

Sequence	Sequence Name(s)	Sequence Description	Ratio	Fold Cha	P-value	Sequen	Sequenc
YOL056W	GPM3	converts 3-phosphoglycerate to 2-phosphoglycerate in glycolysis; phosphoglycerate	15.97	15.97		0 SGD	636612
YFR057W	YFR057W		11.83	11.83	6.01E-34	SGD	638201
YLR213C	CRR1	CRH-Related	11.21	11.21		0 SGD	636773
YJR136C	YJR136C		10.31	10.31	1.11E-18	SGD	637037
YEL033W	YEL033W		9.85	9.85	9.33E-35	SGD	638229
YBR250W	YBR250W		9.16	9.16		0 SGD	635338
YJL051W	YJL051W		9.11	9.11		0 SGD	636319
YNL175C	NOP13	Nucleolar Protein 13	8.75	8.75	2.02E-37	SGD	636784
YOL150C	YOL150C		8.52	8.52	6.41E-26	SGD	634857
YBL023C	MCM2	Member of complex that acts at ARS's to initiate replication; Null mutant is inviable,	8.14	8.14	1.02E-08	SGD	637300
YBR247C	ENP1,MEG1	Essential nuclear protein; 57 kDa protein with an apparent MW of 70 kDa by SDS-P	7.76	7.76		0 SGD	637086
YCL050C	APA1,DTP1	diadenosine 5',5'''-P1,P4-tetraphosphate phosphorylase I; null mutant is viable, defe	7.58	7.58		0 SGD	638495
YJR156C	THI11	thiamine regulated gene, homologous to <i>S. pombe</i> NMT1A. Proposed biosynthetic :	7.19	7.19		0 SGD	639311
YJL050W	MTR4,DOB1	Dead-box family helicase required for mRNA export from nucleus; RNA helicase; Ni	7.15	7.15	3.68E-21	SGD	633437
YEL061C	CIN8,KSL2,SDS15	Kinesin-related protein involved in establishment and maintenance of mitotic spindle	7.07	7.07	1.66E-30	SGD	637361
YOR006C	YOR006C		6.97	6.97	1.63E-13	SGD	638441
YPL187W	MF(ALPHA)1	mating factor alpha; Null mutant is viable.	6.88	6.88	5.72E-35	SGD	635007
YDR355C	YDR355C		6.8	6.8	1.21E-39	SGD	634880
YGR152C	RSR1,BUD1	Gtp-binding protein of the ras superfamily involved in bud site selection; random buc	6.52	6.52		0 SGD	633785
YDL244W	THI13	Product of gene unknown	6.5	6.5		0 SGD	633863
YOR305W	YOR305W		6.47	6.47	7.29E-37	SGD	639144
YHR180W	YHR180W		6.33	6.33		0 SGD	634415
YLR215C	CDC123	Product of gene unknown	6.26	6.26	6.46E-17	SGD	639348
YCL031C	RRP7	involved in rRNA processing; Null mutant is inviable	5.85	5.85		0 SGD	634553
YDL242W	YDL242W		5.64	5.64	8.67E-31	SGD	635761
YGL058W	RAD6,UBC2	Involved in DNA repair and sporulation. Rad6p interacts with Ubr1 and Rad18p. mR	5.48	5.48	3.51E-29	SGD	635789
YNL332W	THI12	thiamine regulated gene, homologous to nmt1a in <i>Schizosaccharomyces pombe</i> , pl	5.42	5.42		0 SGD	635939
YBR088C	POL30	Accessory factor for DNA polymerase delta, mRNA increases in G1, peaks in S in n	5.37	5.37	1.89E-32	SGD	635087
YKR070W	YKR070W		5.28	5.28		0 SGD	637789
YNL072W	RNH35	RNase H(35), a 35 kDa ribonuclease H; Null mutant is viable but shows 75% reduct	5.28	5.28		0 SGD	635160
YPL253C	VIK1	vegetative interaction with Kar3p; Cik1p homolog; Null mutant is viable and resistan	5.28	5.28	1.51E-16	SGD	637177
YIL140W	AXL2,BUD10,SRO4	involved in polarity establishment/cellular polarization during budding; AXL2 can ser	5.27	5.27	6.82E-36	SGD	634224
YHR052W	CIC1,NSA3	Core interacting component 1; ribosome biogenesis; Null: lethal. Other phenotypes:	5.18	5.18		0 SGD	636690
YJR044C	YJR044C		5.17	5.17		0 SGD	638213
YNL008C	ASI3	Amino acid Sensor-Independent (ASI) genes encode membrane proteins Asi1p, Asi	5.17	5.17		0 SGD	638796
YBR098W	MMS4,SLX2	Product of gene unknown; null is synthetically lethal with sgs1 null	5.03	5.03	1.29E-14	SGD	636099

YEL070W	YEL070W		5.03	5.03	1.70E-30 SGD	637091
YFL058W	THI5	proposed biosynthetic enzyme involved in pyrimidine biosynthesis pathway above tRNA nucleotidyl transferase	5.01	5.01	0 SGD	633843
YHR204W	MNL1,HTM1	mannosidase like	4.96	4.96	0 SGD	634748
YDL027C	YDL027C		4.83	4.83	2.30E-31 SGD	636774
YGR208W	SER2	phosphoserine phosphatase; serine-requiring	4.75	4.75	4.92E-16 SGD	634544
YDR172W	SUP35,GST1,PNM2,SA1	altered form creates [PSI] prion; translation termination factor eRF3; accumulation of poly(A) tail	4.73	4.73	2.76E-09 SGD	634587
YGL230C	YGL230C		4.65	4.65	0 SGD	638238
YLR325C	RPL38	Homology to rat L38; ribosomal protein L38	4.65	4.65	1.73E-30 SGD	634209
YOR051C	YOR051C		4.63	4.63	0 SGD	636794
YJR158W	HXT16	hexose transporter; hexose permease	4.53	4.53	0 SGD	634051
YAL015C	NTG1,FUN33	endonuclease III like glycosylase involved in DNA repair; DNA glycosylase; Null mutant is viable	4.49	4.49	3.90E-40 SGD	636723
YBL035C	POL12	Required for DNA synthesis and correct progression through S phase, plays an essential role in DNA synthesis	4.45	4.45	0 SGD	634706
YJL220W	YJL220W		4.4	4.4	5.13E-15 SGD	634320
YKL015W	PUT3	Positive regulator of PUT (proline utilization) genes; zinc finger transcription factor of the POU domain class	4.4	4.4	3.48E-26 SGD	634698
YGL015C	YGL015C		4.39	4.39	1.99E-31 SGD	635725
YKR012C	YKR012C		4.38	4.38	0 SGD	633630
YNL233W	BNI4	bud neck involved; required to link Chs3p and Chs4p to the septins; Null mutant is viable	4.32	4.32	0 SGD	634651
YMR277W	FCP1	TFIIF interacting Component of CTD Phosphatase; TFIIF interacting component of the FCP1 complex	4.22	4.22	5.16E-26 SGD	638046
YDL245C	HXT15	High-affinity hexose transporter; hexose transporter	4.13	4.13	0 SGD	638016
YNL076W	MKS1,LYS80	Pleiotropic regulatory factor involved in Ras-CAMP and lysine biosynthetic pathway; involved in the regulation of the Lys80 gene	4.11	4.11	1.92E-28 SGD	639508
YML088W	UFO1	F-box protein; Null mutant is viable and UV sensitive	4.06	4.06	0 SGD	635478
YPR125W	YPR125W		4.05	4.05	0 SGD	636163
YDL028C	MPS1,RPK1	Required for spindle pole body duplication and a mitotic checkpoint function.; Null mutant is viable	4.04	4.04	0 SGD	636299
YER081W		catalyzes the first step in serine biosynthesis, isozyme of SER33; 3-phosphoglycerate kinase	4.02	4.02	0 SGD	639419
YJL030W	MAD2	spindle checkpoint complex subunit; Null mutant is viable, mitotic arrest deficient, se	4.02	4.02	0 SGD	639105
YCR019W	MAK32	Protein necessary for structural stability of L-A double-stranded RNA-containing par	3.99	3.99	1.98E-16 SGD	639330
YGR142W	BTN2	Gene/protein whose expression is elevated in a btn1 minus/Btn1p lacking yeast stra	3.97	3.97	0 SGD	638550
YPR174C	YPR174C		3.92	3.92	1.25E-30 SGD	634469
YGL029W	CGR1	coiled-coil growth-regulated; coiled-coil protein; Null mutant is inviable, CGR1 expre	3.9	3.9	1.47E-40 SGD	635658
YLR260W	LCB5	involved in sphingolipid biosynthesis; sphingoid long chain base (LCB) kinase; Null mutant is viable	3.88	3.88	2.64E-35 SGD	634571
YNR019W	ARE2,SAT1	Acyl-CoA cholesterol acyltransferase (sterol-ester synthetase); acyl-CoA cholestero	3.88	3.88	0 SGD	637179
YER185W	YER185W		3.84	3.84	4.90E-14 SGD	634549
YDR528W	HLR1	LRE1 homolog; Null mutant is viable.	3.8	3.8	3.28E-18 SGD	635263
YOL057W	YOL057W		3.79	3.79	4.62E-21 SGD	634140
YGR214W	RPS0A,NAB1,NAB1A,Y $\epsilon$	Homology to rat Sa; ribosomal protein S0A; Null mutant is viable, yst1 (rps0a) yst2 (rps0b)	3.75	3.75	0 SGD	637047
YDR151C	CTH1	cysteine-three histidine; CCCH zinc finger protein family that has two or more repeats	3.73	3.73	5.79E-43 SGD	638431
YOL065C	INP54	INositol polyphosphate 5-Phosphatase, fourth one identified, has homology to Type	3.71	3.71	6.72E-27 SGD	635217

YDR354W	TRP4	anthranilate phosphoribosyl transferase; tryptophan requiring	3.69	3.69	0 SGD	635173
YPL255W	BBP1	Involved in mitotic cell cycle and meiosis; Null mutant is inviable, cells depleted of B	3.66	3.66	0 SGD	635170
YDR257C	RMS1	Transcription regulator; null mutant is viable with no apparent defects	3.65	3.65	6.36E-20 SGD	637095
YDR042C	YDR042C		3.64	3.64	6.68E-22 SGD	637630
YLL042C	APG10	Involved in autophagy, protein-conjugating enzyme involved in the Apg12p-Apg5p c	3.64	3.64	3.53E-31 SGD	636477
YHR084W	STE12	Involved in pheromone and pseudohyphal growth signal transduction pathways; trar	3.63	3.63	0 SGD	637275
YPL251W	YPL251W		3.62	3.62	1.16E-06 SGD	634216
YLR217W	YLR217W		3.58	3.58	3.92E-44 SGD	634834
YLR076C	YLR076C		3.57	3.57	1.47E-29 SGD	634253
YCR105W	YCR105W	Alcohol dehydrogenase	3.53	3.53	0 SGD	639279
YDL241W	YDL241W		3.52	3.52	1.06E-09 SGD	637493
YCL044C	YCL044C		3.5	3.5	4.30E-37 SGD	637023
YNL065W	AQR1	A(acids, azoles) Q(quinidine, quinine) Resistance; multidrug resistance transporter;	3.49	3.49	0 SGD	639491
YMR067C	YMR067C		3.48	3.48	1.02E-29 SGD	638607
YGR211W	ZPR1	Involved in nucleolar function, similar to murine ZPR1 protein; zinc finger protein; Nu	3.47	3.47	4.01E-35 SGD	637101
YLR026C	SED5	Sed5p is a t-SNARE (soluble NSF attachment protein receptor) required in ER to Gr	3.46	3.46	6.43E-26 SGD	637799
YBR184W	MEL1	alpha-galactosidase; lack of melibiose fermentation	3.42	3.42	8.80E-35 SGD	635403
YKL043W	PHD1	protein similar to StuA of Aspergillus nidulans; transcription factor (putative); Null mu	3.42	3.42	0 SGD	637779
YER050C	RSM18	protein similar to bacterial ribosomal subunit S18; mitochondrial ribosome small sub	3.41	3.41	1.34E-16 SGD	635815
YNL108C	YNL108C		3.41	3.41	0 SGD	635879
YNL102W	POL1,CDC17,CRT5,HPf	Required for mitotic DNA synthesis, premeiotic DNA synthesis, recombination, and	3.4	3.4	9.16E-17 SGD	638965
YFL016C	MDJ1	involved in protection against heat-induced protein aggregation but not necessary fo	3.38	3.38	0 SGD	635329
YDR004W	RAD57	Required for X-ray damage repair, meiotic recombination, wild-type levels of sporula	3.36	3.36	4.90E-43 SGD	639440
YHR124W	NDT80	Meiosis-specific gene, mRNA is sporulation specific, required for exit from pachytene	3.35	3.35	3.92E-44 SGD	636907
YPL124W	NIP29,LPH3,SPC29	Nuclear import protein; spindle pole body associated protein; Null mutant is inviable	3.34	3.34	2.44E-11 SGD	638348
YNL123W	YNL123W		3.32	3.32	0 SGD	638836
YNL333W	SNZ2	Snooze: stationary phase-induced gene family; hypersporulation	3.3	3.3	0 SGD	638392
YPR048W	TAH18	Product of gene unknown; tah18-1 mutant is hypersensitive to hydroxyurea, campto	3.3	3.3	0 SGD	636911
YNR064C	YNR064C		3.27	3.27	1.14E-09 SGD	637708
YPL173W	MRPL40	Mitochondrial ribosomal protein MRPL40 (YmL40); ribosomal protein (YmL40)	3.27	3.27	0 SGD	634554
YML047W·ORF:YML047W-A		BioProcess=biological_process unknown MolFunction=molecular_function unknown	3.26	3.26	2.06E-15 SGD	970725
YPL107W	YPL107W		3.26	3.26	0 SGD	635886
YER044C-	MEI4	Functions in early recombination; 88 bp intron at 5' end spliced independently of ME	3.24	3.24	1.07E-21 SGD	633465
YNL231C	PDR16	involved in pleiotropic drug resistance by controlling lipids in various cellular compar	3.21	3.21	0 SGD	633870
YAL010C	MDM10,FUN37	Mitochondrial outer membrane protein involved in mitochondrial morphology and inf	3.2	3.2	5.44E-05 SGD	638631
YDL064W	UBC9	ubiquitin-conjugating enzyme; Null mutant is inviable	3.2	3.2	0 SGD	637637
YNL135C	FPR1,FKB1,RBP1	FK506 binding protein, proline rotamase, rapamycin-binding protein; peptidyl-prolyl	3.18	3.18	1.54E-14 SGD	633543

YOR266W	PNT1	Involved in targeting of proteins to the mitochondrial inner membrane, Pentamidine galactose-1-phosphate uridyl transferase; Null mutant is viable and cannot utilize ga	3.18	3.18	9.37E-14	SGD	635248
YBR018C	GAL7	Septin-related protein expressed during sporulation; Null mutant is viable	3.16	3.16	2.29E-13	SGD	633963
YDR218C	SPR28	Ribonucleotide reductase (ribonucleoside-diphosphate reductase) large subunit; ribo	3.16	3.16	1.42E-16	SGD	635247
YIL066C	RNR3,DIN1,RIR3	phosphoenolpyruvate carboxylkinase; Null mutant is viable.	3.13	3.13	0	SGD	638765
YKR097W	PCK1,JPM2,PPC1	proteasome component Y7	3.13	3.13	1.20E-09	SGD	636201
YML092C	PRE8	high-affinity hexose transporter; high affinity hexose transporter	3.12	3.12	8.94E-22	SGD	636209
YEL069C	HXT13	may be involved in glycolytic gene expression; 33 kDa, serine-rich protein, is a pote	3.11	3.11	2.92E-22	SGD	639251
YOR344C	TYE7,SGC1	similar to mammalian elongin A, interacts with elongin C; elongin A transcription elo	3.08	3.08	3.25E-11	SGD	637669
YLR064W	YLR064W	High level of sequence similarity to HXT1 and HXT9 hexose transporters; putative h	3.06	3.06	0	SGD	638166
YNL230C	ELA1	translation initiation factor eIF3 subunit; Null mutant is inviable.	3.06	3.06	2.91E-18	SGD	636264
YNL077W	YNL077W	may play a role in the oxidative stress response; flavohemoglobin; Null mutant is via	3.05	3.05	0	SGD	635207
YIL171W	HXT12	Spore-specific protein	3.02	3.02	0	SGD	636923
YOR361C	PRT1,CDC63,DNA26	Phospholipase B 2; lysophospholipase, phospholipase B; overexpression confers re	3.02	3.02	2.04E-23	SGD	633380
YGR234W	YHB1,YHB4	3.02	3.02	0	SGD	634186	
YBR148W	YSW1	3.02	3.02	0	SGD	634395	
YMR006C	PLB2	Protein with strong similarity to subtelomerically-encoded proteins such as Cos5p, Y	3.01	3.01	0	SGD	636036
YOL036W	YOL036W	Dispensable for mitosis, premeiotic DNA synthesis, spindle pole body duplication, m	3	3	9.14E-22	SGD	636717
YPL108W	YPL108W	2.99	2.99	1.15E-10	SGD	634936	
YNR075W	COS10	High-Temperature Lethal; Null mutant is viable but shows temperature-sensitive lett	2.98	2.98	2.21E-14	SGD	970797
YHL022C	SPO11	2.98	2.98	0	SGD	639178	
YGR265W	YGR265W	Nap1p Binding Protein; Null mutant is inviable	2.98	2.98	2.09E-16	SGD	634518
YCR020W	HTL1	2.97	2.97	0	SGD	633395	
YDR071C	YDR071C	2.97	2.97	0	SGD	636715	
YLR457C	NBP1	Irregular, involved in sister chromatid cohesion; cohesin complex subunit; Null muta	2.97	2.97	1.01E-33	SGD	635558
YAL068C	YAL068C	histone acetyltransferase; Null mutant is viable	2.97	2.97	1.06E-08	SGD	639338
YHR198C	YHR198C	BioProcess=biological_process unknown MolFunction=molecular_function unknown	2.96	2.96	0	SGD	970700
YIL026C	IRR1,SCC3	predicted membrane protein	2.95	2.95	2.67E-32	SGD	634207
YPL001W	HAT1	47 kDa type I transmembrane protein localized to the Golgi; Null mutant is viable	2.95	2.95	1.21E-25	SGD	637877
YBR255C-	ORF:YBR255C-A	2.94	2.94	0	SGD	639170	
YAR053W	YAR053W	osmoregulation; MAP kinase; Null mutant is viable and unable to grow in high osmo	2.94	2.94	1.90E-22	SGD	637884
YFL048C	EMP47	Emp24p/Erv25p related protein 2; p24 protein involved in membrane trafficking; null	2.93	2.93	6.98E-14	SGD	636524
YLR073C	YLR073C	SH3 domain	2.93	2.93	3.49E-20	SGD	639446
YLR113W	HOG1,SSK3	Processing of Precursors; RNase MRP subunit (putative), RNase P integral subunit	2.92	2.92	1.96E-23	SGD	634346
YAL007C	ERP2	23 kD U4/U6.U5 snRNP associated protein; RNA binding zinc finger protein (putativ	2.92	2.92	2.98E-17	SGD	639106
YHL002W	YHL002W						
YBR167C	POP7,RPP2						
YDL098C	SNU23						

YDR157W	YDR157W		2.92	2.92	3.18E-15 SGD	634938
YOR333C	YOR333C		2.92	2.92	7.29E-05 SGD	634950
YDR131C	YDR131C		2.91	2.91	2.36E-11 SGD	636213
YGR151C	YGR151C		2.91	2.91	9.53E-10 SGD	633578
YJL058C	YJL058C		2.91	2.91	1.88E-13 SGD	636204
YHR062C	RPP1	Ribonuclease P protein 1, required for processing of precursor tRNA and 35S precur	2.9	2.9	2.82E-07 SGD	633808
YKL082C	YKL082C		2.89	2.89	0 SGD	634005
YLR042C	YLR042C		2.89	2.89	8.13E-28 SGD	638274
YFR004W	RPN11,MPR1	Suppressor of mutant (ts on glycerol) tRNA gene deficient in the processing of its 3'	2.87	2.87	0 SGD	635144
YOR214C	YOR214C		2.86	2.86	1.95E-11 SGD	634425
YIL170W	HXT12	High level of sequence similarity to HXT1 and HXT9 hexose transporters; putative h	2.84	2.84	0 SGD	636160
YDR195W	REF2	RNA-binding protein involved in cleavage step of mRNA 3'-end formation, prior to pi	2.83	2.83	1.99E-11 SGD	637154
YMR309C	NIP1	Protein required for nuclear import with some similarity to Nsr1p, another protein inv	2.82	2.82	3.77E-13 SGD	634226
YDR449C	YDR449C		2.81	2.81	7.43E-08 SGD	639393
YGR143W	SKN1	Involved in (1->6)-beta-glucan biosynthesis; highly homologous to Kre6p, type II me	2.81	2.81	2.57E-17 SGD	638077
YKL115C	YKL115C		2.81	2.81	0 SGD	639000
YMR266W	RSN1	overexpression Rescues sro7/sop1 in NaCl; viable in both high and low salinity	2.81	2.81	1.67E-19 SGD	637315
YMR172C-	YMR172C-A		2.8	2.8	4.05E-15 SGD	635745
YOL124C	YOL124C		2.8	2.8	1.39E-12 SGD	636047
YFL017C	GNA1	involved in UDP-N-acetylglucosamine biosynthesis; glucosamine-phosphate N-acet	2.79	2.79	1.54E-30 SGD	638260
YNL183C	NPR1	protein kinase homolog; inactive ammonia-sensitive amino acid permeases	2.78	2.78	9.10E-36 SGD	636375
YLR168C	MSF1'	possibly involved in intramitochondrial sorting	2.77	2.77	6.24E-29 SGD	634446
YGL212W	VAM7,VPS43	Regulator of vacuolar morphogenesis; heptad repeat motif, hydrophilic protein; Null	2.76	2.76	6.11E-12 SGD	638455
YOR050C	YOR050C		2.76	2.76	6.26E-14 SGD	639024
YOR309C	YOR309C		2.76	2.76	1.02E-16 SGD	635731
YKR101W	SIR1	repressor of silent mating loci; silent mating loci repressor	2.75	2.75	1.19E-23 SGD	634630
YLL054C	YLL054C		2.75	2.75	0 SGD	634753
YCR104W	PAU3	member of the seripauperin protein/gene family (see Gene_class PAU)	2.74	2.74	4.77E-20 SGD	633615
YFL059W	SNZ3	Snooze: stationary phase-induced gene family; hypersporulation	2.74	2.74	6.43E-11 SGD	634491
YML093W	YML093W		2.74	2.74	6.98E-36 SGD	637279
YOL079W	YOL079W		2.74	2.74	1.82E-09 SGD	639092
YBL042C	FU1	uridine permease; Null mutant is viable, resistant to 5-fluorouridine and does not grc	2.73	2.73	5.12E-15 SGD	637143
YNL188W	KAR1	involved in spindle pole body duplication and karyogamy, interacts with Cdc31p, loc	2.73	2.73	1.05E-37 SGD	637852
YNL335W	YNL335W		2.71	2.71	7.48E-19 SGD	634381
YLR075W	RPL10,GRC5,QSR1	similar to members of the QM gene family, which is implicated in differentiation in ot	2.7	2.7	3.44E-13 SGD	638296
YJL197W	UBP12	ubiquitin carboxyl-terminal hydrolase	2.69	2.69	0 SGD	635588
YML077W	BET5	Bet5p/18kD component of TRAPP; TRAPP 18kDa component; Null mutant is inviab	2.69	2.69	3.26E-12 SGD	636467

YMR270C	RRN9	Upstream activation factor subunit; upstream activation factor subunit; Null mutant is viable	2.69	2.69	5.23E-27	SGD	639329
YEL072W	YEL072W	Glc7-interacting protein, shares homology with PIG2, contains conserved 25 residues	2.68	2.68	6.28E-19	SGD	636578
YER054C	GIP2	Protein required for sorting proteins to the vacuole; MVP1 was identified as a multicopy suppressor of yeast vacuole targeting mutants	2.68	2.68	0	SGD	637921
YMR004W	MVP1		2.68	2.68	2.39E-09	SGD	637128
YNR048W	YNR048W		2.67	2.67	3.13E-15	SGD	635228
YDR183W	PLP1	Phosducin-Like Protein; Null mutant is viable	2.66	2.66	5.03E-09	SGD	636497
YHL029C	YHL029C		2.65	2.65	2.96E-34	SGD	635458
YLR066W	SPC3	signal peptidase subunit; Null mutant is inviable.	2.65	2.65	6.42E-07	SGD	637549
YCR018C-	ORF:YCR018C-A	BioProcess=biological_process unknown MolFunction=molecular_function unknown	2.64	2.64	2.82E-14	SGD	970824
YJR064W	CCT5,TCP5	Required for assembly of microtubules and actin in vivo; chaperonin subunit epsilon	2.64	2.64	3.80E-14	SGD	634070
YLR037C	DAN2	Delayed anaerobic gene; putative cell wall protein; unknown	2.63	2.63	9.61E-32	SGD	635733
YLR151C	PCD1	peroxisomal nudix hydrolase active towards coenzyme A and its derivatives; coenzyme A ester hydrolase	2.62	2.62	3.69E-26	SGD	637733
YMR046W	ORF:YMR046W-A	BioProcess=biological_process unknown MolFunction=molecular_function unknown	2.62	2.62	2.36E-13	SGD	970695
YMR101C	SRT1	cis-prenyltransferase homologue; cis-prenyltransferase; Null mutant is viable, grows slowly	2.61	2.61	6.77E-17	SGD	639308
YAR008W	SEN34,FUN4	tRNA splicing endonuclease 34kDa subunit, homologous to the 42-kDa subunit, SEC34	2.6	2.6	2.40E-08	SGD	635903
YGL116W	CDC20,PAC5	Required for onset of anaphase; anaphase promoting complex (APC) subunit; Null mutant is viable, grows slowly	2.59	2.59	8.22E-18	SGD	638712
YOR208W	PTP2	protein tyrosine phosphatase; tyrosine phosphatase; Null mutant is viable, grows slowly	2.59	2.59	3.17E-12	SGD	634190
YGR224W	AZR1	MFS-MDR	2.58	2.58	2.07E-09	SGD	636921
YJR024C	YJR024C		2.58	2.58	3.24E-31	SGD	637650
YKL205W	LOS1	Nuclear pore protein involved in pre-tRNA splicing; Null mutant is viable but is defective in nuclear import	2.58	2.58	0	SGD	638890
YDR184C	ATC1	interacts with AIP3, localized to the nucleus	2.57	2.57	5.68E-26	SGD	635068
YGL188C	YGL188C		2.57	2.57	1.45E-08	SGD	634790
YGR291C	YGR291C		2.55	2.55	4.47E-15	SGD	634200
YKL042W	SPC42	involved in SPB duplication, may facilitate attachment of the SPB to the nuclear membrane	2.55	2.55	1.02E-27	SGD	633880
YKL069W	YKL069W		2.55	2.55	0	SGD	635799
YLR214W	FRE1	Ferric (and cupric) reductase; cupric reductase, ferric reductase; Null mutant is viable	2.55	2.55	3.62E-15	SGD	638732
YKL066W	YKL066W		2.54	2.54	4.11E-08	SGD	636377
YOR310C	NOP58	57 kDa nucleolar protein involved in the pre-rRNA processing steps that lead to formation of functional ribosomes	2.54	2.54	6.73E-19	SGD	636848
YPR202W	YPR202W		2.54	2.54	7.66E-07	SGD	635947
YBR042C	YBR042C	Probable membrane-bound small GTPase	2.53	2.53	0	SGD	638502
YNL129W	YNL129W		2.53	2.53	0	SGD	633799
YGL215W	CLG1	cyclin-like protein that interacts with Pho85p in affinity chromatography; Null mutant is viable	2.52	2.52	3.52E-09	SGD	639430
YKL083W	YKL083W		2.52	2.52	5.02E-18	SGD	633286
YGR249W	MGA1	Mga1p shows similarity to heat shock transcription factor; similar to heat shock transcription factor Hsf1p	2.51	2.51	1.91E-23	SGD	634040
YNL151C	RPC31,ACP2,RPC8	31-kDa subunit of RNA polymerase III (C), HMG1 like protein; HMG1-like protein, R	2.51	2.51	2.84E-12	SGD	635024
YNR062C	YNR062C		2.51	2.51	3.98E-07	SGD	638430
YOL068C	HST1	Homolog of SIR2; Overexpression restores transcriptional silencing in a sir2 mutant	2.51	2.51	8.47E-41	SGD	635314

YOR204W	DED1,SPP81	ATP-dependent RNA helicase of DEAD box family, suppressor of a pre-mRNA splicing factor	2.51	2.51	6.68E-05	SGD	636886
YBR100W	YBR100W		2.5	2.5	4.98E-14	SGD	635670
YER179W	DMC1,ISC2	Disp. for double strand breaks, synaptonemal complexes & gene conversion in reticular	2.5	2.5	1.17E-35	SGD	639345
YPL106C	SSE1,LPG3,MSI3	HSP70 family member, highly homologous to Ssa1p and Sse2p; HSP70 family, SS/	2.5	2.5	5.69E-16	SGD	636217
YPL239W	YAR1	YAR1 encodes a 200-amino-acid protein with two ANK repeat motifs and an acidic I	2.5	2.5	9.42E-10	SGD	633732
YBR243C	ALG7,TUR1	ER protein that transfers Glc-Nac-P from UDP-GlcNac to Dol-P; UDP-N-acetyl-glucosamine	2.49	2.49	3.18E-43	SGD	637875
YCL021W-ORF	:YCL021W-A	BioProcess=biological_process unknown MolFunction=molecular_function unknown	2.49	2.49	1.87E-18	SGD	970801
YER091C-	ORF:YER091C-A	BioProcess=biological_process unknown MolFunction=molecular_function unknown	2.49	2.49	1.65E-34	SGD	970807
YJL223C	PAU1	member of the seripauperin protein/gene family (see Gene_class PAU)	2.49	2.49	9.31E-08	SGD	639047
YOR304W	ISW2	has strong homology to Drosophila ISWI; ATPase component of a two subunit chromatin	2.48	2.48	2.48E-25	SGD	637390
YHR065C	RRP3	Required for maturation of the 35S primary transcript of pre-rRNA and is required for	2.46	2.46	9.01E-22	SGD	636144
YPL279C	YPL279C		2.46	2.46	1.80E-12	SGD	637773
YGR062C	COX18	cytochrome oxidase gene 18; Null mutant is viable, respiratory deficient due to inactivation	2.45	2.45	1.36E-07	SGD	636967
YKL106W	AAT1	aspartate aminotransferase, mitochondrial; aspartate aminotransferase; Null mutant	2.45	2.45	2.53E-17	SGD	639355
YKL223W	YKL223W		2.45	2.45	9.02E-25	SGD	638148
YBR172C	SMY2	partial suppressor of myo2-66; Null mutant is viable'	2.44	2.44	6.74E-34	SGD	638074
YDR002W	YRB1,CST20,HTN1,SFC	Yeast Ran Binder #1, suppressor of FUS1, homolog of mouse HTF9a and human RANBP1	2.44	2.44	5.88E-30	SGD	635847
YDR331W	GPI8	Protein involved in the attachment of glycosylphosphatidylinositol (GPI) anchors to proteins	2.44	2.44	5.57E-37	SGD	638566
YER149C	PEA2,DFG9,PPF2	Pea2p is localized with Spa2p to sites of polarized growth and is required for efficient	2.44	2.44	0	SGD	635265
YHR126C	YHR126C		2.44	2.44	4.61E-10	SGD	634328
YIR012W	SQT1	Involved in a late step of 60S ribosomal subunit assembly or modification, contains Ile100	2.44	2.44	5.90E-24	SGD	633938
YJL060W	YJL060W		2.44	2.44	0	SGD	633998
YJR030C	YJR030C		2.44	2.44	1.23E-14	SGD	634191
YKL044W	YKL044W		2.44	2.44	8.78E-14	SGD	636325
YLR020C	YLR020C		2.44	2.44	1.72E-10	SGD	639484
YLR067C	PET309	Involved in expression of mitochondrial COX1 by regulating translation of COX1 mRNA	2.44	2.44	3.72E-35	SGD	638809
YKL068W	NUP100,NSP100	Participates in nucleocytoplasmic transport, member of GLFG-containing family of nucleoporins	2.43	2.43	6.86E-33	SGD	634680
YOL122C	SMF1,SBS1	Isolated as high copy suppressor of a cdc1 mutation & involved in high affinity Mn <sup>2+</sup> binding	2.43	2.43	2.22E-10	SGD	637960
YJL090C	DPB11	Part of the DNA polymerase II complex, acts in a checkpoint pathway during S-phase	2.42	2.42	7.74E-20	SGD	638079
YLR372W	SUR4,ELO3,SRE1,VBM	Required for conversion of 24-carbon fatty acids to 26-carbon species; Null mutants	2.42	2.42	0	SGD	633875
YNL036W	NCE103	involved in secretion of proteins that lack classical secretory signal sequences; An unnamed protein product	2.42	2.42	0	SGD	634452
YJR070C	YJR070C		2.41	2.41	0	SGD	636646
YLR313C	SPH1	SPa2-Homolog, protein involved in shmoo formation and required for bipolar bud site	2.41	2.41	2.73E-16	SGD	636890
YMR325W	YMR325W		2.41	2.41	1.10E-15	SGD	633616
YNR034W	SOL1	Multicopy Suppressor Of los1; Null mutant is viable	2.41	2.41	3.30E-09	SGD	638480
YDR194C	MSS116	Mitochondrial RNA helicase of the DEAD box family; RNA helicase DEAD box; mss116	2.4	2.4	0	SGD	635479
YGL260W	YGL260W		2.4	2.4	2.59E-30	SGD	634788

YHL046C	YHL046C			2.4	2.4	1.25E-10 SGD	635674
YNR066C	YNR066C			2.4	2.4	0 SGD	633950
YPL212C	PUS1			2.4	2.4	0 SGD	634064
YDR213W	UPC2,MOX4	Involved in tRNA biogenesis; tRNA pseudouridine synthase; pus1 los1 double mutant involved in sterol uptake; zinc finger transcription factor of the Zn(2)-Cys(6) binuclear cluster.		2.39	2.39	3.10E-11 SGD	638813
YFR043C	YFR043C			2.39	2.39	5.83E-07 SGD	635095
YGL244W	RTF1,CSL3	Directly or indirectly regulates the DNA-binding properties of Spt15p, the TATA box-associated transcription factor.		2.39	2.39	4.69E-17 SGD	637917
YGR039W	YGR039W			2.39	2.39	3.80E-32 SGD	634841
YJR072C	YJR072C			2.39	2.39	1.48E-09 SGD	636748
YLR223C	IFH1	Interacts with fork head protein. Protein controlling pre-rRNA processing machinery.		2.39	2.39	2.89E-26 SGD	637340
YNL061W	NOP2,YNA1	May participate in nucleolar function during the transition from stationary phase to regulation of ribosome biogenesis.		2.39	2.39	3.06E-14 SGD	636935
YCR102W	ORF:YCR102W-A	BioProcess=biological_process unknown MolFunction=molecular_function unknown		2.37	2.37	0 SGD	970817
YDL185C-	ORF:YDL185C-A	BioProcess=biological_process unknown MolFunction=molecular_function unknown		2.37	2.37	5.48E-05 SGD	970703
YGL214W	YGL214W			2.37	2.37	1.39E-20 SGD	636535
YIL174W	YIL174W			2.37	2.37	1.41E-26 SGD	638103
YJL043W	YJL043W			2.37	2.37	2.20E-17 SGD	634432
YLL046C	RNP1	ribonucleoprotein 1; RNA binding protein (putative); Null mutant is viable		2.36	2.36	1.86E-18 SGD	635885
YDR488C	PAC11	Protein required in the absence of Cin8p; Null mutant is viable.		2.35	2.35	1.06E-17 SGD	636904
YNL064C	YDJ1,MAS5	yeast dnaJ homolog (nuclear envelope protein), heat shock protein; heat shock protein		2.35	2.35	2.24E-08 SGD	638551
YNL211C	YNL211C			2.35	2.35	3.37E-11 SGD	634218
YNR051C	BRE5	protein of unknown function; null mutant is sensitive to brefeldin A		2.35	2.35	5.51E-16 SGD	636861
YPL237W	SUI3	beta subunit of translation initiation factor eIF-2; translation initiation factor eIF-2 beta		2.35	2.35	2.26E-14 SGD	639203
YDL167C	NRP1	asparagine-rich protein		2.34	2.34	6.45E-22 SGD	638049
YJL218W	YJL218W			2.34	2.34	5.21E-22 SGD	637619
YKL055C	OAR1	3-oxoacyl-[acyl-carrier-protein] reductase; Null mutant is viable, respiratory deficient		2.34	2.34	7.51E-12 SGD	635938
YPR136C	FYV15	Function required for Yeast Viability on toxin exposure; Null mutant is viable but a hybrid.		2.34	2.34	3.17E-17 SGD	637480
YBL109W	YBL109W			2.33	2.33	1.48E-12 SGD	633297
YDR426C	YDR426C			2.33	2.33	5.01E-08 SGD	633365
YKR011C	TOS5	Hypothetical ORF		2.33	2.33	1.28E-06 SGD	633902
YLL044W	YLL044W			2.33	2.33	1.68E-04 SGD	638237
YOR143C	THI80	Thiamin pyrophosphokinase; thiamin pyrophosphokinase		2.33	2.33	4.73E-35 SGD	636701
YNR020C	YNR020C			2.32	2.32	2.11E-07 SGD	639231
YDL143W	CCT4,TCP4	cytoplasmic chaperonin subunit required for actin cytoskeleton assembly or function		2.31	2.31	1.09E-19 SGD	636854
YDL202W	MRPL11	Mitochondrial ribosomal protein MRPL11 (YmL11); ribosomal protein (YmL11); Null		2.31	2.31	1.07E-13 SGD	633716
YGL148W	ARO2	Chorismate synthase; chorismate synthase; aromatic amino acid requiring, lack of p		2.31	2.31	2.03E-40 SGD	638516
YGL261C	YGL261C			2.31	2.31	1.10E-15 SGD	637531
YJL209W	CBP1	Protein required for COB mRNA stability or 5' processing; Null mutant is viable, una		2.31	2.31	1.86E-13 SGD	637238
YMR317W	YMR317W			2.31	2.31	2.57E-37 SGD	638871

YOL148C	SPT20,ADA5	Transcription factor; histone acetyltransferase SAGA complex member, transcriptional regulator	2.31	2.31	0 SGD	637195
YBL077W	YBL077W		2.3	2.3	1.37E-14 SGD	634945
YDR153C	YDR153C		2.3	2.3	7.31E-10 SGD	635254
YDR503C	LPP1	Lipid phosphate phosphatase; lipid phosphate phosphatase	2.3	2.3	3.23E-16 SGD	639211
YKL116C	PRR1	protein kinase	2.3	2.3	2.45E-07 SGD	638617
YDR173C	ARG82,ARGR3,IPK2	Regulator of arginine-responsive genes with ARG80 and ARG81; dual specificity inc	2.29	2.29	6.52E-17 SGD	637771
YDR227W	SIR4,ASD1,STE9,UTH2	regulator of silencing at HML, HMR, and telomeres; silencing regulator at HML, HMI	2.29	2.29	7.14E-06 SGD	638953
YER006W	NUG1	NUclear GTPase; Nuclear GTPase involved in Ribosome biogenesis; Null: dead.	2.29	2.29	0 SGD	635324
YFR032C	YFR032C		2.29	2.29	1.12E-06 SGD	633812
YGL217C	YGL217C		2.29	2.29	1.81E-25 SGD	639026
YJL049W	YJL049W		2.29	2.29	2.73E-06 SGD	636114
YJR091C	JSN1,PUF1	benomyl dependent tubulin mutant; Overexpression suppresses some tub2 alleles ↳	2.29	2.29	7.14E-19 SGD	635599
YDR034C- ORF:YDR034C-A		BioProcess=biological_process unknown MolFunction=molecular_function unknown	2.28	2.28	3.21E-10 SGD	970721
YFL034C-/RPL22B		Homology to rat L22; ribosomal protein L22B (L1c) (rp4) (YL31)	2.28	2.28	1.69E-06 SGD	970761
YGL038C	OCH1,NGD29	membrane-bound alpha-1,6-mannosyltransferase; alpha-1,6-mannosyltransferase;	2.28	2.28	7.10E-27 SGD	637072
YJR042W	NUP85,RAT9	Protein in nuclear pore complex, may function in nuclear envelope integrity, may als	2.28	2.28	8.83E-41 SGD	633289
YML043C	RRN11	rDNA transcription factor CF component, which also contains Rrn6p and Rrn7p, whi	2.28	2.28	4.19E-28 SGD	637130
YOR267C	YOR267C		2.28	2.28	2.96E-11 SGD	636265
YPL261C	YPL261C		2.28	2.28	1.65E-27 SGD	634293
YPR137W	RRP9	Rrp9p is an ortholog of the human U3-55k protein, the human cDNA partially compl	2.28	2.28	2.38E-22 SGD	637998
YBR180W	DTR1	dityrosine transporter MFS-MDR; Null: Null mutant is viable, bisformyl dityrosine acc	2.27	2.27	2.25E-19 SGD	634048
YFR003C	YFR003C		2.27	2.27	9.42E-36 SGD	634999
YOL035C	YOL035C		2.27	2.27	3.37E-10 SGD	638194
YOR390W	YOR390W		2.27	2.27	1.98E-22 SGD	639322
YPL282C	YPL282C		2.27	2.27	7.40E-20 SGD	634992
YHR123W	EPT1	sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase; Null mutant is v	2.26	2.26	2.01E-27 SGD	635281
YHR143W	RPC10,RPB12	subunit of RNA polymerase II; RNA polymerase II subunit; Null mutant is inviable	2.26	2.26	2.29E-27 SGD	633413
YIL176C	YIL176C		2.26	2.26	5.01E-40 SGD	635757
YJL148W	RPA34	RNA polymerase I subunit, not shared (A34.5); Null mutant is viable but its RNA pol	2.26	2.26	6.15E-08 SGD	636634
YLR216C	CPR6	a cyclophilin related to the mammalian CyP-40, physically interacts with RPD3 gene	2.26	2.26	1.15E-05 SGD	637775
YNL319W	YNL319W		2.26	2.26	3.18E-09 SGD	636378
YOL032W	YOL032W		2.25	2.25	8.16E-10 SGD	637664
YAL009W	SPO7	dispensable for mitosis, but required for a normal mutation rate, required for premei	2.24	2.24	2.42E-14 SGD	638360
YAL014C	YAL014C		2.24	2.24	0 SGD	639165
YBR029C	CDS1,CDG1	CDP-diacylglycerol synthase, CTP-phosphatidic acid cytidylyltransferase, CDP-digly	2.23	2.23	2.48E-11 SGD	633973
YDR333C	YDR333C		2.23	2.23	1.16E-08 SGD	634153
YFL064C	YFL064C		2.23	2.23	1.55E-16 SGD	637572

YML046W	PRP39	May function to facilitate or stabilize the interaction between U1 snRNP and the 5' splice site of a delayed anaerobic gene; putative cell wall protein; unknown	2.23	2.23	0 SGD	638703
YBR301W	DAN3		2.22	2.22	1.45E-33 SGD	637530
YGL057C	YGL057C		2.22	2.22	7.43E-12 SGD	637694
YGR215W	RSM27	mitochondrial ribosome small subunit component	2.22	2.22	1.55E-05 SGD	636407
YNL184C	YNL184C		2.22	2.22	9.61E-07 SGD	634265
YOL115W	TRF4	TRF5 homolog, Involved in mitotic chromosome condensation, associates with Smc1	2.22	2.22	1.45E-11 SGD	638008
YDL217C	TIM22	Mitochondrial inner membrane protein involved in import of proteins of the ADP/ATP	2.21	2.21	1.53E-06 SGD	637592
YER113C	YER113C		2.21	2.21	0 SGD	638052
YHR184W	SSP1,SPO3	Involved in the control of meiotic nuclear divisions & spore formation, dispensable for vegetative growth	2.21	2.21	5.50E-05 SGD	634049
YIR041W	YIR041W		2.21	2.21	8.19E-09 SGD	637524
YGR113W	DAM1	Duo1 And Mps1 interacting. Localized to intranuclear spindles and spindle pole bodies	2.2	2.2	2.53E-24 SGD	635976
YHR105W	YHR105W		2.2	2.2	4.25E-05 SGD	635045
YKL011C	CCE1,mgt1	cruciform cutting endonuclease; Null mutant is viable, exhibits a higher than normal	2.2	2.2	2.49E-25 SGD	637772
YML041C	YML041C		2.2	2.2	1.74E-11 SGD	635953
YML080W	DUS1	tRNA dihydrouridine synthase	2.2	2.2	1.17E-24 SGD	637036
YMR003W	YMR003W		2.2	2.2	6.95E-07 SGD	639103
YNL174W	YNL174W		2.2	2.2	2.87E-28 SGD	633691
YNL232W	CSL4,SKI4	Represses the replication of double-stranded RNA viruses, protecting the host from	2.2	2.2	2.26E-34 SGD	637690
YBR012C	YBR012C		2.19	2.19	2.88E-39 SGD	634949
YBR074W	YBR074W	Homolog to aminopeptidase Y ( <i>S. cerevisiae</i> )	2.19	2.19	5.92E-12 SGD	637041
YIL030C	SSM4	Protein involved in mRNA turnover; integral membrane protein; Null mutant is viable	2.19	2.19	1.01E-11 SGD	633485
YPL244C	HUT1	similar to UDP-galactose transporter	2.19	2.19	0 SGD	635904
YPL252C	YAH1	Yeast Adrenodoxin Homologue 1, This protein is targeted to the mitochondrial matrix	2.19	2.19	1.45E-13 SGD	637516
YHR217C	YHR217C		2.18	2.18	3.05E-08 SGD	633309
YJL097W	YJL097W		2.18	2.18	1.31E-32 SGD	634387
YBL108C-/ORF:YBL108C-A		BioProcess=biological_process unknown MolFunction=molecular_function unknown	2.17	2.17	4.02E-32 SGD	970780
YBR135W	CKS1	subunit of the Cdc28 protein kinase; Cdc28 protein kinase subunit; Null mutant is in	2.17	2.17	0 SGD	638267
YKL224C	YKL224C		2.17	2.17	2.10E-44 SGD	635735
YML009C-/ORF:YML009C-A		BioProcess=biological_process unknown MolFunction=molecular_function unknown	2.17	2.17	9.69E-19 SGD	970811
YDR189W	SLY1	Hydrophilic suppressor of ypt1 involved in vesicle trafficking between ER and Golgi;	2.16	2.16	1.37E-23 SGD	637250
YIR040C	YIR040C		2.16	2.16	2.31E-32 SGD	634828
YKR105C	YKR105C		2.16	2.16	1.36E-04 SGD	637993
YLR381W	YLR381W		2.16	2.16	4.39E-18 SGD	634715
YDR302W	GPI11	Glycosylphosphatidylinositol (GPI) assembly	2.15	2.15	6.70E-23 SGD	634964
YGR164W	YGR164W		2.15	2.15	1.46E-19 SGD	635656
YGR294W	YGR294W		2.15	2.15	1.91E-21 SGD	633655
YHL005C	YHL005C		2.15	2.15	2.70E-19 SGD	638984

YAL069W	YAL069W		2.14	2.14	0 SGD	633339
YDR542W	YDR542W		2.14	2.14	0 SGD	633654
YNL012W	SPO1	dispensable for mitosis, premeiotic DNA synthesis, synaptonemal complexes, and recombination	2.14	2.14	8.71E-26 SGD	636903
YOR020C	HSP10,CPN10	Homolog of <i>E. coli</i> GroES protein, regulates Hsp60, the yeast mitochondrial chaperone	2.14	2.14	2.06E-11 SGD	636432
YJR157W	YJR157W		2.13	2.13	3.54E-35 SGD	637532
YJL028W	YJL028W		2.12	2.12	6.75E-30 SGD	637447
YKL114C	APN1	major apurinic/apyrimidinic endonuclease/3'-repair diesterase; hypersensitive to both growth inhibitor; Inhibits growth when overexpressed	2.12	2.12	1.31E-20 SGD	636009
YLL065W	GIN11		2.12	2.12	2.26E-19 SGD	639022
YLR009W	RLP24	Ribosomal Like Protein 24; part of a pre-60S complex; Null: lethal. Other phenotype	2.12	2.12	1.35E-25 SGD	637600
YNL166C	BNI5	bud neck involved, localizes to mother-bud neck in a septin-dependent manner, bni5	2.12	2.12	5.85E-19 SGD	637860
YPL260W	YPL260W		2.12	2.12	6.71E-09 SGD	636125
YER056C-	RPL34A	Homology to rat L34; ribosomal protein L34A	2.11	2.11	4.31E-12 SGD	633385
YGR166W	KRE11,TRS65	Involved in biosynthetic pathway for cell wall beta-glucans; Null mutant is viable, kills	2.11	2.11	1.19E-26 SGD	639472
YKL225W	YKL225W		2.11	2.11	1.73E-39 SGD	639039
YLL034C	YLL034C		2.11	2.11	1.14E-08 SGD	638771
YLR212C	TUB4	spindle pole body component that organizes both cytoplasmic and nuclear microtubules	2.11	2.11	3.61E-10 SGD	637893
YLR424W	YLR424W		2.11	2.11	2.60E-23 SGD	636228
YLR437C	YLR437C		2.11	2.11	3.46E-07 SGD	634922
YAL004W	YAL004W		2.1	2.1	4.16E-14 SGD	634373
YAL034W- MTW1		Mis TWelve like (a <i>Schizosaccharomyces pombe</i> kinetochore protein); Null mutant is viable	2.1	2.1	8.16E-07 SGD	639268
YBR049C	REB1,GRF2	DNA binding protein which binds sites found in genes transcribed by both RNA polymerases	2.1	2.1	4.92E-14 SGD	638126
YER103W	SSA4	member of 70 kDa heat shock protein family; HSP70 family; Null mutant is viable, sensitive to heat	2.1	2.1	3.63E-05 SGD	635424
YFL063W	YFL063W		2.1	2.1	4.22E-20 SGD	638282
YOR394W	YOR394W		2.1	2.1	7.40E-17 SGD	638272
YBR166C	TYR1	Step of tyrosine biosynthesis pathway; prephenate dehydrogenase (NADP+); tyrosine kinase	2.09	2.09	4.27E-08 SGD	634043
YBR174C	YBR174C		2.09	2.09	4.86E-39 SGD	638142
YCL024W	KCC4	involved in septin organization; <i>S. pombe</i> Nim1 homolog, protein kinase; Null mutant is viable	2.09	2.09	4.78E-11 SGD	636320
YCL037C	SRO9	Associates with translating ribosomes, may function in the cytoplasm to modulate mRNA processing	2.09	2.09	2.23E-11 SGD	636087
YDR180W	SCC2	Sister chromatid cohesion protein	2.09	2.09	2.22E-06 SGD	635636
YDR366C	YDR366C		2.09	2.09	7.98E-14 SGD	638236
YKL198C	PTK1,KKT8,STK1	Putative serine/threonine protein kinase; Mutant shows decrease in total polyamine levels	2.09	2.09	0 SGD	634015
YOR233W	KIN4,KIN31	protein kinase; Null mutant is viable	2.09	2.09	1.46E-13 SGD	636373
YPL246C	YPL246C		2.09	2.09	4.53E-41 SGD	636547
YER037W	PHM8	involved in phosphate metabolism	2.08	2.08	2.57E-07 SGD	634532
YGR217W	CCH1	calcium channel; calcium channel (putative); Null mutant is viable, exhibits reduced sensitivity to calcium	2.08	2.08	4.82E-25 SGD	637417
YLL064C	YLL064C		2.08	2.08	2.27E-08 SGD	633565
YLR222C	YLR222C		2.08	2.08	1.07E-12 SGD	634225

YBR070C	YBR070C	involved in osmotolerance	2.07	2.07	1.45E-17 SGD	636630
YFL012W	YFL012W		2.07	2.07	1.85E-26 SGD	634355
YJL031C	BET4	catalyzes prenylation of Ypt1p (as a subunit of PGGTase-II); geranylgeranyltransfer	2.07	2.07	5.00E-28 SGD	639267
YNR076W	PAU6	member of the seripauperin protein/gene family	2.07	2.07	5.87E-29 SGD	639048
YAL037W	YAL037W		2.06	2.06	2.66E-44 SGD	637642
YGL185C	YGL185C		2.06	2.06	2.00E-05 SGD	638530
YOL094C	RFC4	RFC is a DNA binding protein and ATPase that acts as a processivity factor for DNA/	2.06	2.06	0 SGD	636977
YGL078C	DBP3	ATP-dependent RNA helicase CA3 of the DEAD/DEAH box family; ATP dependent	2.05	2.05	7.45E-18 SGD	638672
YHR175W	CTR2	Putative low-affinity copper transport protein; ctr2 mutants display a high level of res	2.05	2.05	1.42E-29 SGD	635804
YNL313C	YNL313C		2.05	2.05	1.31E-12 SGD	635482
YOR359W	YOR359W		2.05	2.05	2.10E-07 SGD	638657
YDL227C	HO	Homothallic switching; homothallic switching endonuclease; Null mutant is viable an	2.04	2.04	7.82E-06 SGD	634102
YJR023C	YJR023C		2.04	2.04	7.13E-05 SGD	634369
YNL073W	MSK1	mitochondrial lysine-tRNA synthetase; lysine-tRNA ligase; An uncharacterized allele	2.04	2.04	2.07E-17 SGD	637996
YNL185C	MRPL19	mitochondrial ribosomal protein of the large subunit; ribosomal protein large subunit	2.04	2.04	5.98E-20 SGD	636538
YBR075W	YBR075W		2.03	2.03	1.33E-07 SGD	636106
YCR072C	YCR072C	regulatory protein	2.03	2.03	1.45E-07 SGD	635326
YDR278C	YDR278C		2.03	2.03	7.73E-10 SGD	638141
YHR108W	GGA2	Golgi-localized, gamma-adaptin homology, Arf-binding; ARF-binding protein	2.03	2.03	7.95E-21 SGD	636241
YGR263C	YGR263C		2.02	2.02	1.29E-14 SGD	637051
YNR024W	YNR024W		2.02	2.02	6.60E-05 SGD	639128
YPR167C	MET16	3'phosphoadenylylsulfate reductase; Null mutant is viable, and is a methionine auxc	2.02	2.02	5.30E-16 SGD	634497
YIR020W-I	ORF:YIR020W-B	BioProcess=biological_process unknown MolFunction=molecular_function unknown	2.01	2.01	4.22E-31 SGD	970760
YJL111W	CCT7,TCP7	Required for assembly of microtubules and actin in vivo; chaperonin containing T-cc	2.01	2.01	1.09E-37 SGD	636141
YML037C	YML037C		2.01	2.01	1.20E-08 SGD	633848
YPL273W	SAM4	AdoMet-homocysteine methyltransferase; Slow growth on S-adenosylmethionine us	2.01	2.01	4.41E-41 SGD	635127
YNL292W	PUS4	catalyzes formation of Ps155 (modified uridine) in mitochondrial and cytoplasmic tRN	2	2	1.53E-07 SGD	633356
YOL104C	NDJ1,TAM1	Involved in meiotic chromosome segregation, may stabilize homologous DNA interac	2	2	1.16E-08 SGD	633854
YDL115C	IWR1	Hypothetical ORF	0.5	-2	2.80E-45 SGD	639145
YGR172C	YIP1	Golgi integral membrane protein, binds to the transport GTPases Ypt1p and Ypt31p	0.5	-2	6.57E-08 SGD	633793
YBR149W	ARA1	D-arabinose dehydrogenase; Null mutant is viable but cannot produce D-arabinono-	0.5	-2.01	9.12E-16 SGD	637729
YKL176C	LST4	involved in regulated secretion/recycling of nitrogen regulated permeases; very low	0.5	-2.01	3.65E-12 SGD	634808
YMR235C	RNA1	Protein involved in RNA processing and export from nucleus; GTPase activating prc	0.5	-2.01	2.24E-13 SGD	635272
YNL163C	RIA1	Ribosome Assembly; Null: quasi essential. Other phenotypes: Depletion of Ria1p le	0.5	-2.01	5.27E-10 SGD	638928
YNL288W	CAF40	Hypothetical ORF; Null mutant is viable	0.5	-2.01	1.50E-05 SGD	639339
YOR371C	KRH2	Kelch Repeat Homologue. Homologue of KRH1. Does not act in the cAMP-PKA pat	0.5	-2.01	3.18E-06 SGD	638776
YLR178C	TFS1,DKA1	(putative) lipid binding protein, suppressor of a cdc25 mutation; lipid binding protein (	0.49	-2.02	5.27E-25 SGD	636587

YML001W	YPT7,AST4,VAM4	Gtp-binding protein of the rab family, required for homotypic fusion event in vacuole	0.5	-2.02	6.53E-08 SGD	635841
YMR258C	YMR258C		0.49	-2.02	1.14E-09 SGD	637918
YPL235W	RVB2,TIH2,TIP49B	RUVB-like protein, TIP49b Homologue; transcriptional regulator; Null mutant is inviable	0.49	-2.02	1.95E-25 SGD	636100
YFR044C	YFR044C		0.49	-2.03	6.28E-06 SGD	635311
YLR294C	YLR294C		0.49	-2.03	2.48E-05 SGD	636426
YOR186W	YOR186W		0.49	-2.03	1.06E-06 SGD	636380
YDL067C	COX9	Plays role in cytochrome c oxidase holoenzyme assembly or stability; cytochrome c oxidizes ubiquinol at center P in the protonmotive Q cycle mechanism, transferring electrons	0.49	-2.04	9.97E-21 SGD	636365
YEL024W	RIP1	Involved in myo-inositol biosynthesis, implicated as the sensor of unfolded proteins	0.49	-2.04	3.56E-43 SGD	634389
YHR079C	IRE1,ERN1	negative regulator of cts1 expression; Null mutant is viable and suppresses the failu	0.49	-2.04	2.71E-06 SGD	637337
YPL024W	NCE4	activation mediator subcomplex of RNA polymerase I holoenzyme; Null mutant is viable	0.49	-2.05	6.29E-26 SGD	638898
YCR081W	SRB8,GIG1,NUT6,SSN5	Required for entry into stationary phase, heat shock-resistance, a mating-type funct	0.49	-2.05	3.85E-06 SGD	637287
YDL040C	NAT1,AAA1	BioProcess=biological_process unknown MolFunction=molecular_function unknown	0.49	-2.05	9.70E-27 SGD	970769
YDR381C- ORF:YDR381C-A		alpha subunit of pyruvate dehydrogenase (E1 alpha); pyruvate dehydrogenase alph	0.49	-2.05	1.16E-21 SGD	633945
YER178W	PDA1		0.49	-2.05	0 SGD	638054
YGR266W	YGR266W	YHR077C NMD2,IFS1,SUA1,UPF2 Protein involved in decay of mRNA containing nonsense codons; Null mutant is viable	0.49	-2.05	4.86E-13 SGD	633435
YLR305C	STT4,BLM1	functions in the PKC1 protein kinase pathway, in a pathway with STT1 and MSS4; p	0.49	-2.05	1.10E-26 SGD	638974
YMR247C	YMR247C		0.49	-2.05	0 SGD	635634
YNL097C	PHO23	Involved in expression of PHO5; Null mutant is viable but shows constitutive PHO5	0.49	-2.05	2.26E-13 SGD	638427
YNL224C	YNL224C		0.49	-2.05	1.43E-19 SGD	634820
YOL020W	TAT2,LTG3,SAB2,SCM2	YOL020W TAT2,LTG3,SAB2,SCM2 Tryptophan permease, high affinity; tryptophan permease, high affinity; suppressor of	0.49	-2.05	4.44E-09 SGD	637988
YDL125C	HNT1	Hnt homolog, member of the histidine triad superfamily of nucleotide-binding protein	0.48	-2.06	2.69E-39 SGD	639176
YDR479C	YDR479C		0.49	-2.06	5.05E-34 SGD	634074
YOR213C	SAS5	Involved in silencing at telomeres, HML and HMR; Null mutant is viable	0.48	-2.06	3.99E-43 SGD	635870
YBR105C	VID24	also involved in vacuolar protein targeting; peripheral vesicle membrane protein; Nu	0.48	-2.07	2.95E-36 SGD	633912
YDL231C	BRE4	contains several putative trans-membrane domains; null mutant is sensitive to brefeldin A	0.48	-2.07	1.51E-24 SGD	633495
YLR278C	YLR278C		0.48	-2.07	5.68E-10 SGD	633513
YOR040W	GLO4	Mitochondrial glyoxylase-II; glyoxylase-II; Null mutant is viable, but shows increased sensitivity to	0.48	-2.07	4.69E-08 SGD	639187
YAR035W	YAT1	Outer carnitine acetyltransferase, mitochondrial; carnitine acetyltransferase; Null mutant is	0.48	-2.08	5.90E-06 SGD	635471
YDR166C	SEC5	107 kDa component of the Exocyst complex, required for exocytosis.; exocyst complex	0.48	-2.08	1.62E-10 SGD	634644
YHL047C	TAF1,ARN2	Siderophore transporter for triacytlyfusarinine C; triacytlyfusarinine C transporter; YIL107C	0.48	-2.08	2.68E-39 SGD	637186
YKL023W	YKL023W		0.48	-2.08	3.64E-16 SGD	637718
YMR020W	FMS1	Multicopy suppressor of fenpropimorph resistance (fen2 mutant), shows similarity to	0.48	-2.08	1.22E-09 SGD	638680
YNL032W	SIW14	Synthetic interaction with Whi2; tyrosine phosphatase; Null mutant fails to show cell	0.48	-2.08	2.38E-08 SGD	633834
YBR221C	PDB1	beta subunit of pyruvate dehydrogenase (E1 beta); pyruvate dehydrogenase beta subunit	0.48	-2.09	1.72E-16 SGD	636041
YNL294C	RIM21,PAL3	Regulator of IME2; Unknown function; Null: Affected in sporulation and invasive growth	0.48	-2.09	3.67E-14 SGD	635349
YNL310C	YNL310C		0.48	-2.09	2.21E-10 SGD	639112

YCR044C	PER1	Protein Processing in the ER	0.48	-2.1	3.12E-08 SGD	639281
YDL223C	YDL223C		0.48	-2.1	5.81E-29 SGD	637360
YEL066W	HPA3	Histone and other Protein Acetyltransferase, Has sequence homology to known HATs; GAP for Ypt protein; GTPase-activating protein; Null: viable	0.48	-2.1	5.57E-05 SGD	635784
YFL027C	GYP8	Null mutant is viable and shows transcription-associated hyper-recombination and titration	0.48	-2.1	7.92E-18 SGD	636872
YOL072W	THP1	Product of gene unknown	0.47	-2.11	0 SGD	639444
YJR127C	ZMS1		0.47	-2.11	2.61E-04 SGD	637471
YMR226C	YMR226C		0.47	-2.11	8.03E-15 SGD	639151
YBL095W	YBL095W		0.47	-2.12	3.30E-17 SGD	633710
YBR193C	MED8	Member of RNA Polymerase II transcriptional regulation mediator; RNA polymerase II subunit	0.47	-2.12	4.02E-11 SGD	634450
YBR206W	YBR206W		0.47	-2.12	1.28E-19 SGD	638137
YCR036W	RBK1	ribokinase	0.47	-2.12	6.11E-30 SGD	633806
YDR483W	KRE2,MNT1	N-glycosylation; alpha-1,2-mannosyltransferase; have altered N-linked glycosylation	0.47	-2.12	1.15E-25 SGD	637879
YEL034W	HYP2,TIF51A	Translation initiation factor eIF-5A; translation initiation factor eIF-5A; Null mutant is	0.47	-2.12	1.48E-10 SGD	638261
YIL091C	YIL091C		0.47	-2.12	3.41E-11 SGD	636225
YIL150C	DNA43,MCM10	Protein required for S-phase (DNA synthesis) initiation or completion; Null mutant is	0.47	-2.12	2.14E-18 SGD	636248
YKL077W	YKL077W		0.47	-2.12	2.05E-26 SGD	636979
YKR091W	SRL3	Suppressor of Rad53 null Lethality	0.47	-2.12	1.86E-04 SGD	638266
YMR009W	YMR009W		0.47	-2.12	5.80E-18 SGD	637553
YMR218C	TRS130	targeting complex (TRAPP) component involved in ER to Golgi membrane traffic, 1: sterol C-14 reductase; Null mutant appears to be inviable in some genetic background	0.47	-2.12	1.44E-10 SGD	633497
YNL280C	ERG24	Required for mother cell-specific HO expression; Null mutant is viable	0.47	-2.12	0 SGD	633372
YOR035C	SHE4		0.47	-2.12	1.50E-05 SGD	634800
YPR098C	YPR098C		0.47	-2.12	6.04E-24 SGD	638169
YBR054W	YRO2	Homolog to HSP30 heat shock protein Yro1p	0.47	-2.13	5.35E-14 SGD	639307
YDL215C	GDH2	NAD-dependent glutamate dehydrogenase; Null mutant is viable, grows very poorly	0.47	-2.13	0 SGD	638891
YGL140C	YGL140C		0.47	-2.13	3.11E-11 SGD	637346
YLR038C	COX12	essential during assembly for full cytochrome c oxidase activity; cytochrome c oxidase subunit II	0.47	-2.13	0 SGD	638197
YML002W	YML002W		0.47	-2.13	4.87E-07 SGD	638045
YNL227C	YNL227C		0.47	-2.13	1.60E-24 SGD	634100
YOR031W	CRS5	Metallothionein-like protein; metallothionein-like protein; Null mutant is viable, exhibits	0.47	-2.13	1.61E-17 SGD	638198
YDR466W	YDR466W		0.47	-2.14	4.32E-38 SGD	634665
YML107C	YML107C		0.47	-2.14	0 SGD	636683
YML128C	MSC1	Meiotic Sister-Chromatid recombination	0.47	-2.14	0 SGD	637127
YOR317W	FAA1	cellular lipid metabolism and protein N-myristylation; long chain fatty acyl:CoA synthase	0.47	-2.14	1.88E-15 SGD	634708
YBR223C	TDP1	Tyrosine-DNA Phosphodiesterase	0.47	-2.15	5.73E-04 SGD	637977
YDR436W	PPZ2	serine-threonine phosphatase Z; Null mutant is viable but shows increase in cell size	0.46	-2.15	4.33E-24 SGD	636277
YGL258W-ORF	YGL258W-A	BioProcess=biological_process unknown MolFunction=molecular_function unknown	0.47	-2.15	1.57E-05 SGD	970697
YHR042W	NCP1,CPR1	NADP-cytochrome P450 reductase; Null mutant is viable	0.47	-2.15	8.16E-05 SGD	634569

YMR007W	YMR007W			0.47	-2.15	8.73E-11 SGD	635715
YOL087C	YOL087C			0.46	-2.15	6.47E-08 SGD	638873
YOR251C	YOR251C			0.46	-2.15	3.78E-13 SGD	636665
YAL001C	TFC3,FUN24,TSV115	transcription factor tau (TFIIC) subunit 138; 138 kDa, transcription factor tau (TFIIC)		0.46	-2.16	8.90E-17 SGD	638922
YGR008C	STF2	ATPase stabilizing factor		0.46	-2.16	4.52E-42 SGD	634883
YCR042C	TSM1,TAF150	TATA binding protein-associated factor (TAF); TATA binding protein-associated fac		0.46	-2.17	1.42E-13 SGD	638905
YDR103W	STE5,HMD3,NUL3	Protein of the pheromone pathway; Null mutant is viable but sterile. Overexpression		0.46	-2.17	7.14E-16 SGD	637304
YGL196W	YGL196W			0.46	-2.17	1.23E-27 SGD	634414
YIL090W	YIL090W			0.46	-2.17	3.55E-30 SGD	637081
YKL133C	YKL133C	probable purine nucleotide-binding protein		0.46	-2.17	6.64E-26 SGD	639407
YLR371W	ROM2	Gdp-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein, high c		0.46	-2.17	3.23E-10 SGD	635625
YOL130W	ALR1	aluminium resistance; ion transporter (putative); Null mutant is inviable, overexpress		0.46	-2.17	2.77E-09 SGD	637302
YPL149W	APG5	Involved in autophagy; reduced viability upon nutrient starvation, defective in autoph		0.46	-2.17	7.44E-09 SGD	635925
YJR155W	AAD10	high degree of similarity with the AAD of <i>P. chrysosporium</i> ; aryl-alcohol dehydrogen		0.46	-2.18	3.94E-12 SGD	637760
YOR041C	YOR041C			0.46	-2.18	6.78E-05 SGD	634913
YPL087W	YDC1	Yeast dihydro-ceramidase; alkaline dihydroceramidase with minor reverse activity; I		0.46	-2.18	6.07E-05 SGD	638438
YGL206C	CHC1,SWA5	presumed vesicle coat protein; Clathrin heavy chain; Null mutant is viable, but is slo		0.46	-2.19	8.42E-21 SGD	633363
YGR168C	YGR168C			0.46	-2.19	1.01E-26 SGD	636754
YIL125W	KGD1,OGD1	alpha-ketoglutarate dehydrogenase; Null mutant is viable but is deficient in alpha-ke		0.46	-2.19	9.42E-12 SGD	637309
YLR179C	YLR179C			0.46	-2.19	1.02E-11 SGD	637598
YBR068C	BAP2	contains 12 predicted transmembrane domains; amino acid permease for leucine, v		0.45	-2.2	8.20E-34 SGD	636883
YNL168C	YNL168C			0.46	-2.2	0 SGD	636549
YOR292C	YOR292C			0.45	-2.2	6.80E-23 SGD	635142
YAL058W	CNE1,FUN48	Functions in endoplasmic reticulum protein quality control; calnexin and calreticulin		0.45	-2.21	6.41E-14 SGD	638642
YCL041C	YCL041C			0.45	-2.21	2.99E-24 SGD	634976
YER125W	RSP5,MDP1,MUT2,NPI1	involved in ubiquitin-mediated protein degradation; Null mutant is inviable, an rsp5 n		0.45	-2.21	1.43E-07 SGD	638111
YAL044W- ORF:YAL044W-A		BioProcess=biological_process unknown MolFunction=molecular_function unknown		0.45	-2.22	3.25E-43 SGD	970773
YKR028W	SAP190	190 kDa protein that associates with the SIT4 phosphatase in a cell cycle depender		0.45	-2.22	5.58E-07 SGD	637354
YLR352W	YLR352W			0.45	-2.22	2.10E-18 SGD	634746
YNL317W	PFS2	Polyadenylation Factor I subunit 2; polyadenylation factor subunit; Null mutant is inv		0.45	-2.22	0 SGD	639437
YBR274W	CHK1	checkpoint kinase 1, homolog of the <i>S. pombe</i> and mammalian Chk1 checkpoint kir		0.45	-2.23	9.71E-08 SGD	636873
YCR011C	ADP1	Shows homology to ATP-dependent permeases		0.45	-2.23	3.13E-16 SGD	634685
YDR239C	YDR239C			0.45	-2.23	1.67E-32 SGD	633414
YIL124W	AYR1	Subcellular location of Ayr1p: lipid particles and endoplasmic reticulum of the yeast;		0.45	-2.23	7.13E-23 SGD	636670
YLR358C	YLR358C			0.45	-2.23	1.26E-10 SGD	639061
YML102W	CAC2	Involved in DNA-replication-linked nucleosome assembly, homologous to the p60 st		0.45	-2.23	3.61E-05 SGD	639404
YMR029C	YMR029C			0.45	-2.23	1.18E-28 SGD	638615

YMR153W	NUP53	Component of karyopherin docking complex of the nuclear pore complex; karyopherin subunit B1	0.45	-2.23	0 SGD	634029
YNL144C	YNL144C		0.45	-2.23	4.31E-39 SGD	636287
YCR097W	HMRA1,A1,MATA1	silenced copy of A1, which encodes a homeobox-domain containing protein that, together with its partner A2, forms a dimeric transcription factor	0.45	-2.24	2.26E-05 SGD	970838
YJR062C	NTA1,DEA1	Removes amide group from N-terminal asparagine and glutamine, to generate aspartic acid and glutamic acid respectively	0.45	-2.24	5.04E-30 SGD	636093
YKL020C	SPT23	Dosage dependent suppressor of Ty-induced promoter mutations; Null mutant is viable	0.45	-2.24	1.16E-08 SGD	635600
YLR098C	CHA4,SIL2,SIL3	Zinc-finger protein with Zn[2]-Cys[6] fungal-type binuclear cluster domain; DNA binding	0.45	-2.24	6.12E-10 SGD	634582
YMR162C	DNF3	Drs2 Neo1 Family; Potential aminophospholipid translocase; viable	0.45	-2.24	7.55E-19 SGD	637377
YOR161C	YOR161C		0.45	-2.24	2.15E-20 SGD	634026
YDR291W	YDR291W		0.44	-2.25	8.16E-27 SGD	635565
YHL042W	YHL042W		0.45	-2.25	5.52E-06 SGD	634410
YNL020C	ARK1	actin regulating kinase; serine/threonine kinase (putative); Null mutant is viable and functional	0.45	-2.25	3.62E-08 SGD	637202
YOR329C	SCD5,FTB1	Multicopy suppressor of clathrin deficiency and of ts mutants of IPL1; Null mutant is viable	0.44	-2.25	2.80E-10 SGD	634654
YAR019C	CDC15,LYT1	Required for mitosis and sporulation, cell division cycle blocked at 36 degrees; protein involved in the regulation of the yeast heat shock response	0.44	-2.26	1.63E-16 SGD	635581
YBR117C	TKL2	transketolase, homologous to tkl1; transketolase, similar to TKL1; Null mutant is viable	0.44	-2.26	9.90E-09 SGD	638733
YBR228W	SLX1		0.44	-2.26	3.60E-20 SGD	634548
YDR264C	AKR1	Negative regulator of pheromone response pathway, required for endocytosis of pheromone receptor	0.44	-2.26	1.30E-09 SGD	634754
YER033C	ZRG8	Zinc regulated gene	0.44	-2.26	7.68E-28 SGD	638893
YLR046C	YLR046C		0.44	-2.26	3.42E-08 SGD	633771
YOR122C	PFY1,PRF1	profilin (actin-binding protein); profilin; Null mutant is either inviable or viable (but temperature sensitive)	0.44	-2.26	1.08E-06 SGD	635822
YPR117W	YPR117W		0.44	-2.26	2.80E-05 SGD	638955
YHR099W	TRA1	TRA1 is the homolog of the human protein TRRAP which we have isolated as an essential gene for growth	0.44	-2.27	1.35E-07 SGD	633376
YLL032C	YLL032C		0.44	-2.27	1.74E-23 SGD	634824
YLR368W	YLR368W		0.44	-2.27	0 SGD	634113
YOR241W	MET7	METHionine requiring; folylpolyglutamate synthetase; Null mutant is viable, requires methionine for growth	0.44	-2.27	1.47E-27 SGD	636202
YPL268W	PLC1	Hydrolyzes phosphatidylinositol 4,5-biphosphate (PIP2) to generate two second messengers, diacylglycerol and inositol	0.44	-2.27	1.71E-15 SGD	637284
YBR037C	SCO1,PET161	inner mitochondrial membrane protein; inner membrane protein; required for accumulation of iron-sulfur clusters	0.44	-2.28	1.94E-09 SGD	634493
YBR102C	EXO84,USA3	exocyst complex component, homolog in rat brain called rExo84. pre-mRNA splicing factor	0.44	-2.28	4.70E-29 SGD	638026
YBR222C	FAT2	Fatty acid transporter, very similar to FAT1	0.44	-2.28	2.77E-12 SGD	634080
YDR204W	COQ4	Involved in ubiquinone biosynthesis; Unable to produce ubiquinone, hypersensitivity to paraquat	0.44	-2.28	7.22E-31 SGD	637752
YER119C	YER119C	similar to amino acid transport proteins	0.44	-2.28	4.24E-17 SGD	637812
YNL295W	YNL295W		0.44	-2.28	2.31E-39 SGD	636841
YPR053C	YPR053C		0.44	-2.28	9.08E-34 SGD	634987
YCR077C	PAT1,MRT1	Necessary for accurate chromosome transmission during cell division; Involved in mRNA tRNA nucleotidyl transferase	0.44	-2.29	3.79E-09 SGD	634198
YDR307W	YDR307W		0.44	-2.29	2.34E-07 SGD	637220
YEL071W	DLD3	D-lactate dehydrogenase	0.44	-2.29	9.75E-09 SGD	637094
YMR088C	YMR088C		0.44	-2.29	1.02E-19 SGD	639471
YBR094W	YBR094W		0.43	-2.3	4.50E-06 SGD	638083

YER164W	CHD1	Sole <i>S. cerevesiae</i> member of CHD gene family containing Chromodomain, Helicas	0.43	-2.3	8.99E-07 SGD	635637
YKL076C	YKL076C		0.44	-2.3	1.94E-07 SGD	637488
YNL321W	YNL321W		0.43	-2.3	0 SGD	638829
YDR034C	LYS14	Transcriptional activator of lysine pathway genes with 2-amino adipate semialdehyde dehydrogenase activity	0.43	-2.31	1.90E-37 SGD	634180
YDR089W	YDR089W		0.43	-2.31	2.39E-10 SGD	635504
YDR525W	SNA2	Homology to PMP3/SNA1 (Sensitivity to Na+); Null mutant is viable.	0.43	-2.31	1.37E-18 SGD	970734
YER155C	BEM2,IPL2,SUP9,TSL1	Protein with role in bud emergence; rho GTPase activating protein (GAP); randomizes membrane-bound casein kinase I homolog; casein kinase I homolog; Null mutant is viable.	0.43	-2.31	1.95E-17 SGD	633531
YHR135C	YCK1,CKI2	membrane-bound casein kinase I homolog; casein kinase I homolog; Null mutant is viable.	0.43	-2.31	1.93E-05 SGD	636147
YIL113W	YIL113W		0.43	-2.31	1.54E-23 SGD	635825
YLR189C	UGT51	Udp-glycosyltransferase; UDP-glucose:sterol glucosyltransferase; Null mutant is viable.	0.43	-2.31	1.29E-33 SGD	633490
YOR298C	-MBF1	bridges the DNA-binding region of GCN4 and TBP, similar to multiprotein bridging factor 1	0.43	-2.31	2.82E-34 SGD	970752
YBR183W	YPC1	Yeast Phyto-ceramidase; alkaline ceramidase with reverse activity; Null mutant is viable.	0.43	-2.32	4.55E-24 SGD	636637
YDL112W	TRM3	tRNA ribose methylase; tRNA (Gm18) ribose methylase; Null mutants are defective.	0.43	-2.32	9.62E-13 SGD	637411
YDR388W	RVS167	Involved in endocytosis; cytoskeletal protein (putative); Null mutant is viable but exhibits defects in growth and morphology.	0.43	-2.32	5.84E-29 SGD	637103
YHR001W	QCR10	8.5 kDa subunit of the ubiquinol-cytochrome c oxidoreductase complex; ubiquinol-cytochrome c reductase subunit 1	0.43	-2.32	7.09E-07 SGD	633421
YML103C	NUP188	Localized at both the cytoplasmic and nucleoplasmic faces of the nuclear pore complex.	0.43	-2.32	2.97E-27 SGD	637406
YMR147W	YMR147W		0.43	-2.32	2.02E-04 SGD	635038
YOR228C	YOR228C		0.43	-2.32	0 SGD	634488
YPR122W	AXL1,FUS5,STE22	determinant in axial budding pattern of haploid cells, involved in processing of a-factor precursors; converts phosphatidylserine to phosphatidylethanolamine; phosphatidylserine decarboxylase	0.43	-2.32	3.22E-16 SGD	638867
YGR170W	PSD2	histidine permease; requires supplementation with large amounts of histidine for growth.	0.43	-2.33	5.60E-11 SGD	638887
YGR191W	HIP1	homologous to the medium chain of mammalian clathrin-associated protein complex.	0.43	-2.33	0 SGD	635396
YHL019C	APM2		0.43	-2.33	1.10E-10 SGD	637194
YLR241W	YLR241W		0.43	-2.33	5.47E-42 SGD	634232
YOR303W	CPA1	Carbamoyl phosphate synthetase, arginine specific; arginine specific, carbamoyl phosphate synthetase	0.43	-2.33	3.39E-11 SGD	636795
YDR283C	GCN2,AAS1	Derepression of GCN4 expression; eukaryotic initiation factor 2 alpha (eIF2-alpha) kinase	0.43	-2.34	3.91E-21 SGD	638914
YLR356W	YLR356W		0.43	-2.34	0 SGD	633735
YLR454W	YLR454W		0.43	-2.34	1.13E-17 SGD	635699
YOR014W	RTS1	B-type regulatory subunit of protein phosphatase 2A (PP2A); protein phosphatase 2A regulatory subunit	0.43	-2.34	5.10E-33 SGD	634757
YER080W	YER080W		0.43	-2.35	2.11E-10 SGD	635428
YGL142C	GPI10	Involved in glycosyl phosphatidyl inositol synthesis, could be the target of the GPI synthase.	0.43	-2.35	5.90E-05 SGD	638725
YOR288C	MPD1	Disulfide isomerase related protein; disulfide isomerase related protein; Null mutant is viable.	0.43	-2.35	5.23E-07 SGD	636702
YPL128C	TBF1,LPI16	TTAGGG repeat binding factor; lethal	0.43	-2.35	1.14E-13 SGD	639520
YDR276C	PMP3,SNA1	plasma membrane protein involved in salt tolerance; hypothetical transmembrane protein	0.42	-2.36	5.36E-16 SGD	634221
YDR298C	ATP5,OSC1	Subunit 5 of the mitochondrial ATP synthase complex, homologous to bovine OSCF	0.42	-2.36	0 SGD	634970
YDR474C	YDR474C		0.42	-2.36	8.80E-32 SGD	634073
YER047C	SAP1	interacts with Sin1p; AAA ATPase	0.42	-2.36	1.11E-24 SGD	635515
YGL155W	CDC43,CAL1	may participate in a ras-like C-terminus modification of proteins involved in nuclear envelope	0.42	-2.36	5.19E-40 SGD	636953

YKR031C	SPO14,PLD1	dispensable for mitosis, premeiotic DNA synthesis, recombination, meiosis I, require	0.42	-2.36	8.09E-13 SGD	637421
YLR328W	YLR328W		0.42	-2.36	1.48E-38 SGD	635205
YML035C	AMD1,AMD3	putative alpha-mannosidase; alpha-mannosidase (putative); Null mutant is viable	0.42	-2.36	0 SGD	636371
YPL120W	VPS30,APG6,VPT30	Required for sorting and delivery of soluble hydrolases to the vacuole.; Vacuolar hy	0.42	-2.36	2.35E-13 SGD	634057
YDR294C	DPL1	dihydrophosphingosine phosphate lyase (also known as sphingosine phosphate lyase);	0.42	-2.37	1.91E-06 SGD	636238
YKL168C	KKQ8	Serine/threonine protein kinase of unknown function	0.42	-2.37	8.35E-08 SGD	634193
YLR180W	SAM1,ETH10	S-adenosylmethionine synthetase; Null mutant is viable.	0.42	-2.37	2.25E-06 SGD	635234
YML072C	YML072C		0.42	-2.37	0 SGD	633522
YML100W	TSL1	123 kD regulatory subunit of trehalose-6-phosphate synthase/phosphatase complex	0.42	-2.37	2.66E-05 SGD	637392
YPL096W	PNG1	de-N-glycosylation enzyme; peptide:N-glycanase; Null mutant is viable and shows r	0.42	-2.37	6.12E-06 SGD	637807
YHR078W	YHR078W		0.42	-2.38	0 SGD	634019
YIR036C	YIR036C		0.42	-2.38	1.26E-05 SGD	637660
YLR285W	YLR285W		0.42	-2.38	1.54E-07 SGD	638414
YOL133W	HRT1,RBX1,ROC1	High level expression Reduces Ty3 Transposition; Skp1-Cullin-F-box ubiquitin prote	0.42	-2.38	4.83E-29 SGD	639014
YOR002W	ALG6	Required for glucosylation in the N-linked glycosylation pathway; glucosyltransferas	0.42	-2.38	0 SGD	637923
YPR191W	QCR2,COR2,UCR2	40 kDa ubiquinol cytochrome-c reductase core protein 2; Null mutant is viable and c	0.42	-2.38	2.05E-16 SGD	639274
YLR398C	SKI2	blocks translation of non-poly(A) mRNAs; antiviral protein, helicase (putative); Null r	0.42	-2.39	5.00E-16 SGD	638879
YLR401C	YLR401C		0.42	-2.39	2.64E-30 SGD	638697
YMR152W	YIM1	Mitochondrial inner membrane protease, similar to E. coli leader peptidase; proteas	0.42	-2.39	2.04E-12 SGD	636027
YOR332W	VMA4	vacuolar ATPase V1 domain subunit E (27 kDa); E subunit of V1 sector, vacuolar H	0.42	-2.39	7.14E-23 SGD	635015
YLR425W	TUS1,SOP10	TOR Unique function Suppressor, exchange factor for RHO1; 1307 amino acid hydr	0.42	-2.4	0 SGD	637380
YNL201C	YNL201C		0.42	-2.4	3.87E-34 SGD	635448
YNL268W	LYP1	lysine permease	0.42	-2.4	2.80E-25 SGD	636922
YOL082W	CVT19	Cytoplasm to Vacuole Targeting, Mutant is defective in import of aminopeptidase I tl	0.42	-2.4	1.53E-14 SGD	635252
YPL094C	SEC62,LPG14	membrane component of ER protein translocation apparatus; ER protein translocati	0.42	-2.4	3.63E-38 SGD	635951
YDR377W	ATP17	Subunit f of mitochondrial ATP synthase. Homologous to bovine subunit f.; ATP syn	0.42	-2.41	0 SGD	638181
YGR270W	YTA7	Member of CDC48/PAS1/SEC18 family of ATPases	0.42	-2.41	2.68E-08 SGD	637413
YOR056C	YOR056C		0.41	-2.41	0 SGD	633972
YOR215C	YOR215C		0.42	-2.41	1.76E-08 SGD	639062
YPL022W	RAD1,LPB9	UV endonuclease; radiation sensitive	0.42	-2.41	8.36E-09 SGD	638929
YPL098C	YPL098C		0.42	-2.41	4.90E-27 SGD	635654
YBR263W	SHM1,SHMT1,TMP3	Serine hydroxymethyltransferase, mitochondrial; Null mutant is viable.	0.41	-2.42	0 SGD	637927
YBR270C	YBR270C	Probable ATP/GTP-binding protein	0.41	-2.42	1.43E-29 SGD	636203
YGL162W	SUT1	Involved in sterol uptake; Null mutant is viable	0.41	-2.42	1.32E-26 SGD	638454
YPL049C	DIG1,RST1	Down-regulator of Invasive Growth, Regulator of Sterile Twelve, binds Fus3 and Ste	0.41	-2.42	8.56E-06 SGD	633977
YBR216C	YBR216C		0.41	-2.43	1.09E-20 SGD	635414
YDR306C	YDR306C		0.41	-2.43	3.15E-07 SGD	636837

YIL087C	YIL087C		0.41	-2.43	0 SGD	634403
YJL151C	SNA3	Homology to PMP3/SNA1 (Sensitivity to Na+); Null mutant is viable.	0.41	-2.43	5.92E-25 SGD	634353
YOR133W	EFT1	translation elongation factor 2 (EF-2); Null mutant is viable (eft1 eft2 double mutant	0.41	-2.43	4.32E-13 SGD	634622
YJL132W	YJL132W		0.41	-2.44	6.07E-33 SGD	638084
YJR039W	YJR039W		0.41	-2.44	5.08E-36 SGD	638888
YKL174C	YKL174C	probable transport protein	0.41	-2.44	2.88E-11 SGD	637189
YMR026C	PEX12,PAS11	C3HC4 zinc-binding integral peroxisomal membrane protein; mutant lacks morphol	0.41	-2.45	0 SGD	638517
YMR056C	AAC1	minor species of mitochondrial ADP/ATP translocator, highly homologous to PET9 (	0.41	-2.45	4.95E-15 SGD	638383
YGR070W	ROM1,SKC1	Gdp-GTP Exchange Protein (GEP) for the Rho1p Small GTP-binding Protein; Synth	0.41	-2.46	5.11E-42 SGD	637387
YGR287C	YGR287C		0.41	-2.46	1.98E-16 SGD	634731
YNL025C	SSN8,GIG3,NUT9,SRB1	Component of RNA polymerase II holoenzyme, involved in RNA pol II carboxy-term	0.41	-2.46	5.95E-29 SGD	636961
YHR028C	DAP2,DPP2	Dipeptidyl aminopeptidase B (DPAP B); dipeptidyl aminopeptidase B (DPAP B); Nul	0.4	-2.47	0 SGD	636369
YJL141C	YAK1	Serine-threonine protein kinase; viable, confers growth to strains deleted for tpk1, tp	0.4	-2.47	0 SGD	636372
YKR096W	YKR096W		0.41	-2.47	4.38E-34 SGD	635607
YNL138W	SRV2,CAP	70-kDa adenylyl cyclase-associated protein; 70 kDa adenylyl cyclase-associated pr	0.41	-2.47	1.23E-04 SGD	638655
YAR014C	BUD14	Null mutant is viable, random budding in diploid null mutants	0.4	-2.48	1.23E-35 SGD	634143
YJR121W	ATP2	F(1)F(0)-ATPase complex beta subunit, mitochondrial; F(1)F(0)-ATPase complex b	0.4	-2.48	1.81E-24 SGD	638663
YMR129W	POM152	May be involved in duplication of nuclear pores and nuclear pore complexes during	0.4	-2.48	0 SGD	635585
YFL054C	YFL054C		0.4	-2.49	9.71E-05 SGD	634567
YMR221C	YMR221C		0.4	-2.49	3.77E-04 SGD	635366
YNL091W	YNL091W		0.4	-2.5	4.74E-38 SGD	635604
YOR184W	SER1,ADE9	phosphoserine transaminase; Null mutant is viable, serine-requiring	0.4	-2.5	1.37E-17 SGD	636984
YPR114W	YPR114W		0.4	-2.5	8.78E-12 SGD	635119
YHR001W	OSH7	Oxysterol Binding Protein	0.4	-2.51	5.72E-08 SGD	636074
YIR035C	YIR035C		0.4	-2.51	5.37E-18 SGD	635022
YML117W	YML117W		0.4	-2.51	8.99E-12 SGD	637351
YOR307C	SLY41	multicopy suppressor of ypt1 deletion; chloroplast phosphate transporter homolog; I	0.4	-2.51	4.62E-15 SGD	633992
YPL162C	YPL162C		0.4	-2.51	1.53E-17 SGD	635893
YHR074W	QNS1	Hypothetical ORF	0.4	-2.52	1.53E-09 SGD	636226
YOR356W	YOR356W		0.4	-2.52	8.74E-28 SGD	635369
YAL043C	PTA1,FUN39	pre-tRNA processing; Null mutant is inviable, temperature-sensitive mutant shows d	0.4	-2.53	7.36E-10 SGD	636324
YGR194C	XKS1	Xylulokinase; xylulokinase; Null mutant is viable and cannot grow on media containi	0.39	-2.53	1.25E-23 SGD	634097
YOR015W	YOR015W		0.4	-2.53	1.45E-13 SGD	633658
YOR065W	CYT1,CTC1	Cytochrome c1; cytochrome c1	0.4	-2.53	9.06E-12 SGD	634483
YPL219W	PCL8	PHO85 cyclin; cyclin; Null mutant is viable.	0.39	-2.53	1.65E-12 SGD	635304
YBR287W	YBR287W		0.39	-2.54	1.02E-17 SGD	636770
YHR170W	NMD3,SRC5	putative Upf1p-interacting protein; factor required for a late assembly step of the 60t	0.39	-2.54	0 SGD	635325

YIR007W	YIR007W			0.39	-2.54	6.45E-13 SGD	634805
YMR219W	ESC1	Establishes Silent Chromatin		0.39	-2.54	3.91E-36 SGD	638961
YNL218W	MGS1	Maintenance of Genome Stability 1		0.39	-2.54	6.25E-20 SGD	636180
YIL112W	YIL112W			0.39	-2.55	1.07E-14 SGD	633463
YJL005W	CYR1,CDC35,HSR1,SR	Required for START A of cell cycle, and glucose and nitrogen repression of sporulation		0.39	-2.55	3.13E-14 SGD	633592
YKL091C	YKL091C			0.39	-2.55	1.50E-10 SGD	635140
YAR044W	OSH1	May be involved in ergosterol synthesis; Null mutant is viable but displays pleiotropic effects		0.39	-2.56	1.01E-17 SGD	635490
YCL049C	YCL049C			0.39	-2.56	1.33E-38 SGD	636970
YCR073W	SOL2	multicopy suppressor of los1-1; Null mutant is viable		0.39	-2.56	0 SGD	634537
YML120C	NDI1	NADH dehydrogenase (ubiquinone)		0.39	-2.56	0 SGD	637111
YMR237W	YMR237W			0.39	-2.56	3.96E-20 SGD	638090
YOL098C	YOL098C			0.39	-2.56	1.40E-21 SGD	635534
YBR229C	ROT2,GLS2	Reversal of tor2 lethality. Involved in Beta-1,6-glucan synthesis.; glucosidase II; N-linked glycoside hydrolase family 16 member 1		0.39	-2.57	2.16E-32 SGD	634679
YDL174C	DLD1	mitochondrial enzyme D-lactate ferricytochrome c oxidoreductase; D-lactate ferricytate reductase		0.39	-2.57	0 SGD	639505
YKL197C	PEX1,PAS1	member of the AAA-protein family; AAA ATPase; mutant lacks morphologically recognizable organelles		0.39	-2.57	6.18E-25 SGD	638863
YKR018C	YKR018C			0.39	-2.57	4.92E-05 SGD	636224
YMR256C	COX7	subunit VII of cytochrome c oxidase; cytochrome c oxidase subunit VII; Null mutant is viable		0.39	-2.57	2.27E-05 SGD	634201
YOR109W	INP53,SJL3,SOP2	Synaptojanin-like protein; inositol polyphosphate 5-phosphatase; Null mutant is viable		0.39	-2.57	0 SGD	637391
YBR132C	AGP2	General amino acid permease with broad substrate specificity; amino acid permease		0.39	-2.58	4.73E-32 SGD	639486
YGR127W	YGR127W			0.39	-2.58	1.12E-17 SGD	638442
YJL070C	YJL070C			0.39	-2.58	0 SGD	633293
YJL164C	TPK1,PKA1,SRA3	putative catalytic subunit of cAMP-dependent protein kinase; cAMP-dependent protein kinase regulatory subunit type 1		0.39	-2.58	0 SGD	636740
YOL048C	YOL048C			0.39	-2.58	2.57E-09 SGD	634301
YBL105C	PKC1,CLY15,HPO2,STT	Protein Kinase C; The null mutant is inviable and lyses rapidly in hypotonic media. C-terminal domain homologous to PKC		0.39	-2.59	3.38E-16 SGD	637403
YGL173C	KEM1,DST2,RAR5,SEP	Kar1-1 nuclear-fusion-defect Enhancing Mutation. Plays a role in cytoplasmic mRNA/		0.39	-2.59	1.43E-09 SGD	638901
YJL127C	SPT10,CRE1,SUD1	chromatin maintenance and transcriptional regulation; transcriptional regulator; superoxide dismutase		0.39	-2.59	1.37E-04 SGD	636878
YNL104C	LEU4	leucine biosynthesis; alpha-isopropylmalate synthase (2-isopropylmalate synthase);		0.39	-2.59	0 SGD	635434
YDR385W	EFT2	translation elongation factor 2 (EF-2); Null mutant is viable (eft1 eft2 double mutant)		0.38	-2.6	0 SGD	637270
YJL047C	RTT101	Regulator of Ty1 Transposition; Null mutant is viable and causes an increase in Ty1		0.38	-2.6	9.16E-35 SGD	637289
YKL010C	UFD4	Ubiquitin Fusion Degradation; Null is viable, defective in proteolysis of fusion proteins		0.38	-2.6	0 SGD	638949
YLR090W	XDJ1	Homolog of E. coli DnaJ, closely related to Ydj1p; Null mutant is viable, displays no		0.38	-2.6	0 SGD	639425
YAL028W	YAL028W			0.38	-2.61	0 SGD	638653
YMR154C	RIM13,CPL1	calpain-like protease involved in proteolytic processing of Rim1p; cysteine protease		0.38	-2.61	0 SGD	636290
YMR196W	YMR196W			0.38	-2.61	0 SGD	638876
YPL111W	CAR1,LPH15	arginase; Null mutant is viable but defective in arginine catabolism		0.38	-2.61	2.26E-27 SGD	637738
YAR023C	YAR023C	membrane protein		0.38	-2.62	6.94E-04 SGD	637585
YBR053C	YBR053C			0.38	-2.62	0 SGD	633883

YBR111C	YSA1,RMA2	Protein with weak homology to <i>D. melanogaster</i> serendipity protein and <i>X. laevis</i> ba	0.38	-2.62	0 SGD	634444
YKL100C	YKL100C		0.38	-2.62	6.73E-20 SGD	634117
YER166W	DNF1	Drs2 Neo1 Family; Potential aminophospholipid translocase; viable	0.38	-2.63	0 SGD	633581
YOR377W	ATF1	Alcohol acetyltransferase; alcohol acetyltransferase	0.38	-2.63	1.15E-21 SGD	638614
YIL111W	COX5B	Cytochrome-c oxidase chain Vb; cytochrome c oxidase chain Vb; Null mutant is vial	0.38	-2.64	3.26E-16 SGD	637584
YLR120C	YPS1	Gpi-anchored aspartic protease ( <i>Yapsin 1</i> ); GPI-anchored aspartic protease; Null m	0.38	-2.64	0 SGD	638000
YOL013C	HRD1,DER3	Ubiquitin-protein ligase for endoplasmic reticulum-associated degradation.; Null mut	0.38	-2.64	2.49E-16 SGD	639526
YPL084W	BRO1,LPF2	BCK1-like resistance to osmotic shock; Temperature-sensitive growth defect, sensit	0.38	-2.64	1.86E-12 SGD	635493
YDL078C	MDH3	malate dehydrogenase; Null mutant is viable, does not grow on oleate and grows sl	0.38	-2.65	2.05E-06 SGD	633845
YDR154C	YDR154C		0.38	-2.65	5.89E-04 SGD	639037
YGL137W	SEC27	Involved in endoplasmic-to-Golgi protein trafficking; yeast coatomer beta'-subunit; N	0.38	-2.65	1.35E-16 SGD	635578
YGR043C	YGR043C		0.38	-2.65	1.11E-07 SGD	635908
YOL089C	HAL9	involved in salt tolerance; contains zinc finger, transcription factor (putative); Null mu	0.38	-2.65	0 SGD	637308
YJL082W	IML2	Similar to <i>Ykr018p</i>	0.38	-2.66	2.23E-28 SGD	634194
YML058W	SML1	Suppressor of <i>mec</i> lethality; Null mutant is viable and suppresses <i>mec1</i> and <i>rad53</i> l	0.38	-2.66	4.84E-15 SGD	634872
YPR156C	TPO3	Polyamine transport protein	0.38	-2.66	6.56E-07 SGD	636926
YBL099W	ATP1	mitochondrial F1F0-ATPase alpha subunit; F1F0-ATPase alpha subunit; null mutan	0.37	-2.67	0 SGD	634023
YDL237W	YDL237W		0.37	-2.67	1.16E-39 SGD	636681
YER061C	CEM1	homology with beta-keto-acyl synthases; beta-keto-acyl synthase homolog; Null mu	0.37	-2.67	7.67E-09 SGD	637816
YOR270C	VPH1	vacuolar ATPase V0 domain subunit a (100 kDa); V0 sector subunit, essential for v	0.37	-2.67	0 SGD	637271
YFR029W	PTR3,SSY3	Regulator of expression of the PTR2, GAP1, and BAP2 genes, involved in the the c	0.37	-2.68	4.53E-09 SGD	637215
YDL022W	GPD1,DAR1,HOR1,OSC	glycerol-3-phosphate dehydrogenase; lethal under conditions of osmotic stress, una	0.37	-2.7	0 SGD	638523
YDL204W	YDL204W		0.37	-2.7	1.73E-17 SGD	636679
YMR216C	SKY1	SRPK1-like Kinase in Yeast (SRPK1 is a human serine kinase that specifically phos	0.37	-2.7	2.54E-06 SGD	638086
YNR041C	COQ2	para hydroxybenzoate: polyprenyl transferase; Null mutant is viable but is respirator	0.37	-2.7	3.62E-10 SGD	636037
YPR028W	YOP1,YIP2	Ypt Interacting Protein	0.37	-2.7	5.86E-16 SGD	634449
YDR397C	NCB2	Negative Cofactor B2 is the beta subunit of a negative regulator of RNA polymerase	0.37	-2.71	3.55E-08 SGD	633599
YFL041W	FET5	ferrous iron transport; multicopper oxidase, type 1 integral membrane protein; overe	0.37	-2.71	6.89E-06 SGD	637196
YGL156W	AMS1	vacuolar alpha mannosidase; alpha mannosidase; null mutant is viable	0.37	-2.71	0 SGD	633499
YGR183C	QCR9,UCR9	7.3 kDa subunit 9 of the ubiquinol cytochrome c oxidoreductase complex; ubiquinol	0.37	-2.71	7.85E-21 SGD	634349
YIL155C	GUT2	glycerol-3-phosphate dehydrogenase, mitochondrial; glycerol-3-phosphate dehydro	0.37	-2.71	8.45E-10 SGD	638727
YOR350C	MNE1	similar to <i>Lucilia illustris</i> mitochondria cytochrome oxidase	0.37	-2.71	1.01E-14 SGD	638798
YMR316C-YMR316C-B			0.37	-2.72	1.01E-17 SGD	634276
YAL031C	FUN21	Function unknown now; Null mutant is viable	0.37	-2.73	5.12E-14 SGD	636316
YDL024C	DIA3	involved in invasive and pseudohyphal growth; Null mutant is viable and causes inv	0.37	-2.73	1.07E-12 SGD	636101
YFR016C	YFR016C		0.37	-2.73	1.25E-09 SGD	637398
YBL015W	ACH1	Mannose-containing glycoprotein which binds concanavalin A; acetyl CoA hydrolase	0.37	-2.74	0 SGD	636855

YKL019W	RAM2	CAAX farnesyltransferase alpha subunit; lethal	0.36	-2.74	4.52E-42 SGD	636653
YML075C	HMG1	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme; Null mutant	0.36	-2.74	1.05E-40 SGD	638862
YOR178C	GAC1	Regulatory subunit for phosphoprotein phosphatase type 1 (PP-1), also known as G	0.37	-2.74	2.54E-22 SGD	634179
YGL060W	YGL060W		0.36	-2.75	2.98E-27 SGD	637203
YGR271W	SLH1	SKI2-like helicase; null mutant is viable	0.36	-2.75	4.94E-08 SGD	635701
YLR001C	YLR001C		0.36	-2.75	7.22E-22 SGD	635505
YLR082C	SRL2	Suppressor of Rad53 null Lethality	0.36	-2.75	7.52E-08 SGD	636745
YDR406W	PDR15	similar to Pdr5p and Pdr10p; multidrug resistance transporter (putative)	0.36	-2.76	1.52E-33 SGD	638963
YLR375W	STP3	Involved in pre-tRNA splicing and in uptake of branched-chain amino acids	0.36	-2.76	3.26E-13 SGD	636002
YFR021W	AUT10,NMR1	Required for cytoplasm to vacuole targeting of proaminopeptidase I and starvation ii	0.36	-2.78	7.01E-45 SGD	635300
YGL007W	YGL007W		0.36	-2.78	5.86E-09 SGD	637490
YNL118C	DCP2,PSU1	MrnA Decapping. essential suppressor of the respiratory deficiency of a pet mutant	0.36	-2.78	6.20E-36 SGD	635529
YPL076W	GPI2,GCR4	Required for synthesis of N-acetylglucoaminylphosphatidylinositol, the first intermed	0.36	-2.78	2.08E-26 SGD	639207
YDR232W	HEM1	First enzyme in heme biosynthetic pathway; 5-aminolevulinate synthase; Null mutant	0.36	-2.79	0 SGD	637975
YMR264W	CUE1	Cue1p assembles with Ubc7p. Cue1p recruits Ubc7p to the cytosolic surface of the	0.36	-2.79	4.33E-11 SGD	639114
YIL154C	IMP2'	Protein involved in nucleo-mitochondrial control of maltose, galactose and raffinose	0.36	-2.8	1.98E-11 SGD	639236
YDR224C	HTB1,SPT12	Histone H2B (HTB1 and HTB2 code for nearly identical proteins); histone H2B (HTE	0.36	-2.81	3.53E-08 SGD	633622
YKR019C	IRS4	Increased rDNA silencing; Null mutant is viable and shows increased rDNA silencin	0.36	-2.81	0 SGD	635375
YLR093C	NYV1,MAM2	Synaptobrevin (v-SNARE) homolog involved in vacuolar vesicle fusion; vacuolar v-S	0.36	-2.81	6.83E-42 SGD	636570
YLR361C	YLR361C		0.36	-2.81	2.86E-11 SGD	634123
YMR206W	YMR206W		0.36	-2.81	7.19E-05 SGD	636706
YBL029C-/ORF:YBL029C-A		BioProcess=biological_process unknown MolFunction=molecular_function unknown	0.35	-2.82	1.93E-07 SGD	970681
YDR392W	SPT3	Transcription factor; histone acetyltransferase SAGA complex member, transcriptior	0.35	-2.82	3.66E-11 SGD	633866
YGR248W	SOL4	similar to SOL3	0.35	-2.82	4.71E-25 SGD	634500
YOL096C	COQ3	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; Null mutant is viable, fails t	0.35	-2.82	2.35E-34 SGD	635190
YPL262W	FUM1	Fumarase converts l-malate to fumarate as part of the TCA cycle; fumarase (fumar	0.35	-2.82	0 SGD	635307
YML116W-ORF:YML116W-A		BioProcess=biological_process unknown MolFunction=molecular_function unknown	0.35	-2.83	1.50E-20 SGD	970714
YDL185W	TFP1,CLS8,VMA1	Encodes a protein with three regions (ABC) that is spliced to yield the extein AC & tl	0.35	-2.84	3.25E-29 SGD	635582
YDR457W	TOM1	Temperature dependent Organization in Mitotic nucleus; hect-domain-containing pr	0.35	-2.84	6.67E-26 SGD	635626
YIL097W	FYV10	Function required for Yeast Viability on toxin exposure; Null mutant is viable but exh	0.35	-2.84	1.06E-07 SGD	638618
YKL220C	FRE2	Ferric reductase, similar to Fre1p; ferric reductase	0.35	-2.84	2.06E-19 SGD	638051
YDR028C	REG1,HEX2,PZF240,SP	The reg1 locus encodes a gene which is involved in RNA processing and is a negat	0.35	-2.85	1.50E-21 SGD	638833
YDR391C	YDR391C		0.35	-2.85	2.15E-17 SGD	636590
YJL134W	LCB3,LBP1,YSR2	Protein involved in incorporation of exogenous long chain bases in sphingolipids; pl:	0.35	-2.85	7.78E-20 SGD	638564
YPR113W	PIS1	phosphatidylinositol synthase; Null mutant is inviable	0.35	-2.85	0 SGD	636520
YGR032W	GSC2,FKS2	Highly similar to FKS1 (GSC1). GSC2 and FKS1 encode redundant catalytic compo	0.35	-2.86	9.32E-21 SGD	638911
YHR087W	YHR087W		0.35	-2.86	1.37E-23 SGD	635672

YJL167W	ERG20,BOT3,FDS1,FPF	May be rate-limiting step in sterol biosynthesis pathway; farnesyl diphosphate synth	0.35	-2.86	1.29E-06	SGD	639301
YJR074W	MOG1	Required for nuclear-protein import; nuclear protein that interacts with GTP-Gsp1p;	0.35	-2.86	4.71E-27	SGD	634371
YJR151C	DAN4	Delayed Anaerobic Gene; cell wall mannoprotein; unknown	0.35	-2.86	1.71E-24	SGD	638924
YJL016W	YJL016W		0.35	-2.87	0	SGD	639057
YPL221W	BOP1	bypass of PAM1	0.35	-2.87	8.72E-19	SGD	634230
YNL329C	PEX6,PAS8	Required for peroxisome assembly; AAA ATPase; lack of peroxisome biogenesis	0.35	-2.88	0	SGD	637362
YAR027W	YAR027W	membrane protein	0.35	-2.89	3.78E-26	SGD	636632
YGL227W	VID30	vacuole import and degradation (VID), TOR inhibitor (TIN); Null mutant is viable but	0.35	-2.89	9.17E-06	SGD	637371
YLR354C	TAL1	Transaldolase, enzyme in the pentose phosphate pathway; transaldolase, enzyme i	0.35	-2.89	0	SGD	635992
YDR070C	YDR070C		0.34	-2.9	1.40E-37	SGD	634217
YHR093W	AHT1	the AHT1 DNA sequence is upstream of HXT4 and contains an HXT4 regulatory ele	0.34	-2.91	1.11E-16	SGD	637566
YLL040C	VPS13,SOI1,VPT2	vacuolar Protein Sorting; Null mutant is viable but exhibits defects in vacuolar protei	0.34	-2.91	4.41E-12	SGD	638954
YLR450W	HMG2	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme; Null mutar	0.34	-2.91	6.46E-20	SGD	634670
YMR021C	MAC1,CUA1	metal-binding transcriptional activator; Null mutant is viable, has a defect in the plas	0.34	-2.91	1.06E-15	SGD	637055
YMR278W	YMR278W		0.34	-2.91	0	SGD	638726
YNL274C	YNL274C		0.34	-2.91	2.86E-19	SGD	633855
YOR086C	YOR086C		0.34	-2.91	1.49E-24	SGD	637401
YOR370C	MRS6,MSI4	protein of the TCD/MRS6 family of GDP dissociation inhibitors (Rab escort protein);	0.34	-2.91	0	SGD	638649
YPR196W	MAL63	zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type	0.34	-2.91	1.59E-09	SGD	636085
YGR289C	MAL11,AGT1	Part of MAL1 complex locus, encodes funct. maltose permease in all strains, exhibit	0.34	-2.92	1.73E-13	SGD	637205
YHR102W	KIC1,NRK1	Kinase that interacts with Cdc31p, N-rich kinase 1	0.34	-2.94	6.11E-21	SGD	633436
YIR016W	YIR016W		0.34	-2.94	8.33E-19	SGD	637675
YPL083C	SEN54	Trna splicing endonuclease 54kDa subunit; tetrameric tRNA splicing endonuclease	0.34	-2.94	0	SGD	633967
YMR181C	YMR181C		0.34	-2.95	0	SGD	636471
YJR073C	OPI3,PEM2	Second and third steps of methylation pathway for phosphatidylcholine biosynthesis	0.34	-2.96	0	SGD	639181
YMR160W	YMR160W		0.34	-2.96	1.00E-21	SGD	634744
YBR235W	YBR235W		0.34	-2.98	3.12E-27	SGD	637352
YGR240C	PFK1	phosphofructokinase alpha subunit; Null mutant is viable, accumulates fructose-6-ph	0.34	-2.98	0	SGD	637319
YKL038W	RGT1	transcriptional repressor and activator; transcriptional activator, transcriptional repre	0.34	-2.98	0	SGD	637402
YIL136W	OM45	45-kDa mitochondrial outer membrane protein; 45 kDa mitochondrial outer membra	0.33	-2.99	3.22E-10	SGD	638506
YDL085W	YDL085W		0.33	-3	4.90E-44	SGD	636128
YGL035C	MIG1,CAT4,SSN1,TDS2	Transcription factor involved in glucose repression; C2H2 zinc finger protein that res	0.33	-3	0	SGD	637132
YGR100W	MDR1,GYP2,MIC1	Mac1-dependent regulator; GTPase activating protein (GAP) for Ypt6; Null mutant i	0.33	-3	3.51E-11	SGD	634641
YIL047C	SYG1	Protein for which truncation and overexpression can suppress lethality of G-alpha pi	0.33	-3	0	SGD	635498
YBR298C	MAL31,MAL3T	Part of the complex locus MAL3, functional in S288C, highly homologous to MAL61	0.33	-3.01	2.34E-11	SGD	637190
YDR297W	SUR2,SYR2	Suppressor of rvs161 and rvs167 mutations; sphingosine hydroxylase; Null mutant i	0.33	-3.01	0	SGD	639287
YOR173W	YOR173W		0.33	-3.01	2.36E-17	SGD	638535

YKL022C	CDC16	a component of anaphase-promoting complex required for the G2/M transition in mitosis	0.33	-3.02	4.56E-37	SGD	637255
YOR081C	YOR081C		0.33	-3.02	2.60E-10	SGD	634712
YPL270W	MDL2	ATP-binding cassette (ABC) transporter family member; Null mutant is viable	0.33	-3.02	1.70E-16	SGD	638124
YBR140C	IRA1,GLC1,PPD1	Inhibitory regulator of the RAS-cAMP pathway, negatively regulates cAPK by antagonizing Raf-1	0.33	-3.03	1.45E-12	SGD	638971
YOR062C	YOR062C		0.33	-3.03	1.29E-10	SGD	635896
YDL155W	CLB3	Involved in mitotic induction and perhaps in DNA replication and spindle assembly; Involved in mechanism by which mitochondrial shape is established or maintained; transcription is regulated by PHO system	0.33	-3.04	6.42E-17	SGD	635261
YNL330C	RPD3,REC3,SDI2,SDS6	Transcription modifier, required for vegetative repression of early meiosis-specific genes	0.33	-3.04	2.84E-14	SGD	633937
YLL006W	MMM1	Involved in mechanism by which mitochondrial shape is established or maintained; transcription is regulated by PHO system	0.33	-3.05	4.85E-08	SGD	638557
YOL084W	PHM7	adrenodoxin oxidoreductase homolog; Null mutant is inviable	0.33	-3.05	1.49E-24	SGD	637311
YDR376W	ARH1	arginyl-tRNA-protein transferase; Null mutant is viable, but unable to degrade substrates	0.33	-3.06	0	SGD	638575
YGL017W	ATE1	Gtpase activating protein for Ypt1p; GTPase activating protein (GAP); Null mutant is inviable	0.33	-3.07	5.24E-18	SGD	637090
YOR070C	GYP1		0.33	-3.07	7.02E-32	SGD	638690
YPR091C	YPR091C		0.33	-3.07	3.59E-23	SGD	634819
YKR080W	MTD1	NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase; Null mutant is viable	0.32	-3.08	1.57E-42	SGD	634533
YFL031W	HAC1,ERN4,IRE15	Transcription factor that is required for the unfolded protein-response pathway, binds to ER stress response elements	0.32	-3.09	1.21E-06	SGD	633666
YOR042W	YOR042W		0.32	-3.09	0	SGD	636779
YPL026C	SKS1,SHA3	multicopy suppressor of snf3 and grr1 mutants; Null mutant is viable, Sks1 lacking tlp1 is inviable	0.32	-3.09	2.78E-12	SGD	638627
YDR178W	SDH4,ACN18	succinate dehydrogenase membrane anchor subunit; Null mutant is viable, retains a residual activity	0.32	-3.1	4.20E-15	SGD	637551
YDR272W	GLO2	Cytoplasmic glyoxylase-II; glyoxylase-II; Null mutant is viable but shows increased sensitivity to tryptophan synthetase; Null mutant is viable and requires tryptophan	0.32	-3.1	8.02E-26	SGD	635941
YGL026C	TRP5		0.32	-3.1	0	SGD	636278
YMR232W	FUS2	Involved in cell fusion during mating, also required for the alignment of parental nuclei	0.32	-3.1	1.85E-20	SGD	638794
YGL121C	YGL121C		0.32	-3.11	4.48E-09	SGD	638989
YJR115W	YJR115W		0.32	-3.11	1.57E-11	SGD	635706
YGR236C	SPG1	Hypothetical ORF; Null mutant is viable, SPG1 is required for long-term survival in yeast	0.32	-3.13	0	SGD	639001
YKL151C	YKL151C		0.32	-3.15	2.80E-45	SGD	639298
YJL185C	YJL185C		0.32	-3.16	0	SGD	635942
YDR498C	SEC20	membrane glycoprotein, sorted by HDEL retrieval system; membrane glycoprotein, dispensable for haploidization and sporulation, but required for full protein degradation	0.32	-3.17	1.04E-11	SGD	636991
YMR297W	PRC1,LBC1	Translocase of Outer Mitochondrial membrane; forms the outer membrane import complex	0.32	-3.17	0	SGD	636889
YMR203W	TOM40,ISP42,MOM38	Probable serine-type carboxypeptidase (EC 3.4.16.1)	0.31	-3.18	0	SGD	635215
YBR139W	YBR139W		0.31	-3.19	7.76E-17	SGD	635346
YGR141W	YGR141W		0.31	-3.19	2.40E-24	SGD	639420
YMR243C	ZRC1,OSR1	Zinc- and cadmium-resistance protein; Null mutant is viable and sensitive to zinc	0.31	-3.2	1.09E-26	SGD	636120
YGL234W	ADE5,7	glycinamide ribotide synthetase and aminoimidazole ribotide synthetase; aminoimidazole	0.31	-3.21	0	SGD	634747
YER053C	YER053C		0.31	-3.22	0	SGD	635148
YLR087C	CSF1		0.31	-3.22	6.75E-11	SGD	637415
YPL181W	YPL181W		0.31	-3.22	0	SGD	637115
YFR022W	YFR022W		0.31	-3.24	4.23E-20	SGD	636222

YJL084C	YJL084C		0.31	-3.24	1.99E-12 SGD	634701
YML059C	YML059C		0.31	-3.26	1.01E-26 SGD	633520
YNL326C	YNL326C		0.31	-3.26	3.10E-18 SGD	639314
YDL130W-STF1,AIS2	ATPase stabilizing factor		0.31	-3.27	4.22E-34 SGD	970739
YMR302C PRP12, RNA12, YME2	Integral membrane mitochondrial protein; integral membrane protein; Null mutant is		0.31	-3.27	1.19E-34 SGD	634605
YJL142C	YJL142C		0.31	-3.28	3.47E-39 SGD	633608
YOL034W	YOL034W		0.3	-3.28	1.14E-17 SGD	638875
YBR151W APP1	actin patches distal		0.3	-3.3	3.59E-17 SGD	636703
YDR517W GRH1	Yeast (GR)ASP65 (H)omologue; mammalian GRASP protein homolog; Null mutatio		0.3	-3.31	0 SGD	633959
YPR106W ISR1	Inhibition of staurosporine resistance; protein kinase; The null mutant is viable but e		0.3	-3.31	9.02E-17 SGD	639376
YDL222C	YDL222C		0.3	-3.32	1.76E-09 SGD	638398
YGR243W	YGR243W		0.3	-3.32	0 SGD	638207
YJR033C RAV1	Regulator of (H+)-ATPase in vacuolar membrane		0.3	-3.32	1.02E-21 SGD	633528
YMR119W ASI1	Amino acid Sensor-Independent (ASI) genes encode membrane proteins Asi1p, Asi		0.3	-3.32	7.39E-14 SGD	635404
YGL018C JAC1	may be involved in assembly/maturation of mitochondrial iron-sulfur proteins; E. coli		0.3	-3.33	3.64E-15 SGD	635764
YIL045W PIG2	Interacts with Gsy2p; 30% identity to YER054C/GIP2; Null mutant is viable and sho		0.3	-3.34	4.05E-29 SGD	639468
YOL025W LAG2,ECM36	affects longevity; A Tn3 insertion into this gene causes hypersensitivity to the cell su		0.3	-3.34	3.78E-11 SGD	634563
YGR031W YGR031W			0.3	-3.35	1.17E-09 SGD	633861
YMR231W PEP5,END1,VAM1,VPL	peripheral vacular membrane protein, putative Zn-finger protein; Zn-finger protein (p		0.3	-3.35	2.74E-34 SGD	635535
YOR179C YOR179C			0.3	-3.35	7.21E-13 SGD	635793
YLL015W BPT1	bile pigment transporter; ABC transporter, highly homologous to human MRP1 and		0.3	-3.36	1.34E-28 SGD	635691
YNL305C YNL305C			0.3	-3.36	2.01E-29 SGD	638457
YBR203W YBR203W			0.29	-3.4	3.02E-25 SGD	638853
YLR359W ADE13,BRA1,BRA8	Adenylosuccinate Lyase; adenylosuccinate lyase; Unable to grow on complete med		0.29	-3.4	1.61E-39 SGD	638582
YER066W YER066W			0.29	-3.44	4.47E-25 SGD	633678
YHR002W LEU5	mitochondrial carrier protein, involved in the accumulation of CoA in the mitochondri		0.29	-3.44	3.86E-30 SGD	637840
YDR074W TPS2,HOG2,PFK3	Trehalose-6-phosphate phosphatase; trehalose-6-phosphate phosphatase; Null mu		0.29	-3.45	0 SGD	637295
YPL031C PHO85	involved in phosphate and glycogen metabolism and cell cycle progression; cyclin-d		0.29	-3.47	1.86E-15 SGD	635989
YDR043C NRG1	involved in regulation of glucose repression; binds to UAS-1 in the STA1 promoter a		0.29	-3.5	3.86E-16 SGD	636562
YDR399W HPT1,BRA6	enzyme involved in de novo purine biosynthesis; hypoxanthine guanine phosphorib		0.29	-3.5	6.66E-14 SGD	636585
YER187W YER187W	similar to killer toxin		0.29	-3.5	4.39E-12 SGD	636485
YLR128W YLR128W			0.29	-3.5	1.48E-19 SGD	634473
YMR119W YMR119W-A			0.29	-3.5	4.55E-08 SGD	637492
YOR125C CAT5,COQ7	may encode a protein involved in one or more monooxygenase or hydroxylase steps		0.29	-3.51	1.65E-21 SGD	635878
YMR304W UBP15	putative deubiquitinating enzyme; deubiquitinating enzyme (putative)		0.28	-3.52	1.96E-21 SGD	633488
YKL062W MSN4	multicopy suppressor of snf1 mutation; zinc finger protein; Null mutant is viable, msr		0.28	-3.53	2.74E-17 SGD	638719
YCR032W BPH1	beige protein homologue 1; Null mutant is viable, sensitive to low pH		0.28	-3.54	0 SGD	633515

YHR162W	YHR162W							
YML110C	COQ5,DBI56	co-enzyme Q deficient; C-methyltransferase (putative); Null mutant is viable, respira	0.28	-3.55	0 SGD	637501		
YBR001C	NTH2	hydrolyzes trehalose, may be involved in growth transition from glucose to glycerol, s	0.28	-3.56	2.38E-24 SGD	634751		
YGR149W	YGR149W		0.28	-3.56	0 SGD	639368		
YPR161C	SGV1,BUR1	CDC28/cdc2 related protein kinase; Null mutant is inviable.	0.28	-3.56	2.06E-09 SGD	635419		
YMR261C	TPS3	115 kD regulatory subunit of trehalose-6-phosphate synthase/phosphatase complex	0.28	-3.57	2.61E-10 SGD	637305		
YER024W	YAT2	The Yat2p protein shows significant homology with the known carnitine acetyltransf	0.28	-3.58	0 SGD	635574		
YGL193C	YGL193C		0.28	-3.59	6.49E-37 SGD	634873		
YDL239C	ADY3	Accumulation of dyads; Null: forms largely ascospores that contain 2 spores (dyads) when :	0.28	-3.61	2.25E-41 SGD	634164		
YKL150W	MCR1	NADH-cytochrome b5 reductase	0.28	-3.61	8.76E-13 SGD	638404		
YDL128W	VCX1,HUM1,MNR1	Similar to sodium/calcium exchangers, including bovine Na+/Ca2+,K+ antiporter, pu	0.28	-3.63	1.79E-30 SGD	635199		
YMR145C	YMR145C		0.28	-3.63	3.99E-31 SGD	636212		
YNL022C	YNL022C		0.28	-3.63	0 SGD	635290		
YGL248W	PDE1	3',5'-Cyclic-nucleotide phosphodiesterase, low affinity; 3',5'-cyclic-nucleotide phosph	0.28	-3.64	0 SGD	639341		
YKR058W	GLG1	self-glucosylating initiator of glycogen synthesis, similar to mammalian glycogenin; g	0.27	-3.65	6.64E-27 SGD	637088		
YOL016C	CMK2	Calmodulin-dependent protein kinase; calmodulin-dependent protein kinase; Null m	0.27	-3.66	4.57E-20 SGD	636117		
YCL033C	YCL033C	Transcription regulator	0.27	-3.72	3.84E-16 SGD	633605		
YJL186W	MNN5	mannan synthesis; golgi alpha-1,2-mannosyltransferase (putative); Null mutant is vi	0.27	-3.73	0 SGD	636240		
YBR126C	TPS1,BYP1,CIF1,FDP1	Probable regulator of glucose influx into the cell & into glycolytic pathway, indirectly	0.27	-3.74	1.37E-28 SGD	635318		
YGL208W	SIP2,SPM2	Member of a family of proteins, including Sip1p and Gal83p, that interact with Snf1p	0.27	-3.74	1.15E-10 SGD	636792		
YJL163C	YJL163C		0.27	-3.74	1.08E-11 SGD	636214		
YMR213W	CEF1	homolog of <i>S. pombe</i> cdc5+; protein complex component associated with the splicir	0.27	-3.77	1.57E-20 SGD	638004		
YML013W	YML013W		0.26	-3.78	8.83E-43 SGD	636182		
YOR285W	YOR285W		0.26	-3.79	0 SGD	636385		
YMR083W	ADH3	alcohol dehydrogenase isoenzyme III; Null mutant is viable	0.26	-3.8	0 SGD	636035		
YAR015W	ADE1	phosphoribosyl amino imidazolesuccinocarboamide synthetase; Null mutant is via	0.26	-3.81	0 SGD	634502		
YKR049C	YKR049C		0.26	-3.83	0 SGD	636405		
YKL034W	YKL034W		0.26	-3.89	2.13E-10 SGD	634187		
YBR241C	YBR241C	Probable sugar transport protein	0.26	-3.9	0 SGD	636800		
YAL061W	YAL061W		0.26	-3.91	2.51E-39 SGD	637054		
YKR089C	YKR089C		0.26	-3.92	5.44E-38 SGD	634610		
YLR240W	VPS34,END12,PEP15,V	phosphatidylinositol 3-kinase; temperature sensitive, defective vacuolar protein sort	0.25	-3.93	1.67E-15 SGD	638764		
YNL115C	YNL115C		0.25	-3.94	0 SGD	635469		
YPR184W	GDB1	Glycogen debranching enzyme, the enzyme that debranches the glycogen having a	0.25	-3.94	0 SGD	635635		
YOR291W	YOR291W		0.25	-3.96	1.55E-40 SGD	633584		
YDR046C	BAP3	branched-chain amino acid permease; valine transporter	0.25	-3.97	5.30E-26 SGD	635395		
YDL079C	MRK1	putative protein kinase with similarity to mammalian glycogen synthase kinase-3 an	0.25	-3.99	0 SGD	638017		

YHR190W	ERG9	squalene synthetase; Null mutant is inviable	0.25	-3.99	9.90E-11 SGD	637862
YBR086C	IST2	Similar to calcium and sodium channel proteins	0.25	-4.02	3.33E-41 SGD	637330
YPL004C	YPL004C		0.24	-4.09	0 SGD	639241
YNL037C	IDH1	alpha-4-beta-4 subunit of mitochondrial isocitrate dehydrogenase 1; isocitrate dehydrogenase	0.24	-4.13	5.53E-14 SGD	637768
YBR067C	TIP1	cold- and heat-shock induced protein of the Srp1p/Tip1p family of serine-alanine-rich	0.24	-4.15	4.39E-10 SGD	633292
YLR258W	GSY2	Highly similar to GSY1. GSY2 is the predominantly expressed glycogen synthase. A	0.24	-4.17	1.32E-40 SGD	638037
YNR001C	CIT1,CS1,LYS6	citrate synthase. Nuclear encoded mitochondrial protein.; citrate synthase; Null mutant	0.24	-4.17	0 SGD	638640
YER028C	YER028C		0.24	-4.18	6.05E-20 SGD	638520
YJL198W	PHO90	Low-affinity phosphate transporter	0.24	-4.19	3.35E-43 SGD	635502
YFR053C	HXK1	Glucose phosphorylation; hexokinase I (PI) (also called hexokinase A); Null mutant	0.24	-4.2	0 SGD	638580
YER067W	YER067W		0.23	-4.28	0 SGD	634400
YPL101W	ELP4,HAP1	ELongator Protein 4, 50kD subunit; RNA polymerase II Elongator protein subunit; N	0.23	-4.33	2.48E-34 SGD	639443
YMR019W	STB4	binds Sin3p in two-hybrid assay; Null mutant is viable, hypersensitive to caffeine	0.23	-4.34	2.33E-22 SGD	634694
YOR120W	GCY1	Galactose-induced transcript, product is homologous to mammalian aldo/keto reduc	0.23	-4.36	1.78E-15 SGD	634541
YCR091W	KIN82	Putative serine/threonine protein kinase most similar to cyclic nucleotide-dependent	0.23	-4.38	0 SGD	634764
YNL045W	YNL045W		0.23	-4.4	1.22E-42 SGD	638736
YGL197W	MDS3	Mck1 Dosage Suppressor 3, negative regulator of early meiotic gene expression; N	0.23	-4.41	0 SGD	638902
YBR286W	APE3,APY1	Aminopeptidase ysclll; aminopeptidase ysclll; Null mutant is viable but exhibited rec	0.23	-4.42	6.11E-15 SGD	637928
YOL153C	YOL153C		0.22	-4.44	4.65E-34 SGD	639509
YKL035W	UGP1	Uridinephosphoglucose pyrophosphorylase; uridinephosphoglucose pyrophosphory	0.22	-4.46	0 SGD	635301
YCL040W	GLK1,HOR3	Glucose phosphorylation; glucokinase; Null mutant is viable with no discernible diffe	0.22	-4.49	1.35E-06 SGD	638628
YDL019C	OSH2	Oxysterol Binding Protein; Null mutant is viable	0.22	-4.5	0 SGD	637343
YPL006W	NCR1	Niemann-Pick Type C homologous gene; transmembrane protein (putative); Null mu	0.22	-4.58	1.63E-19 SGD	633355
YBR052C	YBR052C	Homolog to YCR004, obr1 ( <i>S. pombe</i> ), trp repressor binding protein ( <i>E. coli</i> )	0.22	-4.62	1.58E-15 SGD	638337
YMR098C	YMR098C		0.22	-4.63	0 SGD	638695
YMR136W	GAT2	Product of gene unknown	0.21	-4.67	5.71E-28 SGD	636195
YNR014W	YNR014W		0.21	-4.7	9.12E-26 SGD	636511
YDR277C	MTH1,BPC1,DGT1,HTR	Negative regulator of HXT gene expression; Msn3p homolog (61% identical); Null m	0.21	-4.72	7.31E-07 SGD	636046
YFR017C	YFR017C		0.21	-4.77	0 SGD	637604
YNL194C	YNL194C		0.21	-4.77	0 SGD	635062
YAL044C	GCV3	H-protein subunit of the glycine cleavage system; glycine cleavage system H-protein	0.21	-4.81	2.98E-14 SGD	637586
YMR105C	PGM2,GAL5	Phosphoglucomutase; phosphoglucomutase; Null mutant is viable, pgm1 pgm2 dele	0.21	-4.81	1.45E-38 SGD	634096
YGR066C	YGR066C		0.21	-4.84	2.56E-24 SGD	633809
YAL060W	BDH1	(2R,3R)-2,3-butanediol dehydrogenase	0.21	-4.86	0 SGD	638512
YBR230C	YBR230C		0.2	-5.12	1.69E-09 SGD	638286
YFR015C	GSY1	Highly similar to GSY2. GSY2 is the predominantly expressed glycogen synthase; g	0.2	-5.12	1.32E-30 SGD	634141
YHL021C	YHL021C		0.19	-5.29	2.84E-40 SGD	636103

YMR291W	YMR291W		0.19	-5.31	0 SGD	634733
YJR148W	BAT2,TWT2	Branched-Chain Amino Acid Transaminase; branched-chain amino acid transamina	0.18	-5.42	0 SGD	635238
YPL082C	MOT1,BUR3,LPF4	involved in TBP (TATA-binding protein) regulation; helicase (putative); Null mutant is Up in StarVation	0.18	-5.46	1.98E-15 SGD	635630
YPL230W	USV1	S-adenosylMethionine Permease; high affinity S-adenosylmethionine permease; Nu	0.18	-5.53	2.02E-20 SGD	637003
YPL274W	SAM3	hexose transporter; high affinity hexose transporter-2; Null mutant is viable	0.18	-5.6	0 SGD	638006
YPL095C	YPL095C	Regulates respiratory functions, encodes divergent overlapping transcripts; transcript glutamate decarboxylase	0.17	-5.79	3.02E-38 SGD	636162
YMR011W	HXT2	Repression of HXT6 expression by glucose requires SNF3; hexose transporter; Null mutant is viable	0.17	-5.91	3.95E-18 SGD	636206
YKL109W	HAP4	Serine/threonine protein kinase; Null mutant is viable	0.17	-5.98	0 SGD	637933
YMR250W	GAD1	May regulate NAM7 function, possibly at level of mRNA turnover; Null mutant is viable	0.16	-6.37	0 SGD	637992
YDR343C	HXT6	Hexose transporter; hexose transporter; Null mutant is viable, snf3 hxt1 hxt2 hxt3 hxt4	0.16	-6.4	9.50E-19 SGD	634095
YKR075C	YKR075C	Glycogen branching enzyme; 1,4-glucan-6-(1,4-glucano)-transferase; Null mutant is viable	0.15	-6.45	0 SGD	636593
YGL158W	RCK1	non-mitochondrial citrate synthase; citrate synthase; Null mutant is viable, disruptor	0.15	-6.53	6.28E-26 SGD	637165
YMR081C	ISF1,MBR3	non-mitochondrial citrate synthase; citrate synthase; Null mutant is viable, disruptor	0.15	-6.84	0 SGD	635974
YDR342C	HXT7	non-mitochondrial citrate synthase; citrate synthase; Null mutant is viable, disruptor	0.14	-6.93	2.00E-06 SGD	638015
YEL011W	GLC3,GHA1	non-mitochondrial citrate synthase; citrate synthase; Null mutant is viable, disruptor	0.14	-7.14	0 SGD	634770
YGL117W	YGL117W	non-mitochondrial citrate synthase; citrate synthase; Null mutant is viable, disruptor	0.12	-8.09	1.24E-39 SGD	635867
YCR005C	CIT2	non-mitochondrial citrate synthase; citrate synthase; Null mutant is viable, disruptor	0.09	-11.4	0 SGD	639424

:e ID

BioProcess=gluconeogenesis\*|MolFunction=phosphoglycerate mutase|CellComponent=cytosol  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cell wall  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=DNA replication initiation\*|MolFunction=chromatin binding\*|CellComponent=cytoplasm\*  
BioProcess=protein amino acid glycosylation|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=ATP adenylyltransferase|CellComponent=not yet annotated  
BioProcess=thiamin biosynthesis|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=35S primary transcript processing|MolFunction=ATP dependent RNA helicase|CellComponent=nucleolus  
BioProcess=mitotic chromosome segregation\*|MolFunction=microtubule motor|CellComponent=kinesin\*  
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BioProcess=pheromone response (sensu *Saccharomyces*)|MolFunction=pheromone|CellComponent=extracellular  
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BioProcess=polar budding\*|MolFunction=signal transducer\*|CellComponent=plasma membrane\*  
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BioProcess=ubiquitin-dependent protein catabolism\*|MolFunction=ubiquitin conjugating enzyme|CellComponent=cytoplasm\*  
BioProcess=thiamin biosynthesis|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=lagging strand elongation\*|MolFunction=DNA polymerase processivity factor|CellComponent=replication fork  
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BioProcess=DNA replication|MolFunction=ribonuclease H|CellComponent=cell  
BioProcess=microtubule-based process|MolFunction=microtubule motor|CellComponent=spindle pole body\*  
BioProcess=axial budding\*|MolFunction=molecular\_function unknown|CellComponent=bud neck\*  
BioProcess=protein catabolism|MolFunction=protease substrate recruitment factor|CellComponent=26S proteasome  
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BioProcess=DNA repair|MolFunction=transcription co-activator|CellComponent=nucleus

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BioProcess=translational termination|MolFunction=translation release factor|CellComponent=cytosol  
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BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=cytosolic large ribosomal subunit (sensu Eukarya)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=nucleus  
BioProcess=hexose transport|MolFunction=glucose transporter\*|CellComponent=not yet annotated  
BioProcess=DNA repair\*|MolFunction=pyrimidine-specific oxidized base lesion DNA N-glycosylase\*|CellComponent=nucleus\*  
BioProcess=DNA replication initiation\*|MolFunction=alpha DNA polymerase|CellComponent=alpha DNA polymerase:primase complex  
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BioProcess=serine biosynthesis|MolFunction=phosphoglycerate dehydrogenase|CellComponent=cellular\_component unknown  
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BioProcess=regulation of pH|MolFunction=molecular\_function unknown|CellComponent=cytosol  
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BioProcess=rRNA processing\*|MolFunction=molecular\_function unknown|CellComponent=nucleolus  
BioProcess=response to heat\*|MolFunction=kinase|CellComponent=not yet annotated  
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BioProcess=not yet annotated|MolFunction=inositol-1,4,5-trisphosphate 5-phosphatase|CellComponent=not yet annotated

BioProcess=tryptophan biosynthesis|MolFunction=anthranilate phosphoribosyltransferase|CellComponent=not yet annotated  
BioProcess=microtubule nucleation|MolFunction=structural constituent of cytoskeleton|CellComponent=spindle pole body  
BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated  
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BioProcess=pseudohyphal growth\*|MolFunction=transcription factor|CellComponent=nucleus  
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BioProcess=transcription from Pol I promoter|MolFunction=not yet annotated|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=pseudohyphal growth|MolFunction=specific RNA polymerase II transcription factor|CellComponent=nucleus  
BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=mitochondrial small ribosomal subunit  
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BioProcess=DNA replication initiation\*|MolFunction=alpha DNA polymerase|CellComponent=alpha DNA polymerase:primase complex  
BioProcess=protein folding\*|MolFunction=heat shock protein|CellComponent=mitochondrial inner membrane  
BioProcess=double-strand break repair via homologous recombination\*|MolFunction=not yet annotated|CellComponent=not yet annotated  
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BioProcess=microtubule nucleation\*|MolFunction=structural constituent of cytoskeleton|CellComponent=central plaque of spindle pole body  
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BioProcess=drug susceptibility/resistance\*|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=mitochondrion organization and biogenesis\*|MolFunction=molecular\_function unknown|CellComponent=mitochondrial outer membrane  
BioProcess=G2/M transition of mitotic cell cycle\*|MolFunction=SUMO conjugating enzyme|CellComponent=nucleus  
BioProcess=biological\_process unknown|MolFunction=peptidyl-prolyl cis-trans isomerase|CellComponent=cytoplasm

BioProcess=inner mitochondrial membrane organization and biogenesis|MolFunction=molecular\_function unknown|CellComponent=mitochondrial inner membra  
BioProcess=galactose metabolism|MolFunction=UTP-hexose-1-phosphate uridylyltransferase|CellComponent=cytoplasm  
BioProcess=cell wall organization and biogenesis\*|MolFunction=structural constituent of cytoskeleton|CellComponent=septin ring (sensu *Saccharomyces*)  
BioProcess=DNA replication|MolFunction=ribonucleoside-diphosphate reductase|CellComponent=cellular\_component unknown  
BioProcess=gluconeogenesis|MolFunction=phosphoenolpyruvate carboxykinase (ATP)|CellComponent=cytosol  
BioProcess=ubiquitin-dependent protein catabolism|MolFunction=proteasome endopeptidase|CellComponent=20S core proteasome  
BioProcess=hexose transport|MolFunction=glucose transporter\*|CellComponent=not yet annotated  
BioProcess=positive regulation of glycolysis|MolFunction=transcription factor\*|CellComponent=not yet annotated  
BioProcess=signal peptide processing|MolFunction=signal peptidase|CellComponent=signal peptidase complex  
BioProcess=RNA elongation from Pol II promoter|MolFunction=transcription elongation factor|CellComponent=transcription elongation factor complex  
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BioProcess=stress response|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
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BioProcess=not yet annotated|MolFunction=lysophospholipase|CellComponent=cell wall (sensu Fungi)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm\*  
BioProcess=meiotic DNA double-strand break formation|MolFunction=endodeoxyribonuclease, producing other than 5-phosphomonoesters|CellComponent=mei  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=DNA replication and chromosome cycle|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mitotic sister chromatid cohesion\*|MolFunction=molecular\_function unknown|CellComponent=cohesin  
BioProcess=chromatin silencing at telomere\*|MolFunction=H3/H4 histone acetyltransferase|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ER to Golgi transport|MolFunction=molecular\_function unknown|CellComponent=Golgi apparatus\*  
BioProcess=protein biosynthesis\*|MolFunction=structural constituent of ribosome|CellComponent=cytosolic large ribosomal subunit (sensu Eukarya)  
BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=cell wall (sensu Fungi)  
BioProcess=ER to Golgi transport|MolFunction=molecular\_function unknown|CellComponent=COPII-coated vesicle  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=endosome  
BioProcess=rRNA processing\*|MolFunction=ribonuclease P\*|CellComponent=ribonuclease mitochondrial RNA processing complex\*  
BioProcess=mRNA splicing|MolFunction=pre-mRNA splicing factor|CellComponent=small nuclear ribonucleoprotein complex

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=rRNA processing\*|MolFunction=ribonuclease P\*|CellComponent=ribonuclease mitochondrial RNA processing complex\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ubiquitin-dependent protein catabolism|MolFunction=proteasome endopeptidase|CellComponent=19S proteasome regulatory particle\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cell wall (sensu Fungi)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=translational initiation|MolFunction=translation initiation factor|CellComponent=cytoplasm\*  
BioProcess=processing of 20S pre-rRNA|MolFunction=snoRNA binding|CellComponent=small nucleolar ribonucleoprotein complex  
BioProcess=cell wall organization and biogenesis\*|MolFunction=not yet annotated|CellComponent=integral membrane protein  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=UDP-N-acetylglucosamine biosynthesis|MolFunction=glucosamine-phosphate N-acetyltransferase|CellComponent=not yet annotated  
BioProcess=regulation of nitrogen utilization|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=non-selective vesicle fusion\*|MolFunction=v-SNARE|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=chromatin silencing at HML and HMR (sensu *Saccharomyces*)\*|MolFunction=not yet annotated|CellComponent=chromatin silencing complex  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=vitamin B6 metabolism|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=processing of 20S pre-rRNA|MolFunction=snoRNA binding|CellComponent=small nucleolar ribonucleoprotein complex  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=spindle pole body duplication (sensu *Saccharomyces*)\*|MolFunction=structural molecule|CellComponent=half bridge of spindle pole body  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=deubiquitination|MolFunction=ubiquitin-specific protease|CellComponent=cellular\_component unknown  
BioProcess=ER to Golgi transport|MolFunction=molecular\_function unknown|CellComponent=TRAPP

BioProcess=transcription from Pol I promoter|MolFunction=RNA polymerase I transcription factor\*|CellComponent=RNA polymerase I upstream activating factor  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=protein phosphatase regulator|CellComponent=protein phosphatase type 1 complex  
BioProcess=protein-vacuolar targeting|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=positive regulation of transcription from Pol II promoter by pheromones|MolFunction=GTPase inhibitor|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein biosynthesis\*|MolFunction=translation regulator|CellComponent=mitochondrial inner membrane\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein folding\*|MolFunction=chaperone|CellComponent=cytoplasm\*  
BioProcess=not yet annotated|MolFunction=cytochrome c oxidase|CellComponent=respiratory chain complex IV (sensu Eukarya)  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein amino acid glycosylation|MolFunction=prenyltransferase|CellComponent=lipid particle  
BioProcess=tRNA splicing|MolFunction=tRNA-intron endonuclease|CellComponent=nuclear inner membrane\*  
BioProcess=ubiquitin-dependent protein catabolism\*|MolFunction=enzyme activator|CellComponent=anaphase-promoting complex  
BioProcess=signal transduction of mating signal (sensu *Saccharomyces*)\*|MolFunction=protein tyrosine phosphatase|CellComponent=nucleus  
BioProcess=transport|MolFunction=transporter|CellComponent=membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=tRNA splicing|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=microtubule nucleation\*|MolFunction=structural constituent of cytoskeleton|CellComponent=central plaque of spindle pole body\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=iron homeostasis|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=rRNA modification\*|MolFunction=snoRNA binding|CellComponent=small nuclear ribonucleoprotein complex\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=cell cycle|MolFunction=cyclin-dependent protein kinase, regulator|CellComponent=cyclin-dependent protein kinase holoenzyme  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transcription from Pol III promoter|MolFunction=DNA-directed RNA polymerase III|CellComponent=DNA-directed RNA polymerase III complex  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transcriptional gene silencing|MolFunction=NAD-dependent histone deacetylase\*|CellComponent=histone deacetylase complex

BioProcess=RNA processing|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=meiosis\*|MolFunction=single-stranded DNA binding\*|CellComponent=nucleus\*  
BioProcess=protein folding|MolFunction=co-chaperone|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=N-linked glycosylation|MolFunction=UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosamine-1-phosphate transferase|CellComponent=r  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mRNA splicing\*|MolFunction=ATP dependent RNA helicase|CellComponent=nucleolus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=cytochrome c oxidase biogenesis|MolFunction=molecular\_function unknown|CellComponent=mitochondrial inner membrane\*  
BioProcess=aspartate catabolism|MolFunction=aspartate aminotransferase|CellComponent=mitochondrion  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=cytoskeleton organization and biogenesis|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=ubiquitin-dependent protein catabolism\*|MolFunction=RAN protein binding|CellComponent=cytoplasm\*  
BioProcess=attachment of GPI anchor to protein|MolFunction=GPI-anchor transamidase|CellComponent=endoplasmic reticulum membrane, intrinsic protein  
BioProcess=establishment of cell polarity (sensu *Saccharomyces*)\*|MolFunction=cytoskeletal regulatory protein binding|CellComponent=actin cap (sensu *Sacch*:  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ribosomal large subunit assembly and maintenance|MolFunction=molecular\_function unknown|CellComponent=cytoplasm\*  
BioProcess=nicotinamide adenine dinucleotide biosynthesis|MolFunction=arylformamidase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ER to Golgi transport\*|MolFunction=t-SNARE|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mRNA-nucleus export\*|MolFunction=structural molecule|CellComponent=nuclear pore  
BioProcess=manganese ion transport|MolFunction=manganese ion transporter|CellComponent=plasma membrane\*  
BioProcess=lagging strand elongation\*|MolFunction=epsilon DNA polymerase|CellComponent=replication fork  
BioProcess=fatty acid biosynthesis\*|MolFunction=molecular\_function unknown|CellComponent=endoplasmic reticulum membrane  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=establishment of cell polarity (sensu *Saccharomyces*)\*|MolFunction=cytoskeletal regulatory protein binding|CellComponent=actin cap (sensu *Sacch*:  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=RNA splicing|MolFunction=RNA helicase|CellComponent=mitochondrial matrix  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=pseudouridylate synthase|CellComponent=not yet annotated  
BioProcess=steroid metabolism|MolFunction=RNA polymerase II transcription factor|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=rRNA processing\*|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=rRNA processing|MolFunction=RNA methyltransferase|CellComponent=nucleolus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=microtubule-based process|MolFunction=microtubule motor|CellComponent=cell  
BioProcess=protein-mitochondrial targeting|MolFunction=chaperone regulator\*|CellComponent=cytosol  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=translational initiation|MolFunction=translation initiation factor|CellComponent=ribosome  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=respiratory gaseous exchange|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=thiamin biosynthesis|MolFunction=thiamin pyrophosphokinase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein folding\*|MolFunction=chaperone|CellComponent=cytoplasm\*  
BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=mitochondrial large ribosomal subunit  
BioProcess=not yet annotated|MolFunction=chorismate synthase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=chromatin modification\*|MolFunction=not yet annotated|CellComponent=SAGA complex  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=phospholipid metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=MAPKKK cascade|MolFunction=receptor signaling protein serine/threonine kinase|CellComponent=cellular\_component unknown  
BioProcess=arginine metabolism\*|MolFunction=inositol/phosphatidylinositol kinase|CellComponent=nucleus  
BioProcess=chromatin silencing at telomere\*|MolFunction=not yet annotated|CellComponent=nucleolus\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=nucleus\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=cytosolic large ribosomal subunit (sensu Eukarya)  
BioProcess=N-linked glycoprotein maturation|MolFunction=alpha-1,6-mannosyltransferase|CellComponent=Golgi cis cisterna  
BioProcess=mRNA-nucleus export\*|MolFunction=structural molecule|CellComponent=nuclear pore  
BioProcess=transcription from Pol I promoter|MolFunction=RNA polymerase I transcription factor|CellComponent=RNA polymerase I transcription factor complex  
BioProcess=ion homeostasis|MolFunction=protein kinase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=rRNA modification\*|MolFunction=snoRNA binding|CellComponent=small nuclear ribonucleoprotein complex\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=phosphatidylethanolamine biosynthesis|MolFunction=ethanolaminephosphotransferase|CellComponent=endoplasmic reticulum  
BioProcess=transcription from Pol II promoter\*|MolFunction=DNA-directed RNA polymerase III\*|CellComponent=DNA-directed RNA polymerase III complex\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transcription from Pol I promoter|MolFunction=DNA-directed RNA polymerase II|CellComponent=DNA-directed RNA polymerase I complex  
BioProcess=protein folding|MolFunction=peptidyl-prolyl cis-trans isomerase|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=meiosis|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=phosphatidylglycerol biosynthesis\*|MolFunction=phosphatidate cytidylyltransferase|CellComponent=mitochondrion\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=mRNA splicing|MolFunction=not yet annotated|CellComponent=snRNP U1\*

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown

BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=mitochondrial small ribosomal subunit

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=mitotic chromosome condensation\*|MolFunction=DNA-directed DNA polymerase|CellComponent=nucleus

BioProcess=mitochondrial translocation|MolFunction=protein transporter|CellComponent=mitochondrial inner membrane translocase complex

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=kinetochore microtubule

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=tRNA processing\*|MolFunction=not yet annotated|CellComponent=mitochondrion

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=35S primary transcript processing\*|MolFunction=3'-5' exoribonuclease|CellComponent=nuclear exosome (RNase complex)\*

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=mRNA polyadenylation|MolFunction=ubiquitin-protein ligase|CellComponent=nuclear membrane

BioProcess=UDP-galactose transport|MolFunction=UDP-galactose transporter|CellComponent=cellular\_component unknown

BioProcess=heme a biosynthesis|MolFunction=Fe2S2 electron transfer carrier|CellComponent=mitochondrial matrix

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown

BioProcess=regulation of cell cycle|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=ER to Golgi transport|MolFunction=SNARE binding|CellComponent=endoplasmic reticulum\*

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated

BioProcess=chromosome segregation|MolFunction=protein binding|CellComponent=kinetochore

BioProcess=GPI anchor biosynthesis|MolFunction=phosphoethanolamine N-methyltransferase|CellComponent=endoplasmic reticulum

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=meiosis|MolFunction=phospholipase|CellComponent=nucleus  
BioProcess=protein folding|MolFunction=chaperone|CellComponent=mitochondrial matrix  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=DNA-(apurinic or apyrimidinic site) lyase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=cytosolic large ribosomal subunit (sensu Eukarya)  
BioProcess=ER to Golgi transport|MolFunction=molecular\_function unknown|CellComponent=TRAPP  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown\*|MolFunction=helicase|CellComponent=cellular\_component unknown  
BioProcess=microtubule nucleation\*|MolFunction=structural constituent of cytoskeleton|CellComponent=inner plaque of spindle pole body\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ergosterol biosynthesis|MolFunction=hydroxymethylglutaryl-CoA reductase (NADPH)|CellComponent=mitochondrial matrix\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=chromosome segregation|MolFunction=molecular\_function unknown|CellComponent=spindle pole  
BioProcess=regulation of transcription from Pol II promoter\*|MolFunction=Pol I transcription termination factor|CellComponent=nucleus  
BioProcess=stress response\*|MolFunction=chaperone\*|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=prephenate dehydrogenase (NADP+)|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein amino acid phosphorylation\*|MolFunction=transcription factor\*|CellComponent=bud neck  
BioProcess=not yet annotated|MolFunction=RNA binding|CellComponent=polysome  
BioProcess=mitotic sister chromatid cohesion|MolFunction=molecular\_function unknown|CellComponent=cohesin  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=polyamine transport|MolFunction=protein kinase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=protein kinase|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=transport|MolFunction=not yet annotated|CellComponent=plasma membrane  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=processing of 20S pre-rRNA|MolFunction=snoRNA binding|CellComponent=small nucleolar ribonucleoprotein complex

BioProcess=stress response|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein amino acid geranylgeranylation|MolFunction=RAB-protein geranylgeranyltransferase|CellComponent=RAB-protein geranylgeranyltransferase  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mismatch repair\*|MolFunction=adenosinetriphosphatase\*|CellComponent=DNA replication factor C complex  
BioProcess=35S primary transcript processing\*|MolFunction=ATP dependent RNA helicase|CellComponent=nucleolus  
BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mating-type switching/recombination\*|MolFunction=endonuclease|CellComponent=nucleus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=lysine-tRNA ligase|CellComponent=not yet annotated  
BioProcess=protein biosynthesis|MolFunction=structural constituent of ribosome|CellComponent=mitochondrial large ribosomal subunit  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=Golgi to vacuole transport|MolFunction=molecular\_function unknown|CellComponent=Golgi trans-face  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=methionine metabolism\*|MolFunction=phosphoadenylyl-sulfate reductase (thioredoxin)|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein folding\*|MolFunction=chaperone|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=sulfur amino acid metabolism|MolFunction=homocysteine S-methyltransferase|CellComponent=cellular\_component unknown  
BioProcess=not yet annotated|MolFunction=pseudouridylate synthase|CellComponent=not yet annotated  
BioProcess=synapsis|MolFunction=molecular\_function unknown|CellComponent=telomere  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=vesicle-mediated transport|MolFunction=molecular\_function unknown|CellComponent=Golgi apparatus\*  
BioProcess=carbohydrate metabolism|MolFunction=D-arabinose 1-dehydrogenase [NAD(P)]|CellComponent=cellular\_component unknown  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=rRNA-nucleus export\*|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=ribosome biogenesis|MolFunction=translation elongation factor|CellComponent=cytoplasm  
BioProcess=regulation of transcription from Pol II promoter|MolFunction=molecular\_function unknown|CellComponent=CCR4-NOT complex  
BioProcess=signal transduction|MolFunction=signal transducer|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=lipid binding\*|CellComponent=cellular\_component unknown

BioProcess=vesicle-mediated transport\*|MolFunction=RAB small monomeric GTPase|CellComponent=vacuole  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=cytochrome c oxidase|CellComponent=respiratory chain complex IV (sensu Eukarya)  
BioProcess=aerobic respiration\*|MolFunction=ubiquinol-cytochrome c reductase|CellComponent=respiratory chain complex III (sensu Eukarya)  
BioProcess=myo-inositol metabolism\*|MolFunction=protein serine/threonine kinase\*|CellComponent=endoplasmic reticulum membrane\*  
BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=negative regulation of transcription from Pol II promoter|MolFunction=RNA polymerase II transcription mediator|CellComponent=transcription factor  
BioProcess=protein amino acid acetylation|MolFunction=peptide alpha-N-acetyltransferase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=not yet annotated|MolFunction=pyruvate dehydrogenase (lipoamide)|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mRNA catabolism\*|MolFunction=protein binding|CellComponent=cytoplasm\*  
BioProcess=not yet annotated|MolFunction=1-phosphatidylinositol 4-kinase|CellComponent=plasma membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=chromatin modification|MolFunction=molecular\_function unknown|CellComponent=nucleus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=aromatic amino acid transport|MolFunction=aromatic amino acid transporter|CellComponent=plasma membrane  
BioProcess=biological\_process unknown|MolFunction=nucleotide binding|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=chromatin silencing at telomere|MolFunction=acetyltransferase|CellComponent=chromatin\*  
BioProcess=vesicle-mediated transport|MolFunction=molecular\_function unknown|CellComponent=cytoplasmic vesicle\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=integral membrane protein  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=carbohydrate metabolism|MolFunction=hydroxyacylglutathione hydrolase|CellComponent=mitochondrion\*  
BioProcess=not yet annotated|MolFunction=carnitine O-acetyltransferase|CellComponent=mitochondrion  
BioProcess=establishment of cell polarity (sensu *Saccharomyces*)\*|MolFunction=not yet annotated|CellComponent=actin cap (sensu *Saccharomyces*)\*  
BioProcess=iron homeostasis\*|MolFunction=siderochrome-iron transporter|CellComponent=plasma membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=pantothenate biosynthesis|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=cell cycle|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=pyruvate dehydrogenase (lipoamide)|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=histone acetylation|MolFunction=histone acetyltransferase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transcription from Pol II promoter|MolFunction=RNA polymerase II transcription mediator|CellComponent=mediator complex  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=ribokinase|CellComponent=not yet annotated  
BioProcess=O-linked glycosylation\*|MolFunction=alpha-1,2-mannosyltransferase|CellComponent=Golgi apparatus  
BioProcess=translational initiation|MolFunction=translation initiation factor|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=DNA replication initiation\*|MolFunction=chromatin binding|CellComponent=nucleus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=nucleobase, nucleoside, nucleotide and nucleic acid metabolism|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ER to Golgi transport|MolFunction=molecular\_function unknown|CellComponent=TRAPP  
BioProcess=ergosterol biosynthesis|MolFunction=C-14 sterol reductase|CellComponent=endoplasmic reticulum  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=glutamate dehydrogenase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cell wall (sensu Fungi)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=heavy metal sensitivity/resistance|MolFunction=copper binding|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=sodium ion homeostasis|MolFunction=protein serine/threonine phosphatase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=ergosterol biosynthesis|MolFunction=electron transporter|CellComponent=microsome

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=transcription initiation from Pol III promoter|MolFunction=RNA polymerase III transcription factor|CellComponent=transcription factor TFIIC  
BioProcess=ATP synthesis coupled proton transport|MolFunction=molecular\_function unknown|CellComponent=proton-transporting ATP synthase complex (serine/threonine kinase)  
BioProcess=transcription initiation from Pol II promoter\*|MolFunction=general RNA polymerase II transcription factor|CellComponent=TFIID complex  
BioProcess=signal transduction of mating signal (sensu *Saccharomyces*)|MolFunction=MAP-kinase scaffold protein|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=establishment of cell polarity (sensu *Saccharomyces*)\*|MolFunction=signal transducer\*|CellComponent=bud tip  
BioProcess=di-, tri-valent inorganic cation transport|MolFunction=di-, tri-valent inorganic cation transporter|CellComponent=plasma membrane  
BioProcess=protein-vacuolar targeting\*|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=aldehyde metabolism|MolFunction=benzyl alcohol dehydrogenase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=sphingolipid metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=vesicle-mediated transport|MolFunction=structural molecule|CellComponent=clathrin vesicle coat  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=tricarboxylic acid cycle\*|MolFunction=oxoglutarate dehydrogenase (lipoamide)|CellComponent=mitochondrial matrix  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=amino acid transport|MolFunction=amino acid transporter|CellComponent=plasma membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ER-associated protein catabolism|MolFunction=molecular\_function unknown|CellComponent=endoplasmic reticulum membrane, intrinsic protein  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=polyubiquitination\*|MolFunction=ubiquitin-protein ligase|CellComponent=plasma membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=G1/S transition of mitotic cell cycle|MolFunction=protein serine/threonine phosphatase|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mRNA polyadenylation\*|MolFunction=cleavage/polyadenylation specificity factor|CellComponent=mRNA cleavage and polyadenylation specificity factor  
BioProcess=cell cycle|MolFunction=kinase|CellComponent=not yet annotated  
BioProcess=transport|MolFunction=ATP-binding cassette (ABC) transporter|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=phosphatidic acid biosynthesis|MolFunction=acylglycerone-phosphate reductase|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=DNA repair\*|MolFunction=molecular\_function unknown|CellComponent=chromatin assembly complex  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=mRNA-nucleus export\*|MolFunction=structural molecule|CellComponent=nuclear pore  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=regulation of transcription, mating-type specific|MolFunction=transcription co-repressor|CellComponent=nucleus  
BioProcess=protein catabolism\*|MolFunction=protein N-terminal asparagine amidohydrolase|CellComponent=cellular\_component unknown  
BioProcess=transcription|MolFunction=transcription factor|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown\*|MolFunction=helicase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein amino acid phosphorylation\*|MolFunction=protein serine/threonine kinase|CellComponent=actin cortical patch (sensu *Saccharomyces*)  
BioProcess=protein secretion|MolFunction=molecular\_function unknown|CellComponent=peripheral membrane protein of membrane fraction  
BioProcess=cell cycle|MolFunction=protein kinase|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=transketolase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=endocytosis\*|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=response to osmotic stress\*|MolFunction=actin monomer binding|CellComponent=actin cap (sensu *Saccharomyces*)\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=histone acetylation|MolFunction=molecular\_function unknown|CellComponent=nucleus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=folylpolyglutamate synthase|CellComponent=not yet annotated  
BioProcess=pseudohyphal growth\*|MolFunction=1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase|CellComponent=cellular\_component unknown  
BioProcess=protein complex assembly\*|MolFunction=molecular\_function unknown|CellComponent=mitochondrial inner membrane  
BioProcess=establishment of cell polarity (sensu *Saccharomyces*)\*|MolFunction=not yet annotated|CellComponent=actin cap (sensu *Saccharomyces*)\*  
BioProcess=lipid transport|MolFunction=plasma membrane long-chain fatty acid transporter|CellComponent=cytoplasm  
BioProcess=ubiquinone metabolism|MolFunction=not yet annotated|CellComponent=mitochondrial inner membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=chromosome segregation\*|MolFunction=not yet annotated|CellComponent=cytosolic small ribosomal subunit (sensu Eukarya)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=lactate metabolism|MolFunction=D-lactate dehydrogenase (cytochrome)|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=lysine biosynthesis|MolFunction=transcription factor|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=establishment of cell polarity (sensu *Saccharomyces*)\*|MolFunction=signal transducer\*|CellComponent=intracellular  
BioProcess=protein amino acid phosphorylation\*|MolFunction=casein kinase I|CellComponent=endoplasmic reticulum\*  
BioProcess=not yet annotated|MolFunction=protein tyrosine phosphatase|CellComponent=cytoplasm\*  
BioProcess=sterol metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=sphingolipid metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=tRNA processing|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=response to osmotic stress\*|MolFunction=cytoskeletal protein binding|CellComponent=actin cortical patch (sensu *Saccharomyces*)  
BioProcess=aerobic respiration\*|MolFunction=ubiquinol-cytochrome c reductase|CellComponent=respiratory chain complex III (sensu Eukarya)  
BioProcess=mRNA-nucleus export\*|MolFunction=structural molecule|CellComponent=nuclear pore  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mating (sensu *Saccharomyces*)\*|MolFunction=metalloendopeptidase|CellComponent=intracellular  
BioProcess=phosphatidylcholine biosynthesis|MolFunction=phosphatidylserine decarboxylase|CellComponent=not yet annotated  
BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=vesicle-mediated transport|MolFunction=clathrin binding|CellComponent=AP-1 adaptor complex  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=arginine biosynthesis|MolFunction=carbamoyl-phosphate synthase (glutamine-hydrolyzing)|CellComponent=cytosol  
BioProcess=protein amino acid phosphorylation\*|MolFunction=protein kinase|CellComponent=cytosolic ribosome (sensu Eukarya)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=protein biosynthesis|MolFunction=protein phosphatase type 2A|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=GPI anchor biosynthesis|MolFunction=molecular\_function unknown|CellComponent=integral membrane protein  
BioProcess=protein folding\*|MolFunction=protein disulfide isomerase|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=nucleus  
BioProcess=cation transport|MolFunction=molecular\_function unknown|CellComponent=plasma membrane  
BioProcess=ATP synthesis coupled proton transport|MolFunction=hydrogen-transporting two-sector ATPase|CellComponent=hydrogen-transporting ATP synthase  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=establishment of cell polarity (sensu *Saccharomyces*)\*|MolFunction=signal transducer\*|CellComponent=intracellular

BioProcess=not yet annotated|MolFunction=phospholipase D|CellComponent=not yet annotated  
BioProcess=nicotinamide adenine dinucleotide metabolism|MolFunction=nicotinamide-nucleotide adenylyltransferase|CellComponent=cellular\_component unknown  
BioProcess=not yet annotated|MolFunction=AMP deaminase|CellComponent=not yet annotated  
BioProcess=protein-vacuolar targeting\*|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=phospholipid metabolism|MolFunction=lyase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=protein kinase|CellComponent=not yet annotated  
BioProcess=methionine metabolism|MolFunction=methionine adenosyltransferase|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=stress response\*|MolFunction=alpha,alpha-trehalose-phosphate synthase (UDP-forming)|CellComponent=alpha, alpha-trehalose-phosphate synthase  
BioProcess=misfolded or incompletely synthesized protein catabolism\*|MolFunction=peptide-N4-(N-acetyl-beta-glucosaminy)asparagine amidase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ubiquitin-dependent protein catabolism\*|MolFunction=protein binding\*|CellComponent=nuclear ubiquitin ligase complex  
BioProcess=protein amino acid glycosylation|MolFunction=transferase, transferring hexosyl groups|CellComponent=endoplasmic reticulum  
BioProcess=aerobic respiration\*|MolFunction=ubiquinol-cytochrome c reductase|CellComponent=mitochondrion\*  
BioProcess=mRNA catabolism\*|MolFunction=RNA helicase|CellComponent=nucleolus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mitochondrial processing|MolFunction=peptidase|CellComponent=cytoplasm\*  
BioProcess=vacuolar acidification|MolFunction=hydrogen-transporting two-sector ATPase|CellComponent=vacuolar membrane (sensu Fungi)\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=basic amino acid transport|MolFunction=basic amino acid transporter|CellComponent=plasma membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=SRP-dependent, co-translational membrane targeting, translocation|MolFunction=transporter|CellComponent=translocon  
BioProcess=ATP synthesis coupled proton transport|MolFunction=hydrogen-transporting two-sector ATPase|CellComponent=proton-transporting ATP synthase  
BioProcess=protein catabolism|MolFunction=ATPase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=nucleotide-excision repair, DNA incision, 5 to lesion|MolFunction=single-stranded DNA specific endodeoxyribonuclease|CellComponent=nucleotide  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=glycine hydroxymethyltransferase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=invasive growth|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=translational elongation|MolFunction=translation elongation factor|CellComponent=ribosome  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=peroxisome organization and biogenesis|MolFunction=molecular\_function unknown|CellComponent=peroxisomal membrane  
BioProcess=ATP/ADP exchange|MolFunction=ATP/ADP antiporter|CellComponent=mitochondrial inner membrane  
BioProcess=establishment of cell polarity (sensu *Saccharomyces*)\*|MolFunction=signal transducer\*|CellComponent=intracellular  
BioProcess=not yet annotated|MolFunction=alpha-glucosidase|CellComponent=not yet annotated  
BioProcess=negative regulation of transcription from Pol II promoter|MolFunction=general RNA polymerase II transcription factor\*|CellComponent=transcription f  
BioProcess=protein processing|MolFunction=dipeptidyl-peptidase and tripeptidyl-peptidase|CellComponent=vacuolar membrane (sensu Fungi)  
BioProcess=protein amino acid phosphorylation\*|MolFunction=protein kinase|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=cytoskeleton organization and biogenesis\*|MolFunction=cytoskeletal protein binding\*|CellComponent=actin cortical patch (sensu *Saccharomyces*)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ATP synthesis coupled proton transport|MolFunction=hydrogen-transporting two-sector ATPase|CellComponent=hydrogen-transporting ATP synthase  
BioProcess=mRNA-nucleus export\*|MolFunction=structural molecule|CellComponent=nuclear pore\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=phosphoserine aminotransferase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=steroid biosynthesis|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=NAD+ synthase (glutamine-hydrolyzing)|CellComponent=cellular\_component unknown  
BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=mRNA polyadenylation\*|MolFunction=cleavage/polyadenylation specificity factor|CellComponent=mRNA cleavage and polyadenylation specificity fa  
BioProcess=not yet annotated|MolFunction=xylulokinase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=complex III (ubiquinone to cytochrome c)\*|MolFunction=electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex|C  
BioProcess=regulation of glycogen biosynthesis|MolFunction=cyclin-dependent protein kinase, regulator|CellComponent=cyclin-dependent protein kinase holoer  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ribosomal large subunit assembly and maintenance|MolFunction=protein binding\*|CellComponent=cytosol\*

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=DNA replication|MolFunction=ATPase\*|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=meiosis\*|MolFunction=adenylate cyclase|CellComponent=plasma membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=steroid biosynthesis|MolFunction=not yet annotated|CellComponent=Golgi trans cisterna\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=complex I (NADH to ubiquinone)|MolFunction=not yet annotated|CellComponent=NADH dehydrogenase complex (ubiquinone) (sensu Eukarya)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=cell wall biosynthesis (sensu Fungi)|MolFunction=alpha-glucosidase|CellComponent=endoplasmic reticulum  
BioProcess=aerobic respiration\*|MolFunction=D-lactate dehydrogenase (cytochrome)|CellComponent=mitochondrial inner membrane  
BioProcess=peroxisome organization and biogenesis|MolFunction=adenosinetriphosphatase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=cytochrome c oxidase|CellComponent=respiratory chain complex IV (sensu Eukarya)  
BioProcess=cell wall organization and biogenesis\*|MolFunction=inositol-1,4,5-trisphosphate 5-phosphatase|CellComponent=membrane fraction  
BioProcess=fatty acid metabolism|MolFunction=hydrogen:amino acid symporter|CellComponent=endoplasmic reticulum membrane\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein amino acid phosphorylation\*|MolFunction=protein serine/threonine kinase\*|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=cell wall organization and biogenesis\*|MolFunction=protein kinase C|CellComponent=cellular\_component unknown  
BioProcess=35S primary transcript processing\*|MolFunction=5'-3' exoribonuclease|CellComponent=cytoplasm  
BioProcess=chromatin modeling\*|MolFunction=molecular\_function unknown|CellComponent=nucleus  
BioProcess=leucine biosynthesis|MolFunction=2-isopropylmalate synthase|CellComponent=cytoplasm\*  
BioProcess=translational elongation|MolFunction=translation elongation factor|CellComponent=ribosome  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=polyubiquitination\*|MolFunction=ubiquitin-protein ligase|CellComponent=cellular\_component unknown  
BioProcess=non-selective vesicle fusion|MolFunction=v-SNARE|CellComponent=vacuolar membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=protein processing|MolFunction=cysteine-type endopeptidase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=arginase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=alcohol\_O-acetyltransferase|CellComponent=not yet annotated  
BioProcess=aerobic respiration|MolFunction=cytochrome\_c\_oxidase|CellComponent=respiratory\_chain\_complex\_IV\_(sensu\_Eukarya)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ER-associated\_protein\_catabolism|MolFunction=ubiquitin-protein\_ligase|CellComponent=endoplasmic\_reticulum\_membrane  
BioProcess=signal\_transduction|MolFunction=molecular\_function unknown|CellComponent=cellular\_component\_unknown  
BioProcess=fatty\_acid\_beta-oxidation\*|MolFunction=malic\_enzyme|CellComponent=peroxisomal\_matrix  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ER\_to\_Golgi\_transport\*|MolFunction=molecular\_function unknown|CellComponent=COPI\_vesicle\_coat  
BioProcess=not yet annotated|MolFunction=transaldolase|CellComponent=not yet annotated  
BioProcess=transcription\_initiation\_from\_Pol\_II\_promoter\*|MolFunction=specific\_RNA\_polymerase\_II\_transcription\_factor|CellComponent=nucleus  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mitochondrion\_organization\_and\_biogenesis\*|MolFunction=molecular\_function unknown|CellComponent=cell  
BioProcess=polyamine\_transport|MolFunction=spermine\_transporter\*|CellComponent=vacuolar\_membrane  
BioProcess=ATP\_synthesis\_coupled\_proton\_transport|MolFunction=hydrogen-transferring\_two-sector\_ATPase|CellComponent=hydrogen-transferring\_ATP\_synthase  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=hexadecanal\_biosynthesis|MolFunction=3-oxoacyl-[acyl-carrier\_protein]\_synthase|CellComponent=mitochondrion  
BioProcess=vacuolar\_acidification\*|MolFunction=hydrogen-transferring\_two-sector\_ATPase|CellComponent=hydrogen-transferring\_ATPase\_V0\_domain  
BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=intracellular\_accumulation\_of\_glycerol|MolFunction=glycerol-3-phosphate\_dehydrogenase\_(NAD+)|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=protein\_kinase|CellComponent=not yet annotated  
BioProcess=ubiquinone\_metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=iron\_transport|MolFunction=multicopper\_ferroxidase\_iron\_transport\_mediator|CellComponent=membrane\_fraction  
BioProcess=carbohydrate\_metabolism|MolFunction=alpha-mannosidase|CellComponent=vacuolar\_membrane  
BioProcess=aerobic\_respiration\*|MolFunction=ubiquinol-cytochrome\_c\_reductase|CellComponent=respiratory\_chain\_complex\_III\_(sensu\_Eukarya)  
BioProcess=carbohydrate\_metabolism|MolFunction=glycerol-3-phosphate\_dehydrogenase|CellComponent=mitochondrion  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component\_unknown  
BioProcess=pseudohyphal\_growth\*|MolFunction=acid\_phosphatase|CellComponent=cellular\_component\_unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=acetate\_metabolism\*|MolFunction=acetyl-CoA\_hydrolase|CellComponent=cytoplasm

BioProcess=pheromone processing|MolFunction=protein farnesyltransferase|CellComponent=cytoplasm  
BioProcess=ergosterol biosynthesis|MolFunction=hydroxymethylglutaryl-CoA reductase (NADPH)|CellComponent=mitochondrial matrix\*  
BioProcess=meiosis\*|MolFunction=protein phosphatase type 1|CellComponent=protein phosphatase type 1 complex  
BioProcess=biological\_process unknown\*|MolFunction=molecular\_function unknown\*|CellComponent=cellular\_component unknown  
BioProcess=regulation of translation|MolFunction=RNA helicase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transport|MolFunction=ATP-binding cassette (ABC) transporter|CellComponent=integral membrane protein  
BioProcess=tRNA splicing|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein-vacuolar targeting\*|MolFunction=molecular\_function unknown|CellComponent=cytosol  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mRNA catabolism|MolFunction=molecular\_function unknown|CellComponent=cytoplasm\*  
BioProcess=GPI anchor biosynthesis|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=not yet annotated|MolFunction=5-aminolevulinate synthase|CellComponent=not yet annotated  
BioProcess=ER-associated protein catabolism\*|MolFunction=protein binding|CellComponent=endoplasmic reticulum membrane, intrinsic protein  
BioProcess=DNA repair\*|MolFunction=transcription factor|CellComponent=cellular\_component unknown  
BioProcess=chromatin assembly/disassembly|MolFunction=DNA binding|CellComponent=nucleosome  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=regulation of transcription, DNA-dependent\*|MolFunction=transcription factor\*|CellComponent=nucleus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=chromatin modification\*|MolFunction=not yet annotated|CellComponent=SAGA complex  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ubiquinone metabolism|MolFunction=hexaprenyldihydroxybenzoate methyltransferase|CellComponent=not yet annotated  
BioProcess=tricarboxylic acid cycle\*|MolFunction=fumarate hydratase|CellComponent=cytosol\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=vacuolar acidification\*|MolFunction=hydrogen-transporting two-sector ATPase\*|CellComponent=hydrogen-transporting ATPase V1 domain  
BioProcess=polyubiquitination\*|MolFunction=ubiquitin-protein ligase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=iron homeostasis|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=glycogen metabolism\*|MolFunction=protein phosphatase type 1|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=sphingolipid metabolism\*|MolFunction=sphingosine-1-phosphate phosphatase|CellComponent=endoplasmic reticulum  
BioProcess=phosphatidylinositol biosynthesis|MolFunction=CDP-diacylglycerol-inositol 3-phosphatidyltransferase|CellComponent=endoplasmic reticulum  
BioProcess=cell wall organization and biogenesis\*|MolFunction=1,3-beta-glucan synthase|CellComponent=actin cap (sensu *Saccharomyces*)\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=ergosterol biosynthesis|MolFunction=dimethylallyltransferase\*|CellComponent=cytosol  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cell wall (sensu Fungi)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=peroxisome organization and biogenesis|MolFunction=adenosinetriphosphatase|CellComponent=peroxisome  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=transaldolase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=Golgi retention|MolFunction=molecular\_function unknown|CellComponent=extrinsic membrane protein  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=transcription factor|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=intracellular protein transport|MolFunction=RAB escort protein|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=nucleus  
BioProcess=alpha-glucoside transport|MolFunction=general alpha-glucoside:hydrogen symporter\*|CellComponent=membrane fraction  
BioProcess=regulation of cell shape and cell size|MolFunction=kinase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=tRNA splicing|MolFunction=tRNA-intron endonuclease|CellComponent=nuclear inner membrane\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=phosphatidylcholine biosynthesis|MolFunction=phosphatidylethanolamine N-methyltransferase|CellComponent=endoplasmic reticulum  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=glycolysis|MolFunction=6-phosphofructokinase|CellComponent=cytoplasm\*  
BioProcess=glucose metabolism|MolFunction=DNA binding\*|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=mitochondrial outer membrane  
BioProcess=biological\_process unknown|MolFunction=NADH dehydrogenase|CellComponent=not yet annotated  
BioProcess=regulation of transcription from Pol II promoter\*|MolFunction=DNA binding\*|CellComponent=cytoplasm\*  
BioProcess=biological\_process unknown|MolFunction=RAB GTPase activator|CellComponent=soluble fraction  
BioProcess=signal transduction|MolFunction=molecular\_function unknown|CellComponent=plasma membrane  
BioProcess=transport\*|MolFunction=general alpha-glucoside:hydrogen symporter\*|CellComponent=membrane fraction  
BioProcess=sphingolipid metabolism|MolFunction=sphingosine hydroxylase|CellComponent=endoplasmic reticulum  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=ubiquitin-dependent protein catabolism\*|MolFunction=protein binding\*|CellComponent=anaphase-promoting complex  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=sporulation (sensu *Saccharomyces*)\*|MolFunction=RAS GTPase activator|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=G1/S transition of mitotic cell cycle\*|MolFunction=cyclin-dependent protein kinase, regulator|CellComponent=cellular\_component unknown  
BioProcess=regulation of transcription, DNA-dependent\*|MolFunction=histone deacetylase|CellComponent=histone deacetylase complex  
BioProcess=mitochondrion organization and biogenesis\*|MolFunction=molecular\_function unknown|CellComponent=mitochondrial outer membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=iron homeostasis\*|MolFunction=NADPH-adrenodoxin reductase|CellComponent=mitochondrial inner membrane  
BioProcess=ubiquitin-dependent protein catabolism\*|MolFunction=arginyltransferase|CellComponent=cytoplasm  
BioProcess=vesicle-mediated transport|MolFunction=RAB GTPase activator|CellComponent=Golgi apparatus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=methylenetetrahydrofolate dehydrogenase (NAD+)|CellComponent=not yet annotated  
BioProcess=regulation of transcription from Pol II promoter\*|MolFunction=specific RNA polymerase II transcription factor|CellComponent=nucleus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=protein kinase|CellComponent=not yet annotated  
BioProcess=tricarboxylic acid cycle\*|MolFunction=succinate dehydrogenase|CellComponent=mitochondrial matrix\*  
BioProcess=carbohydrate metabolism|MolFunction=hydroxyacylglutathione hydrolase|CellComponent=cytoplasm  
BioProcess=tryptophan biosynthesis|MolFunction=tryptophan synthase|CellComponent=cytoplasm  
BioProcess=nuclear fusion during karyogamy\*|MolFunction=molecular\_function unknown|CellComponent=shmoo tip  
BioProcess=signal transduction|MolFunction=signal transducer|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=non-selective vesicle fusion\*|MolFunction=v-SNARE|CellComponent=endoplasmic reticulum\*  
BioProcess=not yet annotated|MolFunction=carboxypeptidase C|CellComponent=cytoplasm\*  
BioProcess=mitochondrial translocation|MolFunction=protein transporter|CellComponent=mitochondrion\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=zinc ion transport\*|MolFunction=di-, tri-valent inorganic cation transporter\*|CellComponent=vacuole (sensu Fungi)  
BioProcess=not yet annotated|MolFunction=phosphoribosylformylglycinamide cyclo-ligase|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown\*|CellComponent=mitochondrion\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ATP synthesis coupled proton transport|MolFunction=molecular\_function unknown|CellComponent=proton-transporting ATP synthase complex (serine/threonine kinase activity)  
BioProcess=rRNA processing\*|MolFunction=exonuclease|CellComponent=mitochondrial inner membrane  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=DNA repair\*|MolFunction=molecular\_function unknown|CellComponent=nucleus  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mitotic spindle checkpoint|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=not yet annotated|MolFunction=protein kinase|CellComponent=not yet annotated  
BioProcess=cell wall organization and biogenesis|MolFunction=molecular\_function unknown|CellComponent=integral membrane protein\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ubiquitin-dependent protein catabolism|MolFunction=ubiquitin-protein ligase|CellComponent=endoplasmic reticulum membrane  
BioProcess=aerobic respiration\*|MolFunction=co-chaperone|CellComponent=mitochondrion  
BioProcess=biological\_process unknown|MolFunction=protein phosphatase regulator|CellComponent=cellular\_component unknown  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=non-selective vesicle docking\*|MolFunction=molecular\_function unknown|CellComponent=vacuolar membrane (sensu Fungi)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=bilirubin transport|MolFunction=bilirubin transporter|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=adenylosuccinate lyase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=stress response\*|MolFunction=trehalose phosphatase|CellComponent=alpha, alpha-trehalose-phosphate synthase complex (UDP-forming)  
BioProcess=protein amino acid phosphorylation\*|MolFunction=cyclin-dependent protein kinase|CellComponent=not yet annotated  
BioProcess=regulation of transcription from Pol II promoter\*|MolFunction=DNA binding\*|CellComponent=nucleus  
BioProcess=purine nucleotide biosynthesis|MolFunction=hypoxanthine phosphoribosyltransferase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=actin cytoskeleton organization and biogenesis|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ubiquinone metabolism|MolFunction=not yet annotated|CellComponent=mitochondrial inner membrane  
BioProcess=deubiquitination|MolFunction=ubiquitin-specific protease|CellComponent=cellular\_component unknown  
BioProcess=transcription\*|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=transport|MolFunction=not yet annotated|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=ubiquinone metabolism|MolFunction=not yet annotated|CellComponent=mitochondrion  
BioProcess=stress response\*|MolFunction=alpha,alpha-trehalase|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=cell cycle|MolFunction=protein kinase|CellComponent=not yet annotated  
BioProcess=stress response\*|MolFunction=alpha,alpha-trehalose-phosphate synthase (UDP-forming)|CellComponent=alpha, alpha-trehalose-phosphate syntha  
BioProcess=not yet annotated|MolFunction=carnitine O-acetyltransferase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=cytochrome b5 reductase|CellComponent=not yet annotated  
BioProcess=calcium ion homeostasis\*|MolFunction=calcium ion transporter\*|CellComponent=vacuolar membrane\*  
BioProcess=ethanol fermentation|MolFunction=NADH dehydrogenase|CellComponent=mitochondrion  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=nucleus  
BioProcess=cAMP-mediated signaling|MolFunction=cAMP-specific phosphodiesterase|CellComponent=cellular\_component unknown  
BioProcess=glycogen metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=protein amino acid phosphorylation\*|MolFunction=calcium/calmodulin-dependent protein kinase|CellComponent=cytoplasm  
BioProcess=response to oxidative stress\*|MolFunction=not yet annotated|CellComponent=cellular\_component unknown  
BioProcess=protein amino acid glycosylation|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=stress response\*|MolFunction=alpha,alpha-trehalose-phosphate synthase (UDP-forming)|CellComponent=cytoplasm\*  
BioProcess=protein amino acid phosphorylation\*|MolFunction=SNF1A/AMP-activated protein kinase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=mRNA splicing|MolFunction=molecular\_function unknown|CellComponent=spliceosome complex  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=acylglycerone-phosphate reductase|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=phosphoribosylaminoimidazole-succinocarboxamide synthase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein amino acid phosphorylation\*|MolFunction=protein kinase\*|CellComponent=membrane fraction  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=glycogen catabolism|MolFunction=4-alpha-glucanotransferase\*|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=amino acid transport|MolFunction=amino acid transporter|CellComponent=plasma membrane  
BioProcess=biological\_process unknown|MolFunction=protein kinase|CellComponent=not yet annotated

BioProcess=ergosterol biosynthesis|MolFunction=farnesyl-diphosphate farnesyltransferase|CellComponent=endoplasmic reticulum  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=tricarboxylic acid cycle\*|MolFunction=isocitrate dehydrogenase (NAD+)|CellComponent=mitochondrial matrix  
BioProcess=cell wall organization and biogenesis|MolFunction=structural constituent of cell wall|CellComponent=cell wall (sensu Fungi)  
BioProcess=glycogen metabolism|MolFunction=glycogen (starch) synthase|CellComponent=cytoplasm  
BioProcess=tricarboxylic acid cycle\*|MolFunction=citrate (SI)-synthase|CellComponent=mitochondrion\*  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=fructose metabolism|MolFunction=hexokinase|CellComponent=cytosol  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=protein kinase|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=meiosis|MolFunction=not yet annotated|CellComponent=cytoplasm  
BioProcess=vacuolar protein catabolism|MolFunction=aminopeptidase|CellComponent=vacuole (sensu Fungi)  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=protein amino acid glycosylation\*|MolFunction=UTP-glucose-1-phosphate uridylyltransferase|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=glucokinase|CellComponent=cytosol  
BioProcess=steroid biosynthesis|MolFunction=molecular\_function unknown|CellComponent=plasma membrane\*  
BioProcess=not yet annotated|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=transcription|MolFunction=transcription factor|CellComponent=nucleus  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=glucose transport|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown\*|CellComponent=cytoplasm\*  
BioProcess=glycine metabolism|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=glycogen metabolism\*|MolFunction=phosphoglucomutase|CellComponent=cytosol  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=butanediol fermentation|MolFunction=(R,R)-butanediol dehydrogenase|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=glycogen (starch) synthase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated

BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=branched-chain amino acid aminotransferase|CellComponent=cytoplasm  
BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=sulfur amino acid transport|MolFunction=amino acid-polyamine transporter|CellComponent=cellular\_component unknown  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=hexose transport|MolFunction=glucose transporter\*|CellComponent=not yet annotated  
BioProcess=transcription|MolFunction=not yet annotated|CellComponent=not yet annotated  
BioProcess=amino acid metabolism|MolFunction=glutamate decarboxylase|CellComponent=cytoplasm  
BioProcess=hexose transport|MolFunction=glucose transporter\*|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cytoplasm  
BioProcess=biological\_process unknown|MolFunction=protein kinase|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=cellular\_component unknown  
BioProcess=hexose transport|MolFunction=glucose transporter\*|CellComponent=not yet annotated  
BioProcess=not yet annotated|MolFunction=1,4-alpha-glucan branching enzyme|CellComponent=not yet annotated  
BioProcess=biological\_process unknown|MolFunction=molecular\_function unknown|CellComponent=not yet annotated  
BioProcess=glutamate biosynthesis\*|MolFunction=citrate (SI)-synthase|CellComponent=peroxisomal matrix





known

ine

iotic chromosome



complex

not yet annotated

aromyces)\*

aromyces)\*









re comple

complex



nsu Eukarya)

actor comple



ise, stator stalk (sensu Eukarya)

own

use complex (UDP-forming)  
nt=nucleus'

complex, coupling factor F(0) (sensu Eukarya)

excision repair factor 1

factor complex

use, catalytic core (sensu Eukarya)

factor complex

CellComponent=mitochondrial inner membrane\*  
enzyme



ise, catalytic core (*sensu* Eukarya)







nsu Eukarya)

use complex (UDP-forming)