/or in creating an acidic microenviron

o carbon source and during infection; may have a role in nutrition and/or in creating an acidic microenviron
not oral tissue, during mouse oral infection; may have a role in nutrition and/or in creating an acidic microe
ource and infection; possible role in nutrition and/or in creating an acidic microenvironment; flow model biof
/or in creating an acidic microenvironment; expressed more strongly during mucosal infections than during
trition and acidic microenvironment; LIP5 and LIP8 expressed at all stages of mucosal and systemic infecti
d during infection; may have a role in nutrition and/or in creating an acidic microenvironment; induced on a
signal sequence for secretion, unlike other family members; may have a role in nutrition or in creating an a
/or in creating an acidic microenvironment; LIP5 and LIP8 are expressed at all stages of both mucosal and
o carbon source and during infection; may have a role in nutrition and/or in creating an acidic microenviron

upstream of MAP kinase Cek1p; has similarity to human ELMO1
systemic infection; macrophage-induced protein; protein present in exponential and stationary phase yeast
tes with overexpression of MDR1 in fluconazole-resistant isolate; stationary phase enriched protein
phatase activity; rat catheter and Spider biofilm induced
nesis; rat catheter biofilm repressed
pathway that controls morphogenesis in response to environmental signals
biosynthesis; flow model biofilm repressed
ential and stationary growth phase yeast cultures; Spider biofilm repressed
n exponential and stationary growth phase yeast cells; Spider biofilm repressed

wth phase yeast cultures; caspofungin repressed; biofilm induced; fungal-specific (no human/murine homo
odel biofilm repressed

not obtained by UAU1 method
unctionally complements S. cerevisiae lys1 mutation; fungal-specific (no human or murine homolog)
s; clade-associated gene expression; protein level decreases in stationary phase cultures; Spider biofilm re
l in the regulation of lysine biosynthesis genes
synthesis genes; fungal-specific
esis genes
synthesis genes
AMP and alpha-aminoadipate; inhibited by lys or thialysine; regulated by Gcn2 and Gcn4; Spider biofilm ind
solate; colony morphology-related gene regulation by Ssn6; ketoconazole-repressed; regulated by Gcn2, G
tationary phase cultures; induced by ketoconazole, Spider biofilm induced; flow model biofilm repressed
human whole blood or PMNs; Hap43-repressed; flow model and Spider biofilm repressed
pha-aminoadipate reductase; functional homolog of S. cerevisiae Lys5p
cn4-regulated; colony morphology-related gene regulation by Ssn6; protein present in exponential and stati
ns; required for copper regulation of SOD1 and SOD3; Spider biofilm induced
crophages and for virulence in a mouse model of systemic candidiasis
ation by Ssn6; Hap43-repressed; Spider biofilm repressed
ngin repressed; Spider biofilm repressed
ofilm induced
ine)
gulated upon adherence to polystyrene
dins
tose, repressed by glucose; Tn mutation affects filamentous growth; upregulated in RHE model; rat cathete
h oral candidiasis; alkaline induced; Spider biofilm induced
ary growth phase yeast cultures
s-induced via Cap1
s

mRNA expression; predicted, conserved MBF binding sites upstream of G1/S-regulated genes
cerevisiae Mca1p; fungal-specific (no human or murine homolog); farnesol-induced
alpha pheromone in SpiderM medium; periodic cell-cycle expression; Hap43-repressed; rat catheter and S

sites; MADS domain DNA-binding motif; similar to S. cerevisiae Mcm1p; greater expression in white than o
cycle
induced
ase; regulated by tyrosol and cell density; repressed by alpha pheromone in SpiderM medium; Hap43-indu
ytosine induced; protein present in exponential and stationary growth phase yeast; YNB biofilm induced; ra

on and membrane raft, plasma membrane localization d in high iron; antigenic during murine and human infection; repressed in Spider biofilms by Bcr1, Tec1, Nd

and stationary growth phase yeast cultures; Spider biofilm repressed

phase yeast; Hap43p-repressed gene

; early-stage flow model biofilm induced

ondria encounter structure (ERMES) complex with a role in protein import into mitochondria

l and Spider biofilm induced

n drug-resistant clinical isolates confers fluconazole resistance; repressed in young biofilms; rat catheter bi

ce in a mouse model of systemic infection and for SD and Spider medium biofilm formation; role in chlamyd

density

benomyl treatment

1 method

1 method

l by UAU1 method

iofilm formation; rat catheter biofilm repressed

ulation of transcription by RNA polymerase II, positive regulation of transcription by RNA polymerase II

in binding, protein-macromolecule adaptor activity, transcription corepressor activity

predicted transmembrane regions; low mRNA abundance; hyphal downregulated; flow model biofilm induce

ane regions; in low nitrogen cytoplasmic C-terminus activates Ras/cAMP and MAPK signal transduction pa

ynthetases are downregulated upon phagocytosis by murine macrophage; protein present in exponential a

le blood or polymorphonuclear (PMN) cells; Hog1p-induced; fungal-specific (no human or murine homolog

uced; possibly adherence-induced; flow model, Spider model, F-12/CO2 biofilm induced

epressed

esent in exponential and stationary growth phase yeast; F-12/CO2 biofilm induced

ence-induced; brown color of mutant in Pb(2+) medium a visual selection; chlamydospore formation induce

ng biofilm formation; fungal-specific; possibly an essential gene, disruptants not obtained by UAU1 method

transcription; Plc1p-regulated

ly biofilm induced, in contrast to many sulfur amino acid metabolic genes; no human or murine homolog; vi

essential, disruptants not obtained by UAU1 method; Hap43-repressed; rat catheter biofilm induced

, caspofungin, white phase-induced; induced on biofilm formation, even in presence of Met and Cys; Spide

herence to silicone substrate; Spider biofilm induced

nethionine synthase); antigenic in murine/human systemic infection; heat shock, estrogen, GCN-induced; S

ulated by Gcn2p and Gcn4p

s, but not MTLalpha; induced by alpha-factor

ge/pseudohyphal-repressed

ion confers hypersensitivity to tubercidin (7-deazaadenosine)

ffects filamentous growth; possibly transcriptionally regulated upon hyphal formation; possibly an essential

e

ecreased transcription is observed upon fluphenazine treatment or in an azole-resistant strain with CDR1 a

tromeres

dependent functions; hyphal, Hap43 and caspofungin repressed; Spider and flow model biofilm induced

nds She3

zole-resistant isolate; induced upon adherence to polystyrene essed by Efg1; fluconazole-induced; stationary phase enriched protein; rat catheter and Spider biofilm repr

zole, caspofungin induced; macrophage-repressed; Spider biofilm induced

cell wall structure/maintenance, caspofungin response; phosphorylated on surface contact, membrane per

lated; mutants are viable and hypersensitive to caspofungin

ent localization to tip polarisome, bud neck in yeast and pseudohyphae; sumoylation target; rat catheter, Sp

utLgamma complex, nucleus localization

hagocytosis, strong oxidative stress induced; stationary phase enriched; flow model biofilm repressed; rat

glutathione, glucuronate, or sulfate; needed for virulence in mouse peritonitis; Spider biofilm induced; flow

n abundance; rat catheter and Spider biofilm repressed

d filamentous growth and stress response

damage; cell-cycle regulated periodic mRNA expression

or adaptation to weak acid stress; activates a subset of the genes that are repressed by Nrg1

101; transcript elevated in chk1 and nik1 mutants, but not in sln1 mutant; Spider and flow model biofilm ind

sylation and mannan polymerase complex localization

fu1p-, and Hap43p

der biofilm induced

ced

vity; iron utilization in low iron; Tn mutation affects filamentous growth; filament induced; increased chitin ex

ocalization

repressed in core stress response; NO, Hog1 induced; confers sensitivity to cell wall perturbing agents; Sp

or white, growth at 42 degrees and have decreased cell wall mannan; flow model biofilm induced

in detergent-resistant membrane fraction (possible lipid raft component); predicted N-terminal acetylation

nal interaction with macrophages; mutant induces inflammatory cytokines in dendritic cells; rat catheter an

ot in chk1 or sln1 null mutants; pheromone induced; Spider biofilm induced

yphal growth; mutant is hygromycin B sensitive and vanadate resistant; has N-terminal membrane-spanni

cosyl hydrolase family 47; ER form is converted by Kex2 to cytosolic form; flow model biofilm repressed

wall mannoprotein biosynthesis; required for wild-type virulence and adherence to epithelial cells; Hap43-in

lant with Mnt1; role in adherence and virulence; expressed in yeast and hyphae; fungal-specific; Hap43-ind

specific (no human or murine homolog)

ctin polarization; required for hyphal growth; phosphorylated by Cdc28 on hyphal induction; activates Cbk1;

erM medium and by Mnl1 under weak acid stress; possibly essential (UAU1 method); flow model biofilm inc

repressed

by heat, germ tube formation, wall regeneration; mycelial antigen; diagnostic marker; fluconazole-represse

oxyurea treatment

by prostaglandins

xidative stress response; periodic mRNA expression, peak at cell-cycle S/G2 phase

e

oxidative stress-induced via Cap1; stationary-phase enriched protein; Spider biofilm induced

ome; transposon mutation affects filamentous growth

viable; flow model and rat catheter biofilm repressed

exponential and stationary growth phase yeast cultures

y Ssn6p

tif; overexpression in S. cerevisiae causes respiratory defect that is reversible upon cessation of C. albican
upregulation of MDR1 (a plasma membrane multidrug efflux pump) and multidrug resistance; Hap43-induc
n; mutants display decreased colonization of mouse kidneys; required for yeast cell adherence to silicone s
l to the mitochondrial membrane; transcription under control of Atf2p; regulated by Sef1p, Sfu1p, and Hap4
lenosine); rat catheter biofilm induced
xpresses CDR1 and CDR2; Spider biofilm induced
ced
ulation of adhesion factors
tress; Rim101-repressed; activation releases extracellular domain into medium; Spider biofilm induced
d gene
ed by tyrosol and cell density
ogous DNA ends; rat catheter biofilm repressed
ion; Hap43p-induced gene
; interacts with Cgr1; transcript regulated by iron; rat catheter biofilm induced; farnesol repressed in biofilm
E. coli MetRS mutant; transcript regulated by Nrg1; flow model biofilm induced
in C. albicans; partly complements STRE-activation defect of S. cerevisiae msn2 msn4 double mutant; flo
biofilm induced
e presence of lysed macrophages; Hap43-repressed; Spider biofilm induced
pha-specific genes; required for hyphal growth
uced; rat catheter biofilm induced
ge/pseudohyphal-repressed; mRNA binds to She3, localized to yeast cell buds and hyphal tips; Hap43-indu
ochondrion localization
ochondrial RNA degradation
essed gene; likely to be essential for growth, based on an insertional mutagenesis strategy
ssembly; mitochondrial translation; Spider biofilm induced
with the large ribosomal subunit; required for mitochondrial translation; rat catheter biofilm repressed
ing and mating (an opaque-specific process); a/alpha mating type may increase virulence by competitive a
ntron; not related to S. cerevisiae MATa2; a/alpha mating type may increase virulence, provides competitiv
nate transport and mitochondrion localization
2-like domain
ent of glucosylceramides; glucosylceramide biosynthesis is important for virulence; Spider biofilm represse
h a single kinetochore microtubule attachment site
biofilm induced
by benomyl treatment; mutant is viable
ed by alpha pheromone in SpiderM medium; transcript regulated by Tup1
ofilm induced
phae compared vs yeast; Hap43-repressed; flow model biofilm induced; Spider biofilm repressed
t on alkaline medium; Hap43p-repressed gene
egulated by carbon source, yeast-hypha switch, growth phase, antifungals; gene has intron; rat catheter, Sp
phage regulated (gene induced, protein decreased); possibly adherence-induced; Spider biofilm induced
y, nuclear organization, migration, hyphal growth; conserved myosin ATPase/tail domains; Hap43-induced;
wth, white-opaque switch; regulatory phosphorylation on S366; downregulated on adherence to polystyrene
ucosamine 6-P to fructose 6-P; reversible reaction in vitro; gene and protein is GlcNAc-induced; Spider bio
ance; in gene cluster that includes genes encoding enzymes of GlcNAc catabolism; Spider biofilm represse
ed for wild-type mouse virulence and wild-type cycloheximide resistance; gene cluster encodes enzymes o
g motif; similar to S. cerevisiae Yor165Wp; in gene cluster that encodes enzymes of GlcNAc catabolism; n

ox olamine treatment

tationary growth phase yeast cultures

ress-induced via Cap1p

gosterol analog

film induced; Spider biofilm induced

; Spider biofilm induced

ential gene, disruptants not obtained by UAU1 method; conditional mutants show decreased susceptibility

m induced; Spider biofilm induced

, normal white-opaque switch; Mnl1-induced in weak acid stress; Hap43-induced gene; F-12/CO2, rat cath

ak at cell-cycle G2/M phase; flow model biofilm induced

thesis; subject to hypoxic regulation; ketoconazole-induced; caspofungin repressed

and Mig1; induced by prostaglandins

catheter biofilm induced; Spider biofilm repressed

chain; required for wild-type filamentous growth; alkaline repressed; Hap43-repressed; Spider biofilm rep

uired for wild-type drug resistance and for Spider biofilm formation; transcript induced by antifungal drug tr

egulation of transcription by RNA polymerase II

nduced histone acetylation at promoters of GlcNAc-inducible genes and activation of their transcription by

localizes to plasma membrane; induced by GlcNAc, macrophage engulfment; 12 transmembrane, major fa

ed; amphotericin B, caspofungin repressed; 5'-UTR intron; rat catheter and Spider biofilm repressed

n of Na+

ed for wild-type virulence in mouse systemic infection but not for wild-type growth or drug sensitivity/resista

coding ribosomal subunits, translation factors, and tRNA synthetases are downregulated upon phagocyto

nduced

se yeast cultures

stress response; merged with orf19.3288.1 in Assembly 21

glandins

3-induced; Spider biofilm induced

at an N-terminal Gly; essential; antifungal drug target; functional homolog of S. cerevisiae Nmt1p

ion confers hypersensitivity to 5-fluorouracil (5-FU), tubercidin (7-deazaadenosine); repressed in core stres

racil (5-FU), and tubercidin (7-deazaadenosine); Spider biofilm induced

ercidin (7-deazaadenosine); repressed by prostaglandins; Hap43-induced

duced

e; rat catheter biofilm induced

racil (5-FU), and tubercidin (7-deazaadenosine); heterozygous mutant is resistant to parnafungin; Spider b

ced

uorouracil (5-FU), and tubercidin (7-deazaadenosine); represses in core stress response

acrophage/pseudohyphal-induced; physically interacts with TAP-tagged Nop1; Spider biofilm repressed

ilm induced

fection; null mutant colonies exhibit slightly decreased filamentation ratio; required for yeast adherence to

mozygous null mutant is avirulent in mouse systemic infection despite persistence in host; repressed in rat

; required for hyphal growth; antigenic during human oral infection; greater expression in yeast-form cells t

Hmt1p; transcript upregulated in RHE model of oralcandidiasis; Spider biofilm repressed

ess response; Hap43p-repressed gene

e homolog

or murine homolog)

cue/stress response genes; effects both Tup1 dependent and independent regulation; flow model biofilm i

cation stress; interacts with Swi4 and Swi6; repressed during core stress response; Spider biofilm represse t catheter biofilm repressed

d by iron; Hap43-repressed gene; Spider biofilm induced

nice; possible regulatory cAMP-dependent phosphorylation at S10,S213; Hap43-repressed gene; Spider bi

id raft component); alkaline repressed; Hap43-repressed; Spider biofilm repressed

h a single kinetochore microtubule attachment site

detergent-resistant membrane fraction (possible lipid raft component)

e, uracil are not; similar to a nucleoside permease of S. pombe; possibly processed by Kex2p

smic transport; rat catheter biofilm repressed

ucleus, ribosomal large subunit export from nucleus, ribosomal small subunit export from nucleus; rat cath

yphal morphogenesis and for SD or Spider media biofilm formation

ulated

viable; mutant shows virulence defect

hows virulence defect

1p; required for wild-type virulence in mouse intravenous infection; fungal-specific (no human or murine hor

poxia; repressed by prostaglandins; Spider biofilm induced

hing and filamentous growth

sed

nce, role in base-excision repair; Spider biofilm induced

and chlamydospore formation; subject to hypoxic regulation; fluconazole-induced; caspofungin repressed;

ecreased production of prostaglandin E2

cific transcript; repressed by alpha pheromone in opaque MTLa homozygotes; fluconazole-induced; Spide

raction domain; interacts with ScSin3, but not CaSin3

orrelates with clinical development of fluconazole resistance; amphotericin B, caspofungin repressed; Hap

S. cerevisiae ptr2-2 mutant defects; induced by BSA or peptides; Stp3p, Hog1p regulated; flow model biof

d after 16h; fluconazole-induced; virulence-group-correlated expression; Hap43-repressed

luced; induced by Rim101 at pH 8; virulence-group-correlated expression; Hap43-repressed; Spider biofilm

s by macrophages; fungal-specific; Hap43-repressed; merged with orf19.2292 in Assembly 20; rat catheter

eptide or pentapeptide

7, or OPT8 does not suppress defect of mutant lacking Opt1p, Opt2p, and Opt3p; alleles are nonidentical

n of OPT6, -7, or -8 does not suppress defect of mutant lacking OPT1-3; Hap43-repressed; F-12/CO2 earl

ic oxide, amphotericin B; expression of OPT6, 7, 8 does not complement mutants lacking Opt1, Opt2, and

ofilm induced

recognition complex subunit

NA replication; mutation confers hypersensitivity to toxic ergosterol analog; induced under hydroxyurea trea

ced by alpha pheromone in SpiderM medium

vity to aureobasidin A

notif; overproducton suppresses cph1 homozygous null filamnetation defect; similar to S. cerevisiae Osh3p

onary phase enriched protein; flow model biofilm induced; Spider biofilm repressed

; stationary phase enriched protein; Hap43p-repressed gene

sylation of newly synthesized proteins; Spider biofilm repressed

43p-repressed; rat catheter biofilm induced

upregulation associated with MDR1 overexpression or benomyl treatment; macrophage-downregulated pro

d

protein import into mitochondrial matrix

protein import into mitochondrial matrix; rat catheter biofilm induced

art of a complex that regulates actin cytoskeleton; Spider biofilm repressed

clear-transcribed mRNA poly(A) tail shortening, postreplication repair and PAN complex localization

on-sex gene located within the MTLa mating-type-like locus

a pheromone in white cells; fluconazole-induced; Spider biofilm induced

ed for stress regulation of Hog1p localization and activity; functional homolog of S. cerevisiae Pbs2p
vity, role in DNA repair and peroxisome localization
ocytosis, H2O2, oral candidasis, Spider/rat catheter/flow model biofilm induced; repressed in biofilm by Bcr
n
expression, peak at cell-cycle G1/S phase; Hap43-induced; rat catheter biofilm repressed
S. cerevisiae via increased Pho85-dependent phosphorylation and degradation of Gcn4; rat catheter and S
ss
onary growth phase yeast cultures; Hap43-induced; Spider biofilm repressed
; Spider biofilm repressed
ed; fluconazole, farnesol induced; amino acid starvation repressed; flow model biofilm induced; Spider biof
activation domain, Glu- and Pro-rich; complements glucose utilization defect of S. cerevisiae pdc2 mutant
ellular acidification; macrophage-repressed; Spider biofilm induced
tching, cell wall, hyphal, not pseudohyphal growth; expressed shortly after hyphal induction; rat catheter an
mentous growth; protein present in exponential and stationary growth phase yeast cultures; flow model bio
e; fluphenazine, 17-beta-estradiol, ethynyl estradiol, NO induced; farnesol-downregulated in biofilm; rat cat
romone in SpiderM medium
nd cohesion; cell-cycle regulated periodic mRNA expression
nase complex; role in the respiratory pathway; protein present in exponential and stationary growth phase
43, caspofungin repressed; present in exponential and stationary phase yeast cultures
influx; rat catheter biofilm induced
vacuolar endosome-like compartments; rat catheter biofilm repressed
required for biofilm formation in RPMI-1640 and for virulence
ciated gene expression
phal growth, chlamydospore formation; similar to S. cerevisiae Pep7p
s filamentous growth
not in hyphal cells; mutation confers hypersensitivity to 5-fluorocytosine, 5-fluorouracil, tubercidin
Hap43-induced; rat catheter and Spider biofilm induced
ted transmembrane helices; flucytosine induced; ketoconazole-induced; downregulated by Efg1p
e
dependent induction by geldamycin; Spider biofilm induced
ubiquitination and integral component of peroxisomal membrane, peroxisomal importomer complex localiz
t induced in an RHE model of oral candidiasis; Hap43-repressed gene
king and Pex17p-Pex14p docking complex, peroxisomal importomer complex, peroxisomal membrane, pe
oxisome matrix, protein polyubiquitination and peroxisomal importomer complex, peroxisomal membrane l
sruptants not obtained by UAU1 method
n induced; Spider biofilm induced
ilar to S. cerevisiae Pas10p peroxisomal targeting receptor; macrophage/pseudohyphal-repressed; Hap43
, receptor recycling, protein targeting to peroxisome, protein unfolding and cytosol, peroxisome localizatior
protein import into peroxisome matrix, docking, protein targeting to peroxisome and cytosol, peroxisome lo
duced on hyphal induction; phagocytosis-repressed; fluconazole, flow model biofilm induced; rat catheter ar
hyphal repressed; fluconazole-induced; stationary-phase enriched; flow model biofilm induced; rat cathete
y Nrg1, Tup1; gene lacks intron (unlike S. cerevisiae PFY1); complements growth of S. cerevisiae srv2 mu
cells and for adherence during Sabouraud biofilm formation; Spider biofilm induced
a/ketoconazole/ciclopirox/hypha-induced; required for RPMI biofilm formation, Bcr1-induced in a/a biofilm;
duced in oralpharyngeal candidasis; Spider biofilm induced; Bcr1-repressed in RPMI a/a biofilms
essed by alpha pheromone in SpiderM medium; macrophage-induced; induced in oralpharyngeal candidias

-related gene regulation by Ssn6

sis; Spider biofilm induced

duced in high iron and during cell wall regeneration; Hap43-repressed

Kex2p substrate; putative GPI-anchored adhesin-like protein

Red and cell wall regeneration; Bcr1-repressed in RPMI a/a biofilms

ralpharyngeal candidasis; flow model biofilm induced; Spider biofilm induced

ene, disruptants not obtained by UAU1 method; rat catheter and Spider biofilm repressed

amily; transcript induced in RHE model of oral candidiasis; fluconazol-induced

hat overexpress CDR1 and CDR2 or MDR1

by Ssn6; Mob2-dependent hyphal regulation; flow model biofilm induced

nase; transcript induced in high iron; flow model biofilm induced; Spider biofilm repressed

l-specific (no human or murine homolog)

sibly an essential gene, disruptants not obtained by UAU1 method

ozygous null mutant than in wild type

lated gene regulation by Ssn6; induced in RHE model; mRNA binds She3; regulated in Spider biofilms by T

ation; mRNA binds to She3 and is localized to yeast-form buds and hyphal tips; induced during chlamydosp

phology-related gene regulation by Ssn6; induced by Tbf1, Hap43; Spider biofilm induced

p43-induced; Spider biofilm repressed

binds She3 and is localized to hyphal tips; Spider biofilm repressed

g cell wall regeneration; Cyr1 or Ras1 repressed; Tbf1 induced

or; flow model and Spider biofilm repressed

uconazole; flow model biofilm induced; Spider biofilm induced; required for RPMI biofilm; Bcr1-induced in a

to polystyrene; repressed by phagocytosis, human neutrophils; flow model biofilm induced; rat catheter an

odel biofilm, Hog1-, Hap43-, GCN-induced; repressed upon phagocytosis; repressed in Spider biofilms by E

; rat catheter biofilm repressed

nt

cted N-terminal acetylation; Hap43p-repressed gene

model biofilm induced; Spider biofilm induced

phosphate catabolic process, polyphosphate metabolic process and cytosol, fungal-type vacuole membran

ngal-specific; Hog1-repressed; repressed by 17-beta-estradiol, ethynyl estradiol; Hap43-induced; Spider bi

e conditions; slight effect on murine virulence; virulence-group-correlated expression; N-glycosylated; F-12

d; DTT-extractable; N-glycosylated; Hap43-induced

ssential gene, disruptants not obtained by UAU1 method

witch

phosphorylation; involved in regulation of white-opaque switch; hyphal repressed; induced in core stress re

es; induced by Mnl1 under weak acid stress

n minimal media at 37 deg; possibly adherence-induced

erence-induced

r alkaline induced; caspofungin, stress repressed; required for normal TORC1 function

genes involved in phosphate metabolism; necessary for geldanamycin-induced filamentation; gene has in

caspofungin repressed; virulence-group-correlated expression; flow model biofilm induced

possibly adherence-induced; F-12/CO2 model, rat catheter and Spider biofilm induced mic, not vaginal virulence (neutral, not low pH); high pH or filamentation induced; Bcr1-repressed in RPMI a

3-induced; Rim101-repressed at pH8; rat catheter biofilm induced; Bcr1-repressed in RPMI a/a biofilms

uman or murine homolog); possibly an essential gene, disruptants not obtained by UAU1 method

sex gene located in MTLa mating-type-like locus; nonidentical gene encoding PI(4)P kinase, PIKALPHA, l

of hyphae, but not yeast-form cells; Hap43, YNB biofilm induced; rat catheter biofilm repressed

aintenance of mitochondria; rat catheter biofilm induced

pressed

tant; Hog1/fluconazole/hypoxia induced; iron/Efg1/Plc1/temp regulated; flow model biofilm induced; hyphal

ncreased virulence and resistance to stresses; macrophage-induced gene

ogy and increased cell lysis; activated by phosphatidylserine; target of antifungal, cercosporamide; R400P

trols endocytosis; mRNA binds She3 and is localized to hyphal tips

quence, N-glycosylation, and Tyr phosphorylation site; induced in fluconazole-resistant strains; rat catheter

signal; no GPI anchor predicted; fungal-specific (no human or murine homolog)

nduced by Tbf1; fluconazole-induced; possible essential gene (UAU1 method); Spider and flow model biofil

eration; clade-associated gene expression; Hap43-induced; rat catheter and Spider biofilm repressed

ll-associated phospholipase A2 activity and attenuates virulence; fluconazole-repressed; flow model biofilm

al growth; upregulated in biofilm; predicted N-linked glycosylation; lacks conserved EF-hand domain

, and regulated by, filamentation, Nrg1 and Tup1; no mouse systemic virulence role; orf19.5797 and orf19.

ype mouse virulence, but not rat oral virulence; mutant defect in hyphal growth on solid substrates; similar t

levels increase at stationary phase transition; fluconazole induced; caspofungin repressed; upregulated in

sed resistance to fluconazole, lithium; increased sensitivity to calcium; Spider biofilm induced

ae, E. coli phosphomannose isomerase; Gcn4-regulated; induced on adherence to polystyrene, phagocytos

nd mannose-l-phosphate; functional homolog of S. cerevisiae Sec53; antigenic in mice; Hap43-induced; flo

required for protein glycosylation and cell wall maintenance; required for hyphal tip oscillation in semisolid s

ved in DNA mismatch repair

al growth and drug sensitivity; Als1, Sec20, Kre9, Pir1 are substrates; 1 of 5 PMT family members

mily which includes Pmt1p, Pmt2p, Pmt4p, Pmt5p, and Pmt6p; induced during cell wall regeneration; esse

rowth and drug sensitivity; one of 5 family members; Axl2 a substrate; Spider biofilm repressed; Bcr1-repre

owth, drug resistance, or virulence in mouse systemic infection; one of five PMT family members

signaling, hygromycin B sensitivity; no major role in cellular PMT activity; Hap4-repressed; Bcr1-repressed

-resistant strain that overexpresses MDR1

irox olamine, ketoconazole or hypoxia; gene of core caspofungin response; Hap43-induced; Spider biofilm

side salvage pathway; Spider biofilm repressed

ion affects filamentous growth; rat catheter biofilm repressed

sity; rat catheter biofilm induced

; periodic mRNA expression, peak at cell-cycle G1/S phase

ng reports about periodic (G1/S) or non-periodic mRNA expression through cell cycle; Hap43p-repressed

undance regulated by tyrosol, cell density; induced by flucytosine, interaction with macrophages; stationary

eriodic mRNA expression

se transcriptase, protease and integrase; downregulated in response to ciclopirox olamine; F-12/CO2 early

ngin and cordycepin in the C. albicans fitness test

ofilm induced

ulated by Nrg1, Tup1; likely essential, based on UAU1 strategy; rat catheter and Spider biofilm induced

nt); antigenic in human, mouse; Hap43p-induced; flucytosine-, macrophage-, farnesol- induced; fluconazol

se; planktonic growth-induced gene; likely to be essential for growth, based on an insertional mutagenesis

ap43-repressed

biofilm induced

oliniensis; A21 sequence updated based on new sequence and analysis, the allelic orf19.10841 was reinsta

ntous growth and haploid invasive growth in S. cerevisiae

ous growth and virulence

n dephosphorylation of septin Sep7p; caspofungin repressed; possibly an essential gene, disruptants not c

sphorylation of Rad53p in response to DNA damage; dephosphorylates Rfa2p in G1 phase; ortholog of S.

ilarity to S. cerevisiae Ppr1p, which is a transcription factor involved in the regulation of uracil biosynthesis

ı homeostasis and cell wall integrity
n thermoautotrophicum (Archaebacterium)
binds to host complement regulators; mediates leukocyte adhesion and migration; immunogenic in mouse;
nan neutrophils; similar to (does not replace) S. cerevisiae vacuolar B protease Prb1p; flow model biofilm i

4
d protein; Hap43-repressed; rat catheter biofilm repressed
cin B repressed
nentous growth; Spider biofilm repressed

:-induced protein
-AT); Spider biofilm repressed
udohyphal-repressed gene; regulated by Gcn2p and Gcn4p; removed from/reinstated in Assembly 20 (see
transcription is positively regulated by Tbf1p; stationary phase enriched protein

iofilm repressed

ne; protein induced during the mating process

m; transcript induced by Mnl1 in weak acid stress; rat catheter and Spider biofilm induced

sed gene; early-stage flow model biofilm induced gene
cn2p and Gcn4p
tionary phase enriched protein; Spider biofilm repressed

acid stress
biofilm induced

ider biofilm induced
heromone in SpiderM medium

esis; essential; flucytosine induced; macrophage/pseudohyphal-induced
ess response
encoding ribosomal subunits, translation factors, tRNA synthetases are downregulated upon phagocytosis
2p-downregulated; caspofungin repressed; protein present in exponential and stationary growth phase yea
mone in SpiderM medium; possibly essential, disruptants not obtained by UAU1 method; Spider biofilm ind
in; Spider biofilm induced; rat catheter biofilm repressed
ed
s, phosphatidylethanolamine biosynthetic process and endosome localization
DNA replication machinery; flow model biofilm induced
lication, mitotic DNA replication

but not MTLa/MTLalpha cells; telomere-proximal gene; mutation does not affect white-to-opaque phenotyp

uctase; hyphal-induced; regulated by Cyr1, Ras1, Efg1, Nrg1, Rfg1, Tup1; Hap43-induced; Spider biofilm in
eductase; similar to 1,4-benzoquinone reductase; induced by benomyl, oxidative stress via Cap1; fungal-sp
/ phase enriched protein; rat catheter and Spider biofilm repressed

iae Ptc1p; mutant shows virulence defect
ntrols hyphal elongation through regulation of phosphorylation of transcription factor Ume6p and its stabilit
, potassium and azole drugs; decreased expression in hyphae compared to yeast-form cells
g response and cadmium tolerance
olog of S. cerevisiae Ptc6p; mutant shows virulence defect
-spanning segment and mitochondrion-targeting signal
ress; flow model biofilm induced; Spider biofilm induced
uptants not obtained by UAU1 method
e status; Spider biofilm induced
camycin; YPD flow model biofilm induced; rat catheter and Spider biofilm induced

1 under weak acid stress; rat catheter and Spider biofilm induced
thways; mutants are viable; Spider biofilm induced; rat catheter biofilm repressed; flow model biofilm repre
n in both C. albicans and C. dubliniensis
l upon phagocytosis by macrophage; repressed by Rim101 at pH 8; flow model biofilm induced
an ssr1 null mutant
ssed
n4p; protein present in exponential and stationary growth phase yeast cultures
e-tRNA(Tyr); F-12/CO2 early biofilm induced
d
l and stationary growth phase yeast cultures; flow model biofilm induced; Spider biofilm induced
gulation of proline utilization genes
ocess
hysically interacts with TAP-tagged Nop1; Hap43-induced
rter
cn4p-regulated
ue specific transcript; putative peroxisome targeting signal; Spider biofilm induced
atment, or in an azole-resistant strain overexpressing MDR1; stationary phase enriched protein; flow mode
oxide; in detergent-resistant membrane fraction (possible lipid raft component); levels decrease in stationar
ology-related gene regulation by Ssn6; Hap43-repressed; Spider biofilm repressed
in repressed; repressed during chlamydospore formation; flow model biofilm induced; Spider biofilm repres
Spider biofilm induced
facilitator superfamily (MFS); Hap43p-repressed gene
wth; dynamic localization at plasma membrane and nucleus; similar to, but not interchangeable with, Cdc42
ely sensitive to UV irradiation; transcript repressed in alkaline conditions
at catheter and Spider biofilm induced
UV irradiation; transcript induced by interaction with macrophages
of RNA polII initiation factor TFIIH and Nucleotide Excision Repair Factor 3 (NEF3)
ciated with azole resistance; Hap43p-repressed gene
e; flow model biofilm repressed
ased white-to-opaque switching frequency in null mutant
nduced LOH; constitutive expression, MMS-induced; weakly complements S. cerevisiae rad52 mutant; slo
e checkpoint; ortholog of S. cerevisiae Rad53p, protein kinase required for cell-cycle arrest in response to D
ssential role during mitotic growth; mutants display aberrant cell and nuclear morphology
ated by Nrg1, Mig1, and Tup1; essential protein; S. cerevisiae ortholog is essential
erminal similarity with Rad52p
sistance; acts in pathway with Efg1; ; transcript is UV-induced, slightly repressed during hyphal growth; gen
ed under hydroxyurea treatment
owth; induced by alpha pheromone in SpiderM medium
l fluconazole; Hap43p-repressed gene
transcript; lovastatin, fluconazole regulated; GGTase I binds zinc, is Mg-dependent; Cdc42 substrate; rat ca
represses hyphal growth under yeast-favoring conditions; similar to (but shorter than) S. cerevisiae Rap1
lence, apoptosis, heat-shock sensitivity; nonessential; plasma membrane-localized; complements viability o
rat catheter and Spider biofilm induced
xem1 mutant slow growth, mating defect, and haploid invasive growth defect
ion affects filamentous growth
nent induced, repressed by Rim101, Tup1; Hap43-induced; Spider biofilm induced
4-regulated; caspofungin repressed; Spider biofilm induced
ed; ketoconazol induced; regulated by Sef1, Sfu1, Hap4; flow model biofilm induced; rat catheter and Spide
ear; mutation causes accelerated induction of filamentous growth; antigenic during human oral infection; S
n resistance; regulated by Gcn4p; macrophage-induced protein; repressed in response to 3-AT; functional
expression repressed by Rim101 and activated by Nrg1; Hap43-induced

ssed by alpha pheromone in SpiderM medium; macrophage-induced gene
/ UAU1 method
pressed; farnesol, alpha factor, serum, hyphal and alkaline induced; Rfg1, Rim101-regulated
NA binds She3, is localized to hyphal tips; Hap43-induced; in both yeast and hyphal culture supernatants; S
rum, alkaline pH, antifungal drugs, geldamycin repressed; Hap43 induced; required for RPMI biofilms; Spid

cription factor of the ATF/CREB family; null mutant displays slow growth, abnormal colony morphology and

ensitivity to calcium and resistance to azoles and terbinafine; rat catheter biofilm induced
2p; induced by osmotic stress via Hog1p; macrophage/pseudohyphal-repressed; mutants are sensitive to r
isiae ortholog is essential; represses in core stress response;
cineurin function
3; induced in oralpharyngeal candidasis; rat catheter biofilm repressed
r murine homolog)
iduced by interaction with macrophages
nduced; regulated by Nrg1, Tup1; protein levels low in stationary phase yeast
ed; possibly regulated upon hyphal formation; flow model biofilm induced

gative regulation of MDR1 transcription; mutants show increased resistance to azole drugs
tein sorting; flow model biofilm induced
e transport between Golgi and ER; interacts with Crk1 in the two-hybrid system; Spider biofilm repressed
e translesion synthesis and mitochondrion, zeta DNA polymerase complex localization
8S rRNAs; rat catheter biofilm induced

nal mutagenesis strategy; rat catheter biofilm repressed
phase

ak at cell-cycle G1/S phase
phase
dependent pathways; binds DNA; transcript not regulated by oxygen or serum; not responsible for hypoxic
uced
ne mucosal, systemic infections; RFX domain; regulated by Nrg1, UV-induced; partially complements S. ce
controlling cell polarity; induced by low-level peroxide stress; flow model biofilm induced
ce area in G1 phase and in the bud tip during S and G2 phases

enes; ortholog of S. cerevisiae Rgt1; mutants display decreased colonization of mouse kidneys
rowth under nitrogen starvation; involved in activation of TOR1C during starvation response
ell wall phosphopeptidomannan; 9-gene family memebr; regulated on yeast-hypha and white-opaque switcl
; overlaps blocked reading frame orf19.2668.1; yeast-enriched transcript; rat catheter biofilm induced
ot essential for cell wall integrity; fluconazole-repressed; flow model and Spider biofilm repressed
cted to be geranylgeranylated by geranylgeranyltransferase type I; plasma membrane-localized
egulation of fungal-type cell wall (1->3)-alpha-glucan biosynthetic process
se type I; greater transcription in hyphal form than yeast form; plasma membrane-localized
nodel biofilm induced; regulated by macrophage, stress, yeast-hyphal switch, pheromone, Gcn4, Hog1, Nrg
nthetases are downregulated upon phagocytosis by murine macrophage
homolog); regulated by Sef1p, Sfu1p, and Hap43p
ribulose 5-phosphate to L-3,4-dihydroxy-2-butanone 4-phosphate; transcription regulated on yeast-hyphal
ep in the synthesis of riboflavin; Hap43-induced; rat catheter and Spider biofilm repressed
n present in exponential and stationary growth phase yeast cultures
essed
eter biofilm repressed
mice; activated by C-terminal proteolytic cleavage; mediates both positive and negative regulation; Spider b
nt is viable
red for alkaline pH-induced hyphal growth and for normal chlamydospore formation; Hap43-repressed; flov

iced
scaffold to facilitate the C-terminal proteolytic cleavage that activates Rim101; required for alkaline pH-indu
ctivation of Rim101 and for alkaline pH-induced hyphal growth; Spider biofilm induced
aline pH-induced hyphal growth; colony morphology-related gene regulation by Ssn6p negative feedback re
and A. nidulans palI; Spider biofilm induced
ull mutants are hypersensitive to caspofungin

pider biofilm repressed
hal growth and biofilm formation
osynthetic process
Sef1p, Sfu1p, and Hap43p
ent; regulates caspofungin-induced transcription of SKO1
to 5-fluorocytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine); Spider biofilm induce
al development of fluconazole resistance; Upc2-regulated in hypoxia; flow model biofilm induced; Spider bi
ulated degradation of daughter cell-specific mRNAs; rat catheter and Spider biofilm induced
tants not obtained by UAU1 method; rat catheter and Spider biofilm induced
essed
possibly essential (UAU1 method); rat catheter biofilm induced; flow model biofilm repressed
n; farnesol upregulated in biofilm; regulated by cell cycle, tyrosol, cell density; regulated by Sef1, Sfu1, and
e or flucytosine induced; regulated by Sef1, Sfu1, and Hap43
ipt regulated by tyrosol and cell density; Hap43-repressed; Spider biofilm induced
n induced
enesis and cytosol, extracellular region, fungal-type vacuole, vacuole localization
ny morphology and invasive growth; caspofungin repressed; flow model biofilm induced; rat catheter biofilm
mutant is viable
; Spider biofilm induced
nsmembrane region; possibly an essential gene, disruptants not obtained by UAU1 method
esis; alkaline downregulated
ffects filamentous growth
tation of an S. cerevisiae rpb4 mutant; suppresses defects of S. cerevisiae rpb4 and ess1 mutants; Spider
starvation (3-aminotriazole treatment); heterozygous null mutant exhibits resistance to parnafungin
uced; Spider biofilm induced
ey, compared to growth in vitro; has murine homolog
lymerase III complex localization
ssion in white cells than opaque cells; has conserved deacetylation motif
ssential for growth; rat catheter and Spider biofilm induced
ytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine)
d upon phagocytosis by murine macrophage; Spider biofilm repressed
iption regulated by yeast-hypha switch; Spider biofilm repressed
pider biofilm repressed
-induced; Spider biofilm repressed
r cells; genes encoding cytoplasmic ribosomal subunits are downregulated upon phagocytosis by macroph
macrophage; Spider biofilm repressed
pf1; Spider biofilm repressed
e macrophages; Hap43-induced; Spider biofilm repressed
by macrophage; Hap43-induced; Spider biofilm repressed
rophage; Hap43p-induced; Spider biofilm repressed
er biofilm repressed
t not NGY152, strain background; Spider biofilm repressed
5' UTR; Hap43-induced; Spider biofilm repressed
target; Spider biofilm repressed
ap43-induced; Spider biofilm repressed
morphology-related gene regulation by Ssn6
er biofilm repressed
Ssn6; intron in 5'-UTR; Spider biofilm repressed

osomal subunits are downregulated upon phagocytosis by murine macrophages; Hap43-induced gene; Spi

uctive transcripts; temp-regulated splicing; colony morphology-related regulation by Ssn6, Tup1, Nrg1 regu

orphology-related gene regulation by Ssn6; Hap43-induced; Spider biofilm repressed

rs, tRNA synthetases are downregulated upon phagocytosis by murine macrophage

lation by Ssn6; Hap43-induced

gene regulation by Ssn6; positively regulated by Tbf1; Spider biofilm repressed

repressed

lated gene regulation by Ssn6; Spider biofilm repressed

epressed

ation-related genes are downregulated upon phagocytosis by murine macrophage; Hap43-induced; Spider

and Spider biofilm induced

synthetases are downregulated upon phagocytosis by murine macrophage

acrophage; Spider biofilm repressed

otein levels decrease in stationary phase; Hap43-induced; Spider biofilm repressed

ng, mitochondrial translation; virulence-group-correlated expression; likely essential (UAU1 method); rat ca

y Gcn2 and Gcn4; Spider biofilm repressed

and Gcn4; gene used for strain identification by multilocus sequence typing

ess-induced via Cap1p

AAA) enriched in regions upstream of proteasome genes; induced in core stress response; Hap43-induced

al and stationary growth phase yeast cultures

ulated by Mig1, Gcn2 and Gcn4; Spider biofilm repressed

model biofilm repressed

icans fitness test

ced by Tbf1; overlaps orf19.7014; Spider biofilm repressed

Spider biofilm induced

1 of 4 similar C. albicans ribosomal proteins (Rpp1A, Rpp1Bp, Rpp2A, Rpp2B); Hap43-induced; Spider bio

2A; 1 of 4 similar C. albicans ribosomal proteins (Rpp1A, Rpp1B, Rpp2A, Rpp2B); induced by Tbf1; Spide

ibosomal proteins (Rpp1A, Rpp1B, Rpp2A, Rpp2B); CUG start codon; upstream uORFs; Tbf1-induced; Sp

Rpp1A; 1 of 4 similar C. albicans proteins (Rpp1A, Rpp1B, Rpp2A, Rpp2B); macrophage/pseudohyphal-inc

cleolar ribonuclease P complex localization

nduced during active growth; Spider biofilm repressed

essed

AT); protein abundance is affected by URA3 expression in CAI-4 strain background; sumoylation target; Sp

ated by Tbf1; Spider biofilm repressed

murine macrophage; Spider biofilm repressed

r biofilm repressed

; Hap43-induced; Spider biofilm repressed

ed

ated by Tbf1; Spider biofilm repressed

vely regulated by Tbf1; Spider biofilm repressed

tively regulated by Tbf1, Hap43; Spider biofilm repressed

transcriptionally activated by Tbf1; Spider biofilm repressed

macrophage; transcript positively regulated by Tbf1; 5'-UTR intron; Hap43-induced; Spider biofilm repress

tively spliced intron in 5'-UTR; Spider biofilm repressed

ent in exponential and stationary phase cells; Spider biofilm repressed

n repressed

urine macrophage; positively regulated by Tbf1; mutant is defective in filamentous growth and sensitive to

murine macrophage; Hap43-induced; Spider biofilm repressed

by murine macrophage; possibly essential; Hap43-induced; Spider biofilm repressed

etases are downregulated upon phagocytosis by murine macrophage; Spider biofilm repressed
e macrophage; 5'-UTR intron; Hap43-induced; Spider biofilm repressed
ated upon hyphal formation; Spider biofilm repressed
verlaps orf19.442
Spider biofilm repressed
hase cultures
rotein level decreases in stationary phase
ted by Gcn2 and Gcn4
repressed; repressed in core stress response; repressed by prostaglandins
glandins
ced
ty to 5-fluorocytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine)
idin (7-deazaadenosine); physically interacts with TAP-tagged Nop1; Hap43-induced; Spider biofilm induce
nsitivity to 5-fluorocytosine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine)
process; Hap43-repressed
n vitro; has murine homolog; possibly an essential gene, disruptants not obtained by UAU1 method
ce; role in systemic virulence in mouse; geranylgeranylation predicted; suppresses S. cerevisiae cdc24-4 n
nse and resistance to azoles; Plc1p, Ca2+, calcineurin-regulated;
ne; involved in biofilm formation; putative drug-responsive regulatory site; rat catheter biofilm induced
ous growth; alkaline downregulated; caspofungin induced; possibly an essential gene; Hap43p-repressed
nscriptional rewiring, performs role analogous to Gal4p in S. cerevisiae; involved in regulation of sphingolip
logous to Gal4p in S. cerevisiae; regulates carbon source-dependent stress response; regulates sphingolip
ast-hyphal switch
ha pheromone in SpiderM medium
ased white-to-opaque switching and increased susceptibility to killing by macrophages
ullin subunit (Cdc53p) modulates the ubiquitin ligase activity of the SCF complexes
vity to virgineone
curvature; null mutant exhibits defects in hyphal growth, virulence, cell wall integrity, and actin patch localiz
oes not display the endocytic, hyphal growth, virulence, or cell wall defects exhibited by mutants in related
yphal growth, virulence, cell wall integrity, and actin patch localization; cosediments with phosphorylated My
enesis
ntial gene, disruptants not obtained by UAU1 method
transcript regulated by Nrg1 and Mig1; protein level decreases in stationary phase
e/pseudohyphal-repressed; transcript is upregulated in RHE model of oral candidiasis and in clinical oral ca
azole-induced expression; Gcn4-regulated; amino acid starvation (3-AT) repressed; flow model biofilm indu
mutant has virulence defect; Spider biofilm induced
arnesol-downregulated; F-12/CO2 early biofilm induced; Spider biofilm repressed
mbrane, involved in protein import into mitochondria
volved in insertion of proteins into the outer membrane; mutants show loss of mtDNA
er biofilm repressed
sembly; member of the Omp85 protein family
complicated by URA3 effects; regulated by growth phase, alpha-pheromone; produced by opaque cells
ity from Sap9; at cell membrane and wall; GPI-anchored; induced in low iron; Tbf1-activated; Spider biofilm
URA3 effects; immunoprotective; regulated by growth, albumin, drugs, white cell-type; flow model biofilm
complicated by URA3 effects; regulated by growth phase; produced by opaque phase cells; alpha-pheromo
isiae Bar1; a-cell specific; induced by alpha pheromone
nplicated by URA3 effects; expressed during mucosal and systemic infections; N-glycosylated; rat catheter,
ized to hyphal tip via She3; rat catheter and Spider biofilm induced
ffecte by URA3; N-glycosylated; rat catheter biofilm induced
6p-regulated; role in murine intravenous infection; induced during, but not required for, murine vaginal infec
d in opaque cells and upon deep epidermal invasion; greater expression in vaginal than oral infection; pron
phase, or in white-phase cells; farnesol-downregulated in biofilm; autocatalytic processing; GPI-anchor; Sp
l only in opaque MTLa/MTLa cells
omone in SpiderM medium; possibly essential (UAU1 method); regulated by Sef1, Sfu1, and Hap43; Spide
imilar to small GTPase superfamily proteins; gene has intron; Hap43-induced; rat catheter biofilm represse
s resistance to 5-fluorocytosine (5-FC); repressed upon high-level peroxide stress

iofilm repressed
vel decreases in stationary phase cultures; Hap43-repressed
protein
hlamydospore formation, filamentous growth, and virulence; prevents hyphal growth in hypoxia at high CO
low model and Spider biofilm repressed
atus
sed; Spider biofilm induced
ossibly an essential gene, disruptants not obtained by UAU1 method; rat catheter and Spider biofilm repre
itch; alkaline repressed; possibly essential (UAU1 method); flow model biofilm induced; Spider biofilm indu
biogenesis; rat catheter biofilm induced; Hap43-induced
xide
ated by Efg1p; repressed by nitric oxide; protein present in exponential and stationary growth phase yeast c
iron and during log phase aerobic growth; repressed by nitric oxide, Hap43
r to deactivate DNA damage checkpoint; macrophage/pseudohyphal-repressed
1 and Tup1; fluconazole-induced; flow model biofilm induced
cking involved in exocytosis and cellular bud neck, cellular bud tip, plasma membrane, prospore membran
yst localization
otein; protein level decreases in stationary phase cultures; Spider biofilm repressed
line transfer protein that regulates choline-phosphate cytidyltransferase and thereby affects secretion; biofil
GTPase Rsr1p; ortholog of S. cerevisiae SEC15
ot glycosylated
sites of polarized growth; phosphorylation by Cdc28 needed for normal hyphal growth; Hap43-repressed;
sitivity; expression regulated by growth phase; O-mannosylation regulates proteolysis; does not complemen
iated transport, Golgi to endoplasmic reticulum and COPI vesicle coat, endosome localization
ort, retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum, vesicle fusion, vesicle fusion w
Spider biofilm repressed
eptin ring formation; interacts with septins Cdc3p, Cdc10p, and Cdc11p; localizes to a crescent on the surf
d on adherence to polystyrene; localizes to the Spitzenkorper during hyphal growth; functional homolog of
e hyphal tip; Hap43p-repressed
partially functionally complements S. cerevisiae sec61 defects; Spider biofilm repressed
nal homolog of S. cerevisiae Sec65; Tbf1-induced
fungin repressed
arvation (3-aminotriazole treatment); sumoylation target
e hyphal tip
Tbf1; promotes virulence in mice; mutants display decreased colonization of mouse kidneys; Spider biofilm
nditions; regulated by Sef1, Sfu1, and Hap43; rat catheter and Spider biofilm induced
mponent of fungal-type vacuolar membrane, nuclear periphery, nuclear pore, nuclear pore outer ring locali
ne treatment
nd to amphotericin B; 5'-UTR intron; Hap43-induced; Spider biofilm induced
stress; flow model biofilm repressed
ent in exponential and stationary yeast growth phases; Spider biofilm repressed
xponential and stationary growth phase yeast cultures; S. cerevisiae ortholog is Gcn4p regulated
t specifies Ser in C. albicans; complements S. cerevisiae ses1 mutant viability; soluble protein in hyphae;
ll adhesion, agar-embedded filamentation, virulence in mice; unique N-terminus immunogenic in human;
/Hos2 function as a complex to regulate white-opaque switching, morphogenesis, and virulence; flow mode
Spider biofilm induced
catheter biofilm induced; Spider biofilm induced

e in SpiderM medium; essential for growth
core caspofungin response; Spider biofilm induced
dioxide levels; required for filamentous growth, for virulence in RHE model but not in mice; Spider biofilm in
ess response; regulates response to oxidative stress; acts as repressor of START; rat catheter biofilm indu
present; Hap43-repressed; promotes gastrointestinal commensalism in mice; Spider biofilm induced
es in populations of cells exposed to fluconazole over multiple generations; Spider biofilm induced
ulated in farnesol treated biofilm
vity to radicicol; sumoylation target
pression in the CAI-4 strain background; Mig1-regulated
duced; ketoconazole-repressed; induced in by alpha pheromone in SpiderM; possibly essential; flow mode
normal filamentation and host epithelial cell damage; ortholog of S. cerevisiae She3 but target mRNAs dif
growth-regulation element; fungal-specific (no human or murine homolog)
m1 null shm2 null gly1-1 triple mutant; protein present in exponential and stationary growth phase yeast cu
2 gly1-1 mutant; antigenic; farnesol-upregulated in biofilm; stationary-phase enriched protein; rat catheter a
on through the cell cycle and response to DNA damage
ge-repressed; repressed by Rim101, Cyr1, Ras1; Spider biofilm induced
nt); has paired amphipathic helix PAH1 domain; interacts with ScOpi1p, not CaOpi1p; transposon mutation
proteins, rDNA silencing; regulates phenotypic switch in strain 3153A, not in WO-1
ss-induced; heterozygous null mutant displays sensitivity to virgineone; rat catheter biofilm induced
itro, not for mouse systemic infection; regulated by iron, Sfu1, Rfg1, Tup1, Hap43; rat catheter and Spider
and virulence in a mouse systemic infection model
shows virulence defect; Hap43p-repressed gene
bolic process and 3'-5' exonucleolytic nonsense-mediated decay, more
ted decay, nuclear-transcribed mRNA catabolic process, exonucleolytic and 3'-5', more
process, 3'-5' exonucleolytic nonsense-mediated decay and nuclear-transcribed mRNA catabolic process,
ot and mRNA length change induced by yeast-hypha transition; induced by Rim101, caspofungin; rat cathe
disruptants not obtained by UAU1 method; Hap43-induced; flow model biofilm induced; rat catheter biofilm
orelay signal transduction pathway; required for normal hydrogen peroxide resistance
utants are caspofungin sensitive; induced by osmotic stress via Hog1; activated by Rlm1p; induced by Mnl1
ino acid starvation (3-aminotriazole treatment)
s regulated by Nrg1 and Mig1; flow model biofilm repressed
al formation; localized to actin patches; rat catheter biofilm repressed
glucosylceramide synthesis, important for virulence; ketoconazole and hypoxia induced; Hap43-represse
19p (a kinetochore protein with roles in mitosis, meiosis); required for wild-type virulence in mouse; macro
osome assembly, endosomal transport and establishment or maintenance of actin cytoskeleton polarity, m
ts are sensitive to growth on H2O2 medium; rat catheter and Spider biofilm induced
ne has intron; Spider biofilm repressed
regulated periodic mRNA expression
chromosome condensation; induced under hydroxyurea treatment
be essential for growth, based on an insertional mutagenesis strategy
single-stranded DNA binding activity
ntous growth
dic mRNA expression; S. cerevisiae ortholog not cell-cycle regulated; Spider biofilm induced
ngin repressed; mutants are viable
ak acid stress; Hap43-repressed
cell wall glucan in mutant; possibly essential (UAU1 method); flow model biofilm induced
ot obtained by UAU1 method

GPI precursor; essential for viability; 8-9 transmembrane regions predicted; has HQEXRF motif; functional I
bud neck; C. albicans septins appear not to be Smt3p-modified, in contrast to S. cerevisiae septins
osine induced
r208 phosphorylation may have regulatory role; up-regulation associated with azole resistance; essential g
of the SWI/SNF chromatin remodeling complex; interacts with Swi1p; SWI/SNF complex is essential for hyp
transposon mutation affects filamentation
s in silicone adherence, biofilm formation, hyphal morphogenesis, cell wall defects; increased cell aggrega
ple roles in RIM101 pathway and in transport from MVB to vacuole; involved in echinocandin and azole sen
l analog; shows colony morphology-related gene regulation by Ssn6p
pendent hyphal regulation
n; rat catheter biofilm repressed
d Hap43; Spider biofilm induced
pider biofilm induced
utation affects filamentation; benomyl-induced transcription; detected at yeast-form cell plasma membrane
on affects filamentous growth; null mutants are viable
be essential for growth, based on an insertional mutagenesis strategy
in overexpressing MDR1; soluble in hyphae; regulated by Gcn4, macrophage; Spider biofilm induced; rat c
ed for full virulence; alkaline induced by Rim101; induced by human blood; rat catheter, flow model and Spi
e; N-terminal 34 amino acids removed on mitochondrial import; H2O2-induced via Cap1p; Hap43p-, alkalir
opirox olamine, induced during stationary phase when SOD1 expression is low; Hap43-repressed; Spider a
que switch; induced under iron starvation; ciclopirox olamine induced; caspofungin repressed; SOD1,4,5,6
th, caspofungin, osmotic/oxidative stress; oralpharyngeal candidiasis induced; rat catheter and Spider biof
contain an intron; Hap43-repressed; flow model and rat catheter biofilm induced
sensitivity; required for hyphal growth; lacks orthologs in higher eukaryotes
film formation, virulence; cell-cycle regulated periodic mRNA expression
dium; induced by alpha pheromone in SpiderM medium; rat catheter and Spider biofilm induced
(CDC4) pathway; CDK phosphorylation predicted
acrophage-downregulated protein; Spider biofilm repressed
eductase activities; NAD-binding site motif; transcriptional regulation affected by chromosome 5 copy numb
p; cell-cycle regulated localization in yeast-form cells; functional domains conserved with S. cerevisiae ; Ha
ential gene, disruptants not obtained by UAU1 method; Spider biofilm induced
chores to spindle microtubules
us growth
signal peptidase activity; predicted integral ER membrane protein; complements spc3 and suppresses sec
spindle microtubules
sion, peak at cell-cycle S/G2 phase
lyamine auxotrophy of S. cerevisiae spe1 mutant; downregulated upon adherence to polystyrene
biofilm induced
epressed
phal growth, biofilm formation and virulence
ependent aminotransferase protein family; predicted to be essential
asexual cycle; produced in mitotically dividing cells; similar to S. cerevisiae Spo11 which functions in recom
embly and condensed nuclear chromosome localization
oling phospholipid biosynthesis; induced by alpha pheromone in SpiderM medium
gic vesicle formation protein; up-regulation associated with azole resistance; Spider biofilm induced
dic mRNA expression
1,3-beta-glucanase; mutant is viable
h noncanonical branch site and 5' splice site, respectively; splicing inhibited upon exposure to alpha-factor
ated in biofilm; protein newly produced during adaptation to the serum
elta-9-fatty acid desaturase
null mutant is hyperfilamentous

us growth

in an RHE model of oral candidiasis and in clinical isolates from oral candidiasis

erol analog, and to amphotericin B

S. cerevisiae psa1; on yeast-form, not hyphal cell surface; alkaline induced; induced on adherence to polys

resses S. cerevisiae diploid filamentous (flo8, ste7, ste12, tec1) or haploid invasive (flo8) mutant growth de

nt induced; fungal-specific (no human or murine homolog)

atheter biofilm repressed

catheter biofilm induced

1 null mutant; flow model biofilm induced; Spider biofilm induced

iosynthetic process, protein glycosylation and dehydrodolichyl diphosphate synthase complex, lipid droplet

formation and for virulence in mice; mutant defects in filamentous growth are rescued by cAMP or dbcAM

ds histatin 5; at hyphal surface, not yeast; farnesol-repressed in biofilm; flow model, Spider biofilm repress

nic in human/mouse infection; macrophage, GCN-induced; possibly essential; sumoylation target; Hap43-in

id starvation (3-AT) or by adherence to polystyrene; macrophage-repressed; sumoylation target; possibly e

omolog of S. cerevisiae Ssd1p, which suppresses various mutant phenotypes; constitutively expressed and

pider biofilm induced

lence, hyphal growth on solid media; expressed in hyphae and yeast; peroxisomal targeting sequence (PT

mine

h phosphorylation of transcription factor Ume6p and its stability; mutants are sensitive to growth on H2O2

Ssn6 and Tup1 regulate distinct sets of genes; overexpression or mutation causes avirulence in mouse IV

e sensitive to hydrogen peroxide medium

able due to internal Ser-Ala tandem repeats; detected at germ tube plasma membrane; repressed in cells t

ivity and mating defect (in opaque MTLa/MTLa background); transcript induced by alpha factor

ated by Gcn2 and Gcn4; induced by nitric oxide; Hap43-repressed; Spider and flow model biofilm induced

hatase activity, protein serine/threonine phosphatase activity, protein tyrosine phosphatase activity

se to oxidative stress to morphogenesis and cell wall biosynthesis; mediates formation of microcolonies; ca

ons; 12 predicted membrane spanning regions; Hap43-repressed; Spider biofilm induced

ponse to amino acid and extrinsic component of plasma membrane localization

catheter biofilm induced

pression and resistance to beauvericin; Hap43p-repressed gene

Spider biofilm induced

affects filamentous growth; induced by low nitrogen, germ tube formation; flow model biofilm repressed

but not MTLa/MTLalpha cells; MTLa1p, MTLalpha2p bind promoter region

for opaque a-form mating and white a-form response; possible Kex2p substrate; a-specific, alpha-factor in

form; Tn mutation affects filamentous growth; Spider biofilm induced

fic transcription

pt is specific to cells homozygous at MTL; induced by alpha pheromone; ortholog of S. cerevisiae Ste4

which is involved in signal transduction via interaction with and regulation of MAPKKK

ed in clinical isolates from HIV+ patients with oral candidiasis; rat catheter, flow model and Spider biofilm in

ble protein in hyphae; protein in exponential and stationary phase yeast cultures; YNB biofilm induced; Spi

activated via amino-acid-induced proteolytic processing; macrophage/pseudohyphal-repressed; Spider bio

by amino-acid-induced proteolytic processing (Ssy1, Csh3 dependent); required for alkalinization of mediu

on by Ssn6; induced by 17-beta-estradiol, ethynyl estradiol; rat catheter and Spider biofilm induced

anssulfuration

downregulated during planktonic growth, whereas related SUA72 is induced; induced by Tbf1; rat catheter

by Mig1; Hap43-induced gene; Spider biofilm repressed

sucrose utilization and mal13 maltase defect; required for yeast cell adherence to silicone substrate; rat ca

tors, and tRNA synthetases are downregulated upon phagocytosis by murine macrophage

RNA synthetases are downregulated upon phagocytosis by murine macrophage; stationary phase enriched

etases are downregulated upon phagocytosis by murine macrophage

Spider biofilm induced

ed; caspofungin repressed; Efg1, Cph1 regulated; O-glycosylated, possible Kex2 substrate; 5'-UTR intron;

revisiae sup35 mutant translation defect; species barrier with S. cerevisiae Sup35p prion; gene not regulat

nder H2O2 stress conditions; Spider and flow model biofilm induced

eisosome subdomains of plasma membrane; 4 transmembrane motifs; cytoplasmic C terminus regulates

ndrial RNA degradation; required for chlamydospore formation, embedded hyphal growth, respiratory grow

sed in response to amino acid starvation (3-AT treatment); fungal-specific (no human or murine homolog)

ylation, histone H3-K79 methylation, mRNA 3'-end processing, sno(s)RNA 3'-end processing, telomere ma

at telomere, histone H3-K4 methylation, regulation of meiotic DNA double-strand break formation, telomere

nt cells are small, rounded, and sometimes binucleate; not required for filamentous growth; mutant is hyper

NF chromatin remodeling complex; interacts with Snf2p; SWI/SNF complex is essential for hyphal growth a

NA expression, peak at cell-cycle G1/S phase; predicted, conserved MBF binding sites upstream of G1/S-r

periodic mRNA expression, peak at cell-cycle G1/S phase

chromatin; required for proper nucleosome positioning on WOR1 promoter

lm; induced upon adherence to polystyrene

ne in zinc cluster region near MTL locus; resequencing indicates that TAC1 spans orf19.3188 and orf19.31

tonylated lysine residues in histone H3; macrophage-induced protein; possibly required for yeast cell adher

tosine repressed; likely to be essential for growth, based on an insertional mutagenesis strategy

nduced via Cap1; induced by nitric oxide independent of Yhb1p; sumoylation target; rat catheter biofilm rep

ne on the opposite strand; induced by Tbf1

l membranes; rat catheter biofilm induced

t of promoters; recruits Fhl1 and Ifh1 to promoters; role is analogous to that of S. cerevisiae Rap1; Spider

ssed; functional homolog of S. cerevisiae and human TATA-binding proteins; Spider biofilm induced

lates hypha-specific gene expression; contains 4 tetratricopeptide repeat (TPR) motifs; flucytosine repress

the regulation of growth and cell wall integrity; heterozygous null mutant displays sensitivity to rapamycin

ase enriched protein

ic in infection; farnesol-repressed; stationary phase-enriched; GlcNAc-induced; flow model biofilm induced;

3p-repressed gene

and RPMI biofilm formation; regulates BCR1; Cph2 regulated transcript; alkaline, rat catheter, Spider, flow

al-induced; induced in RHE model of oral candidiasis, in clinical oral candidiasis isolates; possibly essential

nthetases are downregulated upon phagocytosis by murine macrophage

nthetases are downregulated upon phagocytosis by murine macrophage

vity

-hypha switch; Spider biofilm induced

activity; has telomerase-specific motif T and other conserved reverse transcriptase motifs

a basal transcription initiation factor of RNA Polymerase II; possibly an essential gene, disruptants not obta

d

weak acid stress; possibly essential gene, disruptants not obtained by UAU1 method

s filamentous growth; possibly an essential gene, disruptants not obtained by UAU1 method

ssed

ted gene regulation by Ssn6

n

le-turnover enzyme that provides histidine for HMP-P formation; induced by nitric oxide independent of Yhb

protein; Spider biofilm induced

induced

Spider biofilm repressed

n4p-regulated; sumoylation target

murine macrophages; stationary phase enriched protein; Spider biofilm repressed

human; flucytosine induced; downregulated upon phagocytosis by macrophages; Spider biofilm repressed

ıg ribosomal subunits, translation factors, and tRNA synthetases are downregulated upon phagocytosis by
ıetases are downregulated upon phagocytosis by murine macrophage
rin A; downregulated upon phagocytosis by murine macrophages; Spider biofilm repressed
pressed
ıage-induced; genes encoding some translation factors are downregulated upon phagocytosis by murine m
pressed
ıer membrane
flow model biofilm induced
n protein import into mitochondria
ıto mitochondria; Hap43, ketoconazole-repressed; Spider biofilm repressed
biofilm induced; Spider biofilm repressed
n mitochondrial protein import; Spider biofilm repressed
ɛr membrane; Spider biofilm repressed
ɛmbrane and cytosol
pressed
ɛnsitivity to toxic ergosterol analog
CF complexes; binds unnedddylated cullin Cdc53; mutants are viable
asmic reticulum; similar to S. cerevisiae Tip20p
d53p during recovery from DNA damage
ɛgulated by Nrg1, Mig1, and Tup1; antigenic in human or murine infection; possibly essential (by UAU1 me
ɛr biofilm repressed
.6337.1, which is a region annotated as blocked reading frame
s extended, relative to that of other family members; overlaps orf19.2662
f oral candidiasis; Hap43-repressed
ofilm repressed
ipt induced upon phagocytosis by macrophage; rat catheter biofilm induced
abundance not affected by reintegration of URA3 in CAI4; flucytosine induced; possibly an essential gene (
); very similar to S. cerevisiae Tok1p; Bcr1-repressed in RPMI a/a biofilms
mitochondria
ın into mitochondria; flucytosine induced
hecin; induced upon adherence to polystyrene; rat catheter biofilm induced
to be catalytic; functional homolog of S. cerevisiae Top2p; sensitive to amsacrine or doxorubicin; farnesol-
ed in regulation of ribosome protein synthesis, starvation response, and adhesion
or Kex2 processing in vitro; fluconazole-induced; induced by alpha pheromone in SpiderM medium; Hap43
ıesis; forms complex with catalytic subunit Pph21p that dephosphorylates septin Sep7p
ɛssed; protein in exponential and stationary growth phase yeast; possibly essential; flow model biofilm induc
ıotypic switching and mating; WT nuclear localization requires Bcy1; produced during stationary, not expor
henotypic switching and mating; needed for epithelial cell damage, engulfment and oral virulence in mice
ɛd; protein levels decrease in stationary cells; Hap43-induced; rat catheter and Spider biofilm repressed
ɛd expression in hyphae vs yeast-form cells; regulated by Nrg1; Spider biofilm repressed
omoter bound by Tec1 and Ndt80; Bcr1-repressed in RPMI a/a biofilms
; macrophage induced
in presence of human neutrophils; macrophage/pseudohyphal-repressed after 16h; stationary phase enric
e virulence; possible drug target; 2 conserved phosphohydrolase motifs; no mammalian homolog; Hap43-re
ınder H2O2 stress conditions; flow model biofilm induced (reports differ)
ɔt1 null mutant

y direct uptake, possibly related to membrane permeability; contains 5' UTR intron; Spider biofilm induced

ring alkyl or aryl (other than methyl) groups activity and role in tRNA methylation, wybutosine biosynthetic pr

enzyme of some other fungi; complements E. coli trpC, S. cerevisiae trp1 mutant; CCT1 and TRP1 overlap
n4p
e activities; regulated by Gcn2p and Gcn4p
revisiae ortholog is Gcn4p regulated
onent); predicted N-terminal acetylation; Gcn4p-regulated; S. cerevisiae ortholog is Gcn4p regulated; upreg
ced in response to amino acid starvation (3-AT treatment)
-induce via Cap1; induced by human neutrophils; stationary phase enriched protein
le-mediated transport and TRAPPI protein complex, TRAPPII protein complex, TRAPPIII protein complex

3 induced; amphotericin B, caspofungin repressed; induced by human neutrophils; macrophage-repressed
ive site (Trp-Cys-Gly-Pro-Cys); TRX1 encodes all of the cytoplasmic/nuclear thioredoxin function in C. albic
ate; Spider biofilm induced
cone substrate; Spider biofilm induced
to silicone substrate; Spider biofilm induced
cone substrate
silicone substrate; Spider and F-12/CO2 biofilm induced; repressed by alpha pheromone in SpiderM mediu
lative stress signaling; antigenic; hyphal surface, nucleus; yeast-form nucleus, cytoplasm; biofilm, phagocyt
3p role under oxidative/reductive stress, hyphal cell wall formation; in hyphal nucleus, cell wall; yeast-form n
affects filamentous growth
; mutants are viable
atients with oral candidiasis; Nrg1-regulated

eatment; alkaline repressed; regulated by Gcn2 and Gcn4; required for virulence in mouse model; Spider b
single alpha-tubulin gene, whereas S. cerevisiae has two (TUB1, TUB3); farnesol-upregulated in biofilm; su
GlcNAc, hypha fluconazole-induced; slow growth, ectopic expression increases white-to opaque switch; rat
eriodic mRNA expression, peak at cell-cycle S/G2 phase
rine macrophage; levels decrease in stationary phase cells; Spider biofilm repressed
, farnesol response; in repression pathways with Nrg1, Rfg1; farnesol upregulated in biofilm; rat catheter, S
ed

Cyr1; flucytosine, Hog1 induced; amphotericin B, caspofungin repressed; induced in flow model biofilm and
ne homolog)
e enriched protein; Spider biofilm repressed
TP and N-acetylglucosamine 1-phosphate; functional homolog of S. cerevisiae Qri1p; alkaline upregulated

e complex, nucleus localization
xpression

onjugating enzyme activity, ubiquitin-protein transferase activity
e-induced ubiquitination of fructose-1,6-bisphosphatase; induced by alpha pheromone in SpiderM medium
appears to be degraded; functional homolog of S. cerevisiae RPS31; Hap43-induced; Spider biofilm repres
individual units; transcript induced by stress; mRNA in yeast and mycelia at similar abundance; Spider biofi
ation, protein deubiquitination and cytoplasm, endoplasmic reticulum localization
rat catheter biofilm repressed

xygen availability; transposon mutation affects filamentous growth; Spider biofilm induced
wnregulation correlates with clinical fluconazole resistance; Ras1-regulated; Hap43-repressed; flow model b
scription induced on contact with vascular endothelial cells; not highly conserved
asmic reticulum; functional homolog of S. cerevisiae Ufe1p, which is an ER t-SNARE that mediates the retr
rat catheter and Spider biofilm induced
s a region annotated as a blocked reading frame; Spider biofilm induced
ulated by Mig1, Tup1, Gcn4; mutants are viable
ce; mutants display decreased CFU in mouse kidneys; Spider biofilm induced
d in the regulation of gamma-aminobutyrate metabolism genes; rat catheter biofilm induced
olism gene expression; required for yeast cell adherence to silicone substrate; rat catheter biofilm induced
sence of preferred N sources; transcriptionally induced upon phagocytosis by macrophage; gene regulatio
zole-resistant strain that overexpresses MDR1

ionary phase enriched; induced in oralpharyngeal candidasis; rat catheter biofilm repressed; Bcr1-represse
has UDP-sugar binding domain; activity is UDP-glucose-specific in vitro; enzyme does not use UDP-mannc

lm induced

L : B9J08_000281 and Candida tenuis NRRL Y-1498 : CANTEDRAFT_119330
tion to filamentous growth; stability controlled by Grr1p, Ubr1p, Ptc2p in response to CO2 and O2 levels
transcription factor involved in the regulation of meiotic genes
oter; induced by ergosterol depletion, by azoles, anaerobicity; macrophage/pseudohyphal-repressed; flow m
g1/Tup1; flow model biofilm induced; rat catheter and Spider biofilm repressed
crophage/pseudohyphal-induced; 5'-UTR intron; flow model biofilm repressed
xpression when integrated at ectopic chromosomal locations can cause defects in hyphal growth and virule

4 strain background; flucytosine induced; protein level decreased in stationary phase cultures
biosynthetic process, nucleobase-containing compound metabolic process and cytoplasm, nucleus localiza
ures
n infectious prion form called [URE3]; forms [URE3] prion when expressed in S. cerevisiae

vesicle-mediated transport and ER to Golgi transport vesicle membrane, Golgi membrane localization
ced upon filamentous growth and in response to alpha pheromone in SpiderM medium

racts with TAP-tagged Nop1
cally interacts with TAP-tagged Nop1p
racts with TAP-tagged Nop1
e stress response; mutation confers resistance to 5-fluorocytosine (5-FC) and parnafungin
ced
tant to parnafungin
r biofilm induced
osine (5-FC), 5-fluorouracil (5-FU), and tubercidin (7-deazaadenosine); physically interacts with TAP-taggec
sis; physically interacts with TAP-tagged Nop1; Spider biofilm induced
P-tagged Nop1
n; chitin-binding, glycosyl hydrolase domains; induced during cell wall regeneration; mRNA in yeast-form ce
rphology; mutants are viable

an or murine homolog)
es are downregulated upon phagocytosis by murine macrophage

ypersensitivity to toxic ergosterol analog; fungal-specific (no human or murine homolog)
uolar acidification; rat catheter biofilm repressed
equired for hemoglobin-iron utilization; Spider biofilm repressed
er biofilm repressed
membrane localized; amphotericin B repressed, caspofungin repressed
rting V-type ATPase complex assembly
ses in stationary phase cultures; rat catheter biofilm repressed

erevisiae Vma7p; interacts with phosphatidylinositol 3-kinase Vps34p
ells exposed to fluconazole over multiple generations; rat catheter and Spider biofilm repressed

Gcn4p
; role in hyphal growth, possibly via vacuole expansion into hypha; role in killing of and survival within macr

for growth, based on insertional mutagenesis; downregulated in biofilm or in azole-resistant strain that ove

d protein retention in Golgi apparatus, more
cr1-repressed in RPMI a/a biofilms
e; involved in filamentous growth and virulence; Spider biofilm induced
m8p; Hap43p-repressed gene
esponse; ortholog of S. cerevisiae Stp22/Vps23
regulated upon adherence to polystyrene

, which regulates pH response; role in echinocandin, azole sensitivity

wth, fibroblast adherence, virulence in mouse systemic infection; growth-regulated; caspofungin and hydro

., which regulates pH response; role in uptake of Histatin-5 into vacuole

decreases SAP secretion and virulence in murine intravenous infection; regulated by Gcn2p, Gcn4p; requ

on mutation affects filamentous growth; regulated by Gcn4p; induced in response to amino acid starvation (

othelial cells; required for normal hyphal growth and stress resistance; induced in presence of host oral or v

endosome to Golgi and GARP complex, Golgi apparatus localization

revisiae Vrg4p, which imports GDP-mannose from cytoplasm to Golgi for protein and lipid mannosylation; r

with Wal1p and Myo5p; downregulated upon adherence to polystyrene

otion is opaque-specific; fungal-specific (no human or murine homolog)

specific (no human or murine homolog); virulence-group-correlated expression

transport, macroautophagy, vacuole fusion, non-autophagic, vesicle fusion

le morphology; similar to Wiskott-Aldrich syndrome protein; localizes to cortical actin patches and hyphal ti

erence to silicone substrate; Spider biofilm induced

; Hap43, hypoxia, ketoconazol induced; required for RPMI biofilm; Bcr1-induced in RPMI a/a biofilm; rat ca

urine homolog

tain the opaque state; opaque-specific, nuclear; regulates its own expression; suggested role in regulation

tate; Hap43-induced

overexpression at 25 degr shifts cells to opaque state; deletion stabilizes opaque cells at higher temperatu

ng; activator of the opaque cell type

re downregulated upon phagocytosis by murine macrophages

l biofilm induced

sis inhibitors; not required for yeast-to-hypha transition or for virulence in mice; Hap43-induced; Spider biof

f the Nucleobase-Ascorbate Transporter/Nucleobase-Cation Symporter (NAT/NCS2) family; rat catheter b

, Hog1 and during cell wall regeneration; Mnl1-induced in weak acid stress; stationary phase enriched; flow

sfer and Yae1-Lto1 complex localization

n histone H3; subunit of the NuA4 histone acetyltransferase complex; transcript regulated by Mig1p

nodel biofilm induced; induced in core caspofungin response

to H_2O_2; essential for macrophage killing

nil-induced; oxidative stress-induced via Cap1; possible association with multidrug resistance; possibly ess

nd morphogenesis; transcription is activated in weak acid stress or on contact with with host cells

pider biofilm repressed

cript is regulated by Nrg1 and Mig1; Hap43-repressed

nthesis; induced by alpha pheromone in SpiderM medium

d by Nrg1, repressed if iron absent induced by macrophage interaction; Hap43-repressed gene

activated by NO, macrophage interaction; Hap43, hypha repressed; mRNA binds She3

FAD-binding, and NAD(P)-binding domains but lacks some conserved residues of flavohemoglobins; Hap4

(P)-binding domains but lacks some conserved residues of flavohemoglobins; filament induced; rat cathet

ne

ced; Spider biofilm repressed

omyl treatment; macrophage-downregulated gene

and actin; transcript induced by yeast-to-hypha switch; regulated by Nrg1, Tup1; Spider and flow model bio

essed

pair repair; Hap43-repressed gene; flow model biofilm induced

ced

ilm induced

ced; biofilm induced; macrophage-induced protein; stationary phase enriched protein; Spider biofilm repres
eobasidin A; white cell type-specific transcript; Spider biofilm induced
, peak at cell-cycle G1/S phase
phosphoacceptor histidine; predicted to be soluble and cytosolic; functional homolog of S. cerevisiae Ypd1p
sed sensitivity to alpha pheromone
n secretion at ER-to-Golgi; dominant-negative mutation causes SAP secretion defect and accumulation of i
ap43-repressed gene
d virulence
plasmic transport and cytoskeletal dynamics; transcript is not regulated by white-opaque switch or by dimor
O-acetyl-ADP-ribose to AMP and acetylated ribose 5'-phosphate; rat catheter biofilm repressed
ninin receptor; predicted S/T phosphorylation, N-glycosylation, myristoylation, Hap43-, Gcn4-regulated; Spic
s filamentous growth; induced by Mnl1 under weak acid stress
l switch; decreased expression in hyphae compared to yeast-form cells; fluconazole or flucytosine induced
poson mutation affects filamentous growth; protein level decreases in stationary phase cultures; Hap43p-in
ofilm repressed
ed for wild-type growth rate and for wild-type virulence in mouse model of systemic infection; Hap43p-induc
opeptide; growth phase, phosphate, Ssk1/Ssn6/Efg1/Efh1/Hap43 regulated; mRNA binds She3; flow and S
decreased colonization of mouse kidneys; flow model biofilm induced; Spider biofilm induced
s display decreased colonization of mouse kidneys
creased colonization of mouse kidneys
e through expression of SSU1 and CDG1; Hap43-repressed; Spider biofilm induced
; Spider biofilm induced
biofilm induced
ed
morph; Hap43-repressed; mutants have decreased CFU in mouse kidneys and defects in filamentous grov
tosine; possibly an essential gene, disruptants not obtained by UAU1 method; Hap43-repressed; Spider an
luced
o Calcofluor White; required for yeast cell adherence to silicone substrate
ilicone substrate; Spider biofilm induced
s unable to utilize mannitol as a carbon source; mutants have increased colonization of mouse kidneys
erence to silicone substrate
of mouse kidneys; required for yeast cell adherence to silicone substrate; Spider biofilm induced
nosome 5, near the MTL locus; required for yeast cell adherence to silicone substrate; Spider biofilm induce
inotriazole treatment); upregulation correlates with clinical development of fluconazole resistance
macrophage-induced; alkaline induced upon adherence to polystyrene; induced in oralpharyngeal candidas
in B, interaction with macrophages; induced in oralpharyngeal candidiasis; Spider biofilm induced
ow model biofilm induced; Spider biofilm repressed
, based on an insertional mutagenesis strategy; Spider biofilm repressed
menadione, macrophage; caspofungin repressed; induced in core stress response; regulated by Gcn2, Gc

m induced			
itro by Gin4p			
and F-12/CO2 biofilm induced			
43p-induced; GlcNAc-induced			
biofilm repressed			
erevisiae Abd1; rat catheter biofilm induced			
t catheter biofilm repressed			
model biofilm repressed			
hase-enriched protein			
and Spider biofilm repressed			
essed, Spider biofilm induced			
r biofilm repressed			
silicone substrate			
vels decrease in stationary phase			
phase-enriched protein			
ADE2; stationary phase-enriched			
ast to S. cerevisiae ortholog			
biofilm repressed			
cultures			
induced; Spider biofilm repressed			
induced			
utant is viable			
iofilm induced			
Spider biofilm repressed			
ed			
d			
pider biofilm induced			

d; rat catheter biofilm repressed			
chloride			
ytosis by murine macrophages			
n; stationary phase enriched			
n induced			
otained by UAU1 method			
ned by UAU1 method			
obtained by UAU1 method			
creases in stationary phase			
t catheter biofilm repressed			
se model of systemic infection			
c1, Efg1, Ndt80, and Brg1			
on; regulated by Sfu1p			
del biofilm repressed			
ring chlamydospore formation			
tion; can form amyloid fibrils			
, cell-surface glycoproteins			
evisiae; Hap43p-repressed			
c1, Ndt80, Brg1			
er biofilm repressed			
repressed			
ced in a/a RPMI biofilms			
ence; Spider biofilm induced			

ilm induced			
biofilm induced			
ter, Spider biofilm induced			
Spider biofilm induced			
pressed			
ein decreases in stationary phase			
tionary phase enriched			
pider biofilm repressed			
tional mutagenesis strategy			
uced			
ed; Spider biofilm repressed			
repressed yeast, hyphae			
uced			
ed; Spider biofilm induced			
ed; Spider biofilm repressed			

hases; Spider biofilm repressed			
wth phases; Hap43-induced			
in 5' UTR			
hase yeast cultures			
he3; Spider biofilm induced			
S. cerevisiae cdc24-4 mutant			
dy localization			
d by Vhr1p			
kines in mouse dendritic cells			
uced; Spider biofilm induced			
atheter biofilm repressed			
an; Spider biofilm induced			
w model biofilm induced			
azole-resistant strain; Hap43p-induced			
causes decreased colony wrinkling			
3; rat catheter biofilm repressed			
e oral epithelial cells			
n at septum			
nthase III)			
RPMI a/a biofilms			

M medium			
ess			
m repressed			
film induced			

e mouse cecum

ivity

plex localization

ecombination

clease activity

2835

rane localization

localization			
ST_32780			
30203			
OB_00081			

ane, nucleus localization

mitochondrion localization

pressing MDR1

4439

T_30337			
localization			
pathway			
m induced			
)			
induced			

ctivity

_02885

deaminase complex localization

membrane localization

(no human/murine homolog

localization

upon hyphal formation

T_2506

localization

film induced

; Spider biofilm repressed

r biofilm induced

PGUG_05223

ation			
99722			
l			
2709			
ation			

T_29111			
4			
iquid media			
uced; flow biofilm repressed			
ding			
pider biofilm induced			
sine induced			
m repressed			

d new sequence data

T_2287

xygen activity

gene

ed reading frame

T_2351			
ation			
_01196			
nd cytoplasm, polysome localization			
duced			

3			
arge subunit biogenesis			

liquid media

bly

ST_32327

processing

ization

OB_00124			
_05051			
otype; no expression detected			

ed			
e ion transmembrane transport			
d mitochondrion localization			
ion			
alization			
T_2098			
pressed			

T_2127

_02365

alization

1 method

G_00248

d Spider biofilm repressed

LY : CORT1C04470			
us localization			
CAWG_02618			
3333			
localization			

30078

tosol, nucleus localization

ion

ulum membrane localization

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ss

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JAU1 method

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ot obtained by UAU1 method

ing activity

DRAFT_58603

some localization

atheter biofilm induced

G_00335			
a			
30926			
esicle localization			
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plex assembly

UAU1 method

_03191

transport

catheter biofilm induced

argeting to membrane			
nplex localization			
er and Spider biofilm induced			
nembrane localization			
T_1253			

azoles

eter biofilm repressed

nt decay

te endosome localization

ization			
Spider biofilm induced			
PADRAFT_55715			
_04763			
eromone in SpiderM medium			

nduced

98

d

flow model biofilm induced

osomal complex localization

dy localization

ST_31932

nsferase I complex localization

on localization

n induced

biofilm repressed			
rane localization			
omolog)			
uclear periphery localization			
; overlaps orf19.5621			
localization			

and Spider biofilm induced

6820

alization

del biofilm induced

lization			
iofilm repressed			
der biofilm induced			
, and Hap43p			
od; Spider biofilm induced			
786			
processing			
ssed			
eter biofilm repressed			
m localization			

ilm induced

; Spider biofilm induced

y phase cultures
s; rat catheter biofilm repressed
ene (by UAU1 method)
nd flow model biofilm induced
d; promoter bound by Efg1
hil, Spider biofilm induced
induced
pider biofilm repressed
biofilm repressed
; Spider biofilm induced
; Spider biofilm induced
induced
Spider biofilm repressed
s
biofilm induced
ap43; Spider biofilm induced
se systemic infection
bits pheromone response
neter biofilm repressed
ofilm repressed
ider biofilm repressed
r biofilm repressed
epressed
) tem1 mutant phenotypes
duced; Spider biofilm repressed
buds of yeast cells and to hyphal tips
ring human oral infection
n; Spider biofilm repressed
tron

Gcn4p			
lization to hyphal tip			
in SpiderM medium			
embly 21			
yeast; Spider biofilm repressed			
pider biofilm repressed			
ntial and stationary phase			
ofilm induced			
flow model biofilm induced			
se; possibly essential			
s; Spider biofilm induced			
s filamentous growth			
x olamine			
/amphotericin B repressed			
stationary phase enriched			
repressed			
duced in a/a biofilm			
der biofilm repressed			
del biofilm repressed			
pider biofilm induced			
of S. cerevisiae Chs4p			
model biofilm repressed			
er biofilm induced			
phal cells			
Spider biofilm repressed			
p, Cyr1p, Ras1p			
yeast-to-hyphal switch			
er biofilm induced			

catheter biofilm induced

a systemic mouse model

tant caspofungin sensitive

A in clb4 mutant

e has intron
osphorylated; Hap43p-repressed

l to null mutant

nduced

athether biofilm repressed
nd Spider biofilm induced
a pheromone in SpiderM medium;

cess

egulated by Vhr1p

cess, snRNA modification

ne

ucleus localization

duced; Spider biofilm induced

n induced

, caspofungin repressed

g, more

g, more

erase I

JAU1 method

s CDR1 and CDR2

ation

3

32997

a Cap1p

1066			
lization			

on, exosome-dependent

tion-dependent decay

tation

d Spider biofilm induced

er biofilm repressed

riched; flow biofim repressed

ced

erase II

lycoprotein ERAD pathway			
.			
tion			
cation			
uble-strand break localization			
y			
ation			
43; Spider biofilm induced			
d; Hap43-repressed gene			
induced			
e sgv1 mutant; Hap43p-repressed			
nt			
lel biofilm induced			
se; Spider biofilm induced			
3cr1-induced in a/a biofilms			

hase; Spider biofilm repressed			
neter biofilm repressed			
egulated by Gcn2p and Gcn4p			
biofilm induced			
ched; GlcNAc-induced			
rmal Spider biofilms			
wth regulation			
mone; Hap43p-repressed			
epressed			
n folding			
reduced virulence			
r, Spider biofilm induced			
Spider biofilm induced			
model/Spider biofilm induced			
del biofilm induced			
tionary phase			
ofilm induced			
d stationary phase cells			
gnaling			
flow model biofilm induced			
se yeast cultures			
pider biofilm induced			
ider biofilm induced			
ider biofilm repressed			

sion			
anslational termination			
utagenesis			
biofilm induced			
v model biofilm induced			
ultures			
; Spider biofilm induced			
-induced, fungal-specific			
der biofilm induced			
biofilm induced			

ultures			
r and flow model biofilm induced			
eter, Spider biofilm repressed			
er biofilm repressed			
ressed in a/a biofilms			
ed; rat catheter biofilm induced			
ofilm induced			
eter and Spider biofilm induced			
ssed			
pressed			
and hypoxia			
pider biofilm induced			
ron; Spider biofilm repressed			
onse; binds E-box			
tinal tract colonization			
amount in stationary phase			
biofilm repressed			
ofilm repressed			
rease in stationary phase			
film induced			

Spider biofilm induced			
er biofilm induced			
r biofilm repressed			
tive; may be essential			
nduced			
sed			
uced; Spider biofilm repressed			
otein; GlcNAc-induced protein			
uced; hypoxia regulated			
athway			
sed; Spider biofilm repressed			
er biofilm induced			
biofilm repressed			
on affects filamentous growth			
der biofilm repressed			
at catheter biofilm induced			
iofilm repressed			
S/G2 phase			
e Ess1p			
1 method; Hap43p-repressed			
dherence to HeLa cells			
ed, flow model biofilm repressed			

eromone response and cell cycle arrest			
pider biofilm repressed			
nduced			
uced; Spider biofilm repressed			
erlaps orf19.6179			
n			
pider biofilm repressed			
ofilm repressed			
pider biofilm induced			
3; Spider biofilm induced			
r biofilm repressed			
ungin sensitivity			
ted in RHE model			
H motif; has LUFS domain			

ter, Spider biofilm induced			
Spider biofilm induced			
biofilm induced			
Assembly 21			
nd flow model biofilm induced			
ponential and stationary phase			
Sfu1p, and Hap43p			
Hap43p-repressed			
Spider biofilm induced			
hage			
d			
rease in stationary phase			
el biofilm induced			
er biofilm induced			
nodel biofilm induced			
d			
ow model biofilm induced			
nfection model			
n RPMI a/a biofilms			
ofilms			
flow and Spider biofilm repressed			
tion; Spider biofilm induced			

ed			
olog of S. cerevisiae Gda1p			
er and flow model biofilm induced			
sed; rat catheter biofilm induced			
owth-phase regulated; catalytic Cys			
associates with septins			
epressed			
ein			
ofilm induced			
growth phase yeast cultures			
riched protein			
n induced			
el biofilm induced			
temic infection			
er biofilm repressed			
heter, flow model biofilm induced			
osmotic stress			
pa2; regulates HWP1 and ECE1			
sponse; Spider biofilm induced			
iofilm induced			
ofilm induced			
Spider biofilm repressed			
sed			

ECE1; required for WT hyphal growth			
er polyamine limitation			
rotein; Spider biofilm induced			
pider biofilm induced			
fluphenazine, benomyl			
der biofilm induced			
RPMI a/a biofilms			
ed; Spider biofilm repressed			
n induced			
phase enriched			
19 correction)			
ted by Gcn2p, Gcn4p			
cultures			
eter biofilm repressed			
She3; Spider biofilm induced			
ced			
o1-dependent induction in low iron			
n RPMI a/a biofilms			
m induced			
r, Spider biofilm induced			
ent expression in low iron			
ofungin-downregulated			
theter, Spider biofilm repressed			
ofilm repressed			
hemoglobin			

by trichostatin-A;			
, Spider biofilm repressed			
iofilm induced			
sential gene (UAU1 method)			
d by Nrg1, Tup1, farnesol			
ed gene			
membrane segments			
se			
uced			
edium with 2% glucose			
ucose			
nduced			
ch medium with 2% glucose			
; Spider biofilm induced			
ch medium; Hap43p-repressed			
film repressed			
; flow model biofilm induced			
%) glucose in rich media; intron			
r and Spider biofilm repressed			
repressed			
ssed			
epressed			
uman or murine homolog)			
e adhesion to human calls			
se			
hyphae			
ced			
e immune response			

ast cultures; GlcNAc-induced protein			
ssed			
irulence			
ouse systemic infection			
Spider biofilm induced			
and azoles			
m induced			
3-repressed			
er biofilm induced			
n and biofilm azole resistance			
duced switching; nicotinamide target			
yeast-hyphal switching			
e hypersensitive to caspofungin			
ains; Spider biofilm repressed			
pider biofilm induced			
and Rbt1 domains			
Spider biofilm repressed			
film induced			
eter, Spider biofilm induced			
Brg1; Spider biofilm induced			
al; Spider biofilm induced			

; rat catheter biofilm repressed			
pressed; Tac1p-regulated			
ec1, Efg1, Ndt80, Rob1, Brg1			
res			
d; Spider biofilm repressed			
er biofilm repressed			
R54 encoded within IMH3 intron			
brane targeting domain			
biofilm repressed			
ene has intron			
get; Spider biofilm repressed			
n induced			
catheter biofilm repressed			
gulation			
ider biofilm induced			
atricopeptide repeats			

sed			
rat catheter biofilm induced			
paque independent			
flow model biofilm repressed			
roxide; Hap43p-repressed gene			
g1p-downregulated			
induced			
in RPMI a/a biofilms			
pressed in RPMI a/a biofilms			
I a/a biofilms			
y Pmt1p			
model biofilm induced			
biofilm repressed			
te; Spider biofilm induced			
asm, nucleus localization			
vild-type pathogenesis			
ment			

ment			
nvironment			
ilm induced			
systemic infections			
ion; affects filamentation			
dherence to polystyrene			
cidic microenvironment			
systemic infection			
ment			
cultures; Hap43p-repressed			
olog); sumoylation target			
epressed			
luced, flow model repressed			
cn4, Hap43			
onary growth phase yeast			
er and Spider biofilm induced			
pider biofilm repressed			
paque cells; intron in 5'-UTR			
ced gene			
catheter biofilm repressed			

t80, Rob1, Brg1			
iofilm induced			
dospore formation			
ed			
thways to induce filamentation			
nd stationary phase yeast			
); Hap43p-repressed			
d, F-12/CO2 biofilm induced			
; Hap43p-repressed gene			
rulence-group-correlated expression			
r, F-12/CO2 biofilm induced			
Spider biofilm repressed			
gene (by UAU1 method)			
nd CDR2 overexpression			

ressed			
rturbation, or cell wall stress			
pider biofilm repressed			
catheter, Spider biofilm induced			
model biofilm repressed			
uced			
xposes beta-glucan			
pider biofilm repressed			
and transmembrane helix			
d Spider biofilm induced			
ng segment (positions 18-34)			
duced			
luced; Spider biofilm induced			
mRNA binds She3			
duced; Spider biofilm induced			
d; Spider biofilm induced			

s gene expression			
ced			
substrate			
3p			
; sumoylation target			
w model biofilm induced			
ced; Spider biofilm induced			
dvantage; Spider biofilm induced			
e advantage			
d			
ider biofilm repressed			
flow model biofilm repressed			
film induced			
ed			
f GlcNAc catabolism			
o human or murine homolog			

to azoles

neter, Spider biofilm induced

ressed
eatment

Rep1p; Hap43-induced gene
acilitator superfamily

nce; 9 HAMP domains
sis by murine macrophage

ss response

iofilm induced

silicone substrate
oral candidiasis
nan hyphae

nduced; Spider biofilm repressed

ed

ofilm induced			
neter biofilm repressed			
molog)			
Hap43p-induced			
r biofilm induced			
43-induced			
ilm induced			
n induced			
r and Spider biofilm induced			
ly biofilm induced			
Opt3; Spider biofilm induced			
atment			
)			
otein; Spider biofilm induced			

1, Tec1, Ndt80, Rob1, Brg1			
pider biofilm induced			
ilm repressed			
d Spider biofilm induced			
film repressed			
heter biofilm induced			
east; Spider biofilm repressed			
ation			
roxisome localization			
calization			
p-repressed			
n			
calization			
nd Spider biofilm repressed			
r/Spider biofilm repressed			
tant; nonessential			
rat catheter biofilm repressed			
is; Spider biofilm induced			

ec1, Egf1, Ntd80, Rob1, Brg1
ore formation

/a biofilm
d Spider biofilm repressed
cr1, Ndt80, Rob1, Brg1

e, nucleus localization
ofilm induced
/CO2 early biofilm induced

sponse

tron

a/a biofilm			
ocated in MTLalpha locus			
, Spider biofilm repressed			
mutant is activated			
biofilm repressed			
m induced			
repressed			
1586 are almost identical			
o S. cerevisiae Spo14p			
RHE model; Spider biofilm repressed			
sis; 3-AT, Spider biofilm repressed			
w model and Spider biofilm repressed			
ubstrate			
ntial			
ssed in RPMI a/a biofilm			
in RPMI a/a biofilms			
induced			
phase enriched protein			
biofilm induced			
e, caspofungin repressed			
strategy			
ated; Spider biofilm induced			
btained by UAU1 method			
cerevisiae Pph3p			
genes			

produced at ambient pH
nduced; Spider biofilm induced

e Locus History)

by murine macrophages
ast cultures
uced

ic switching

nduced
ecific

y

ssed			
l biofilm repressed			
y phase; Hap43p-repressed			
ssed			
p; lacks S. cerevisiae homolog			
w growth, increased white-to-opaque switch			
NA damage			
e has two introns			
atheter biofilm repressed			
f S. cerevisiae ras1 ras2 mutant			
er biofilm repressed			
ko1p-repressed			
homolog of S. cerevisiae Rbp1p			

Spider biofilm induced			
der biofilm induced			
invasive growth			
rapamycin			
repression; Spider biofilm induced			
erevisiae rfx1 mutant defects			
hes; Spider biofilm repressed			
g1, Tup1			
switch, macrophage interaction			
iofilm induced			
v model biofilm induced			
ced hyphal growth			
egulation target			

d
ofil
Hap43
n repressed
biofilm repressed
nage; Tbf1p-activated; Hap43p-induced

der biofilm repressed			
lated; Spider biofilm repressed			
biofilm repressed			
theter biofilm induced			
d; Spider biofilm induced			
ofilm repressed			
r biofilm repressed			
pider biofilm repressed			
luced; Spider biofilm repressed			
pider biofilm repressed			
ed			
osmotic stress			

ed			
nutant heat sensitivity			
oid homeostasis			
oid homeostasis			
ation			
genes RVS161 and RVS167			
yo5p			
andidiasis			
uced; Spider biofilm repressed			
n induced			
induced			
one repressed			
, Spider biofilm induced			
ction; N-glycosylated			
minent role in biofilms			
oider biofilm induced			
er biofilm induced			
d			

2			
ssed			
ced			
ultures; Hap43p-repressed gene			
localization			
lm-regulated			
flow model biofilm induced			
t S. cerevisiae sec20-1 mutant			
ith Golgi apparatus			
ace of the hyphal tip			
. cerevisiae Sec4p			
induced			
ation			
macrophage-regulated			
at catheter biofilm repressed			
l biofilm induced			

nduced			
uced			
l biofilm induced			
fers			
ltures			
and Spider biofilm repressed			
affects filamentous growth			
biofilm induced			
more			
ter and Spider biofilm induced			
repressed			
under weak acid stress			
d; Spider biofilm induced			
phage-downregulated			
ore			

homolog of S. cerevisiae Smp3p			
ene in some experiments			
hal growth and virulence			
tion during yeast form growth			
sitivity			
by mass spec			
atheter biofilm repressed			
ider biofilm repressed			
e-downregulated, farnesol-induced			
and flow model biofilm induced			
gene family			
ilm induced			
er; Hap43p-induced gene			
p43p-induced gene			
61 S. cerevisiae mutants			
bination during meiosis			

tyrene; Spider biofilm repressed			
efects			
localization			
P; Spider biofilm repressed			
ed; caspofungin repressed			
nduced; Spider biofilm repressed			
ssential			
not cell-cycle regulated			
S1); Spider biofilm induced			
medium			
nfection; TPR motifs			
reated with Congo Red;			
aspofungin repressed			
duced, A1p-Alpha2p repressed			
duced			
der biofilm induced			
ofilm repressed			
n; Spider biofilm induced			
, Spider biofilm induced			
atheter biofilm induced			
d protein			

Spider biofilm induced			
ed by yeast-hyphal switch			
morphogenesis and stress response			
th, alkaline-induced morphogenesis			
intenance			
maintenance			
sensitive to caspofungin			
nd virulence			
egulated genes			
89; Spider biofilm induced			
ence to silicone substrate			
ressed			
biofilm induced			
ed; Tbp1-induced			
Spider biofilm repressed			
model biofilm induced			
; Spider biofilm repressed			
ained by UAU1 method			
1; Spider biofilm induced			
d			

murine macrophage			
acrophage			
ethod)			
UAU1 method)			
upregulated in biofilm			
-induced			
ced; Spider biofilm repressed			
nential growth			
hed protein; Hap43-repressed			
pressed; flow model biofilm induced			

rocess

; Spider biofilm repressed

gulated in biofilm;

localization

l gene

cans; Hap43p-induced

um

tosis, peroxide induced

nucleus, cytoplasm

iofilm induced

moylation target

catheter biofilm repressed

Spider biofilm repressed

planktonic cultures

ssed

ilm induced

biofilm induced

rograde traffic

n by nitrogen source requires Gat1p

ed in RPMI a/a biofilms			
ose; Mig1-regulated			
model biofilm induced			
ence; Spider biofilm repressed			
ation			
d Nop1p			
lls; Spider biofilm induced			
ophage			
erexpresses MDR1			

gen peroxide sensitivity

ired for normal Rim8p processing

(3-aminotriazole treatment)

vascular cells

no mammalian homolog

ps

atheter, Spider biofilm induced

of adhesion factors

res; Spider biofilm induced

ilm induced

iofilm induced

v model biofilm induced

ential; Spider biofilm induced

3p-repressed gene

er and Spider biofilm induced

ofilm induced

ssed			
o			
ntracellular secretory vesicles			
rphic transition			
der biofilm repressed			
duced gene			
ed gene			
Spider biofilm repressed			
vth; Spider biofilm induced			
d flow model biofilm induced			
ed			
sis; Spider biofilm induced			
n4; rat catheter biofilm repressed			