

Run	Bins	Run Details	Motif	Z-score	Known Match	Match details	Pos.-Bias	Best Domain	Best Domain	Domain Overlap	Best GO term	Motif-Motif Interaction <sup>2</sup>	Mutual Information	Robustness
Z-score												2-score		
protein_40_YPR119W	2	CLB2: B-type cyclin involved in cell cycle pro	SP[RK]	312	SP[RK]	CDK kinase substrate motif	Y	Pkinase	1:E-04	3.5	cell cycle (1e-16)	Y	0.055	10
protein_40_YBR160W	2	CDC28: Catalytic subunit of the main cell cyc	SP[RK]	295	SP[RK]	Glycosaminoglycan attachment	Y	Pkinase	1:E-04	3.5	cell cycle (1e-16)	Y	0.053	10
yeast-256_GO-0016462	2	pyrophosphatase activity	G.G[KTS]	227	SG.G	Glycosaminoglycan attachment	ABC, tran	1:E-19	4.5	nucleoside-triphosphatase activity (1e-11)	Y	0.047	10	
yeast-238_GO-0017111	2	nucleotide-triphosphatase activity	G.G[KST]	221	SG.G	Glycosaminoglycan attachment	AAA	1:E-18	5.5	nucleoside-triphosphatase activity (1e-11)	Y	0.048	10	
yeast-335_GO-0016772	2	transf erase activity, transferring phosphorus-c	[KVJ][LVJ].DFG	205			Pkinase	1:E-85	8.1	protein kinase activity (1e-85)	Y	0.046	10	
yeast-335_GO-0016772	2	transf erase activity, transferring phosphorus-c	H.D[LIC]K	197			Pkinase	1:E-09	8.5	protein kinase activity (1e-09)	Y	0.044	10	
protein_40_YAR019C	2	CDC15: Protein kinase of the Mitotic Exit Net	H[RQSD][ILM]K	167			Pkinase	1:E-29	5.4	protein kinase activity (1e-24)	Y	0.018	10	
protein_40_YNL270	2	proteasome activator	H[YVQ][ILV].V	165			Pkinase	1:E-30	4.6	protein kinase activity (1e-24)	Y	0.017	10	
protein_40_YNL270	2	Guanyl-nucleotide exchange factor	H[YVQ][ILV].V	154			Pkinase	1:E-30	4.6	protein kinase activity (1e-31)	Y	0.017	10	
yeast-174_GO-0005634	2	Guanyl-nucleotide exchange factor	K[KR][R]	154	K[KR][R]	Nuclear localization motif	Zn_clus	1:E-07	6.4	nuclear lumen (1e-10)	Y	0.032	10	
yeast-685_GO-0016740	2	transf erase activity	H[RCWD][ILMV]K	151			Pkinase	1:E-09	8.7	protein kinase activity (1e-97)	Y	0.033	10	
protein_40_YAR019C	2	CDC15: Protein kinase of the Mitotic Exit Net	H[KVJ][LVJ].DFG	148			Pkinase	1:E-28	4.9	protein kinase activity (1e-28)	Y	0.015	10	
protein_40_YNL168W	2	transf erase activity	H[KVJ][LVJ].DFG	148			Pkinase	1:E-89	8	protein kinase activity (1e-88)	Y	0.033	10	
yeast-238_GO-0017111	2	nucleotide-triphosphatase activity	[WFLD][GQ]EDP]	136	D...G	motif that binds phosphate in	Ras	1:E-37	2.7	GTPase activity (1e-38)	Y	0.020	10	
protein_40_YNL272C	2	SEC2: Guanyl-nucleotide exchange factor	Y[ASPGE]	132	E.Y QSG	Protein TEVProtease TEV	Pkinase	1:E-89	7.4	protein kinase activity (1e-29)	Y	0.014	10	
yeast-335_GO-0016772	2	transf erase activity, transferring phosphorus-c	I[LLMVIV][SQAQ]	132	PWDLW	LIG_Clastr_ClaBox_2	Pkinase	1:E-23	4.4	protein kinase activity (1e-23)	Y	0.029	10	
protein_40_YNL163C	2	SAS10: Component of the small (ribosomal) :	D[FLS][F]CF	131			Pkinase	1:E-23	4.4	protein kinase activity (1e-23)	Y	0.014	10	
protein_40_YNL163C	2	nucleolus	D[FLS][F]CF	131	YDE[PDV]	SH2 ligand for Nck1 and Nck	Pkinase	1:E-28	3.9	protein kinase activity (1e-25)	Y	0.014	10	
protein_40_YNL168W	2	Guanyl-specific protease that deus	D[FLS][F]CF	129	DALDL	14-3-3 binding motif in ExoS	Pkinase	1:E-83	7.9	protein kinase activity (1e-85)	Y	0.029	10	
protein_40_YNL168W	2	nucleolus	D[FLS][F]CF	129	YDE[PDV]	SH2 ligand for Nck1 and Nck	Pkinase	1:E-72	6.6	protein kinase activity (1e-68)	Y	0.028	10	
protein_40_YNL168W	2	transf erase activity	I[LLMVIV][SQAQ]	128			IBN_N	1:E-05	-0.4	Golgi apparatus (1e-08)	Y	0.021	10	
ubiquitin_penc003	2	ubiquitin_penc003	I[LLMVIV][SQAQ]	125	L...[LD]S		Helicase_C	1:E-06	-1.9	DNAbeta metabolism (1e-11)	Y	0.027	10	
protein_40_YNL163C	2	Component of the small (ribosomal) :	K[KR][R]	124	K[KR][R]	Nuclear localization motif	Pkinase	1:E-25	3.8	protein kinase activity (1e-22)	Y	0.012	10	
protein_40_YNL163C	2	nucleolus	K[KR][R]	122	[KR]R	CLV_PCSK_KEX2_1	Pkinase	1:E-23	4.2	phosphotransferase activity, alcohol group as ac	Y	0.022	10	
protein_40_YNL163C	2	Guanyl-specific protease that deus	K[DIFWP]G	121			Pkinase	1:E-27	4.9	protein kinase activity (1e-23)	Y	0.013	10	
protein_40_YNL163C	2	nucleolus	K[DIFWP]G	121	YDE[PDV]	SH2 ligand for Nck1 and Nck	Pkinase	1:E-03	-1.2	nucleolus (1e-98)	Y	0.029	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	119	K[KR][R]	Nuclear localization motif	Zn_clus	1:E-07	-1.4	regulation of biological process	Y	0.027	10	
protein_40_YNL163C	2	transf erase activity, transferring phosphorus-c	K[NINSEN][CVI]	117			Pkinase	1:E-09	-1.1	regulation of metabolism (1e-09)	Y	0.023	10	
protein_40_YNL163C	2	transf erase activity, transferring phosphorus-c	K[NINSEN][CVI]	117	WIA_GISH  LF	BOMBESIN PATTERN	Pkinase	1:E-68	2.2	protein kinase activity (1e-62)	Y	0.026	10	
protein_40_YNL163C	2	transf erase activity, transferring phosphorus-c	K[NINSEN][CVI]	117	MR[DE][IL]	TUBULIN_B_AUTOREG_PA	Pkinase	1:E-86	7.8	kinase activity (1e-85)	Y	0.024	10	
protein_40_YNL163C	2	Component of the small (ribosomal) :	KPN[LIV][L]MF	109			Pkinase	1:E-25	4.4	protein kinase activity (1e-25)	Y	0.012	10	
protein_40_YNL163C	2	nucleolus	KPN[LIV][L]MF	109	YDE[PDV]	SH2 ligand for Nck1 and Nck	Zn_clus	1:E-06	-1.1	nuclear lumen (1e-18)	Y	0.022	10	
protein_40_YNL163C	2	regulation of physiological process	DE[DEK][DEJ]	107			Pkinase	1:E-26	5.1	protein kinase activity (1e-24)	Y	0.012	10	
protein_40_YNL163C	2	Guanyl-specific protease that deus	NISNE[N]SNV	105			Pkinase	1:E-19	3.6	kinase activity (1e-17)	Y	0.012	10	
protein_40_YNL163C	2	nucleolus	NISNE[N]SNV	104	WISAG JL C G	ERK1, ERK2 Kinase substr	Pkinase	1:E-20	4.7	protein kinase activity (1e-20)	Y	0.010	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	103	SP	ERK1, ERK2 Kinase substr	Ras	1:E-30	2.5	GTPase activity (1e-26)	Y	0.014	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	101			Pkinase	1:E-29	5.1	protein kinase activity (1e-26)	Y	0.013	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	101	[AG R]	Protease matrilysin protease	Pkinase	1:E-25	4.6	protein kinase activity (1e-25)	Y	0.012	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	99	KKR	OLV_PCSK_FC1ET2_1	Zn_clus	1:E-06	-1.1	regulation of metabolism (1e-09)	Y	0.022	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	99	S.G	Chitosaminidase attachment	Pkinase	1:E-26	5.1	protein kinase activity (1e-24)	Y	0.012	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	99	[FW FW]	EH3(F) hand domain bindi	Pkinase	1:E-03	-1.2	endoplasmic reticulum part (1e-31)	Y	0.019	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	99	[FW FW]	EH3(F) hand domain bindi	Helicase_C	1:E-05	-1.8	regulation of metabolism (1e-09)	Y	0.023	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	97	[ST FCG EDP]	PDK1 phosphorylation motif	Pkinase	1:E-13	4.2	kinase activity (1e-11)	Y	0.011	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	97	Y [AS P E]		Pkinase	1:E-18	3.9	protein kinase activity (1e-18)	Y	0.011	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	97	R K R S	PKC epsilon kinase substr	Pkinase	1:E-25	4	protein kinase activity (1e-23)	Y	0.012	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	[L M K.. N L F ]		Pkinase	1:E-25	4.6	protein kinase activity (1e-25)	Y	0.012	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	E.Y QSG	Protein TEVProtease TEV	Pkinase	1:E-81	7.3	protein kinase activity (1e-77)	Y	0.021	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	E.Y QSG	Protein TEVProtease TEV	Pkinase	1:E-20	4.6	protein kinase activity (1e-77)	Y	0.010	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	N N P L C J L		Pkinase	1:E-08	-1.4	regulation of metabolism (1e-27)	Y	0.020	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	[FW FW]	SH3 general ligand,	MFS_1	1:E-03	-0.1	endoplasmic reticulum part (1e-31)	Y	0.023	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	P.P.		Pkinase	1:E-02	-1.1	nucleolus (1e-11)	Y	0.019	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	actin cytoskeleton organization and biogenesis (	Y	0.010	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Mit_carr	1:E-06	-0.5	regulation of cellular metabolism (1e-26)	Y	0.010	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.018	10	
protein_40_YNL163C	2	transf erase activity	K[KR][R]	95	LLG	Beta2-Integrin binding motif	Pkinase	1:E-08	-1.3	regulation of cellular metabolism (1e-26)	Y	0.0		



yeast-256_GO-0016462	2	pyrophosphatase activity	[DGEIK_TLAHJT]	60	K_{[ST]}	PKA kinase substrate motif	E1-E2_ATPase	1.E-09	-1.2	nucleoside-triphosphatase activity (1e-16)	0.009	10	
protein_40_YPL131W	2	RPL5: Protein component of the large (60S) ribosomal subunit	[RIGST]DAQDIP	60	F..LF	Androgen receptor motif that	DEAD	1.E-05	-1.1	ribosome biogenesis (1e-08)	0.007	10	
protein_40_YHR0052W	2	Catalytic subunit protein that interacts with proteins	[DLRPA_PIGVQUR_F..F]AWCK	60	F..LF	Ankyrin B C-terminal motif th	Helicase_C	1.E-05	-0.0	RNA helicase activity (1e-08)	0.006	10	
protein_40_YDR303C	2	RSC3: Component of the RSC chromatin remodelling complex	[RLR]RSQI[GQV]	60	EED	[DKS]E[AEDP]	Sugar_Ir	1.E-05	-0.0	plasma membrane (1e-83)	0.013	10	
protein_40_YMR229C	2	RRPP5: Protein required for the synthesis of tRNA	[REVID_KPHEHQ]	60	P IV IND R_K	SH3 binding motif for HBP S'	DEAD	1.E-08	3.1	nuclear nucleosome (0.001)	0.007	10	
yeast-238_GO-0017111	2	nucleoside-triphosphatase activity	[ALUR]_PI[GDIJR	60	P IV IND R_K	Ankyrin B C-terminal motif th	Pkinase	1.E-13	3.7	rRNA metabolism (1e-09)	0.013	10	
yeast-256_GO-0016462	2	pyrophosphatase activity	[AERJF]RH[E]DIP	60	Y	[KWF]_DFG	Pkinase	1.E-07	4.4	protein kinase activity (1e-13)	0.008	10	
yeast-706_GO-0043412	2	bisphosphatase modification	[D WV]_LLCV[G]	60	Y	[D WV]_LLCV[G]	Pkinase	1.E-48	6.7	ATPase activity (1e-12)	0.007	10	
yeast-335_GO-0016772	2	transferase activity, transferring phosphorus-chemical groups	[CDA]_C[GRO]L	60	C..C	Motif on TIM mitochondrial tr.	Pkinase	1.E-54	6.9	protein amino acid phosphorylation (1e-65)	0.013	10	
yeast-401_GO-003528	2	transcription regulator activity	[DGR]_C[GRO]L	60	Y	[DGR]_C[GRO]L	GATA	1.E-16	7.8	phosphotransferase activity, alcohol group as ac	Y	0.013	10
protein_40_YMR236W	2	TAF1: Subunit of TFIID and SAGA protein	[TACR]_S[TFIID]	60	Y	[TACR]_S[TFIID]	SLIK (SAGA-like) complex	transcription regulator activity (1e-13)	0.007	10			
protein_40_YLR432W	2	Inosine monophosphate-dehydrogenase	[TACR]_S[TFIID]	60	Y	[TACR]_S[TFIID]	SLIK (SAGA-like) complex	transcription regulator activity (1e-13)	0.006	9			
protein_40_YLR94C	2	Lys12: Homo-isocitrate dehydrogenase, an NADH oxidoreductase	[SE,KHV]E[NAR]	60	[STIE]	G protein-coupled receptor k	Y	0.006	9				
protein_40_YGL019W	2	CCKB1: Beta regulatory subunit of cation kinase	[DE[ESAS]DTR]	60	SEDEE	CII kinase phosphorylation	Y	0.006	10				
protein_40_YDL055C	2	PHOB8: Probable membrane protein, involved in protein transport	[E GDL DLM]	60	Y	[IY C]_LLTM	Y	0.006	10				
protein_40_YBR106W	2	regulation of cellular physiological process	[EE DE ]	59	EE DE YIFFFF	CSK kinase substrate motif	Zn_clus	1.E-03	-1.1	nucleoside-triphosphatase activity (1e-16)	0.012	10	
yeast-630_GO-0051244	2	regulation of cellular physiological process	[L K D]_NP GDL	59	WDL	Binding motif for AP-2 and c-Jun	Zn_clus	1.E-04	-0.8	transcription, DNA-dependent (1e-91)	0.012	10	
protein_40_YJL109C	2	UPT10: Nuclear protein, component of the tRNA processing complex	[L ORL]AV P	59	[K R R]	CLV_PCSK_KEX2_1	PCI	1.E-06	0.1	proteasome complex (sensu Eukaryota) (1e-10)	0.006	9	
protein_40_YJL140C	2	RNA polymerase II largest subunit of the transcription factor	[L N T]_AL R	59	WD40	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-05	0.8	small nuclear ribonucleoprotein complex (1e-01)	0.006	9	
yeast-256_GO-003462	2	RNA polymerase II largest subunit of the transcription factor	[L N T]_AL R	59	[K R R]	Motif for binding guanine nucleic acid	Pkinase	1.E-12	1.4	cytoskeletal protein complex (1e-01)	0.006	9	
protein_40_YGL245W	2	GUS1: Glutathione synthetase (GluRS), m	[W HVS]FLVFV	59	RR SIMIL FVY	PKC kinase substrate motif	Pkinase	1.E-25	5.4	probable protein kinase activity (1e-56)	Y	0.013	10
yeast-1939_GO-0003824	2	catalytic activity	[L G K]_EMAI	59	[V LA F]_PK	Monitored recognition for modifica	Pkinase	1.E-65	7.9	protein kinase activity (1e-66)	Y	0.012	10
yeast-685_GO-0016740	2	transfase activity	[C AF R]RKW K	59	R.RKG S	PKC delta kinase substrate n	Zn_clus	1.E-20	18.1	transcription (1e-57)	0.013	10	
protein_40_YNL178W	2	RP33: Protein component of the small (40S) ribosomal subunit	[A P J]_KV EGV	59	[G SA LNK]	snRNP protein import into nucleus (1e-12)	Y	0.006	8				
protein_40_YMR047C	2	U1P16: Subunit of the nuclear pore complex	[F G N K T]NNM	59	D..D	GDP-mannose nucleotide	Zn_clus	1.E-03	-0.8	regulation of metabolism (1e-19)	0.012	10	
protein_40_YJL187C	2	SWE1: Protein kinase that regulates the G2/M transition	[SD SD WS D]	59	P ST PKKK	Ribose moiety of UDP and m	PCI	1.E-06	0.1	transcription, DNA-dependent (1e-91)	0.012	10	
protein_40_YFR001W	2	LOC1: Nuclear protein involved in asymmetric protein localization	[K K T]_K GEAQ	59	[P ST PKKK]	Cdc12 like protein kinase sub	Zn_clus	1.E-05	-0.8	proteasome complex (sensu Eukaryota) (1e-10)	0.006	9	
protein_40_YER177C	2	BMM1: A3-33 protein, major isoform, control of gene expression	[SQPIS]_T SM P	59	S_{[ST]}	Casine kinase I consensus c	WD40	1.E-05	0.8	small nuclear ribonucleoprotein complex (1e-01)	0.006	9	
protein_40_YGR120C	2	DRP1: Protein component of the small (40S) ribosomal subunit	[V M T]_P L KKR	59	KR	CLV_PCSK_P C1ET2_1	Pkinase	1.E-15	1.6	cytoskeletal protein complex (1e-01)	0.006	9	
protein_40_YJL203C	2	LOC1: Nuclear protein involved in the large (60S) ribosomal subunit	[E E D E ]	59	[S ST]_E	Casine kinase II consensus t	Zn_clus	1.E-03	-0.8	cytoskeletal protein complex (1e-01)	0.006	9	
protein_40_YLR203C	2	regulation of cellular process	[G R V A G RA ]	59	[A G R]	Protease matriceptase protease	DEAD	1.E-05	-1.3	regulation of metabolism (1e-04)	0.012	10	
yeast-631_GO-0050794	2	transcription from RNA polymerase II promoter	[E E D E Y FFF]	59	[D..D]	CSK kinase substrate motif	Zn_clus	1.E-03	-1.1	transcription, DNA-dependent (1e-91)	0.012	10	
yeast-294_GO-0005366	2	RNA processing	[N D NS]_SNH N	59	P ST PKKK	Cdc12 like protein kinase sub	Zn_clus	1.E-03	-0.8	transcription from RNA polymerase II promoter (	0.012	10	
protein_40_YNL00539E	2	matsuyama_Golgi	[K PK P K KT]	59	D..SIL PK	CKII delta kinase phosphor	Zn_clus	1.E-03	-0.8	ribonucleoprotein complex (1e-04)	0.011	10	
yeast-980_GO-0051179	2	localization	I..L FW F	59	[G SA LNK]	GDP-mannose nucleotide	Zn_clus	1.E-03	-0.8	snRNP protein import into nucleus (1e-12)	0.007	10	
yeast-251_GO-0005868	2	plasma membrane	[I G D .. V F J G]	59	[P ST PKKK]	cytoplasm organization and biogenesis (1e-08)	Y	0.006	10				
protein_40_YNL031C	2	H2T2: One of two identical histone H3 proteins	[I G D .. V F J G]	59	D..D	cytoskeletal protein complex (1e-01)	Y	0.011	10				
protein_40_YPL211W	2	NIP10: Nuclear protein required for 60S ribosomal subunit assembly	[I G D .. V F J G]	59	P ST PKKK	cytoskeletal protein complex (1e-01)	Y	0.011	10				
protein_40_YGR230C	2	SP21: GTP binding protein mammalian Ran	[I G D .. V F J G]	59	S ST E	CKII kinase phosphorylation	Zn_clus	1.E-03	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YGR225W	2	RIT102: Component of both the SWI5/SNF and HHT1/HHT2 complexes	[I G D .. V F J G]	59	KR	CLV_PCSK_P C1ET2_1	Pkinase	1.E-15	1.6	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
yeast-312_GO-0006414	2	translational elongation	[I G D .. V F J G]	59	[D..D]	CKII delta kinase binding motif	Zn_clus	1.E-03	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YDL213C	2	LOC1: Putative RNA-binding protein implicated in protein transport	[I G D .. V F J G]	59	[S ST]	MDC1 BRCT domain binding	Zn_clus	1.E-03	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YER181W	2	YEL63C: Putative RNA-binding protein implicated in protein transport	[I G D .. V F J G]	59	[S ST]	MDC1 BRCT domain binding	Zn_clus	1.E-03	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
yeast-248_GO-0016072	2	RNA metabolism	[I G D .. V F J G]	59	[D..D]	CSK kinase substrate motif	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YNL153C	2	matsuyama_Cytosol	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL127W	2	CIC1: Essential protein that interacts with proteins	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120C	2	transcription regulator activity	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YGR120C	2	transcription regulator activity	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1e-08)	0.006	9	
protein_40_YOL120W	2	regulation of physiological process	[I G D .. V F J G]	59	[P ST PKKK]	cytoskeletal protein complex (1e-01)	Zn_clus	1.E-02	-0.8	cytoskeleton organization and biogenesis (1			

protein_40_YDR440C	2	UTP6: Nudelated protein, component of the sr	[L]OKLALVAV[G] K[ETM]PKVJK	55	D.G	motif that binds phosphate in	WD40	1.E-04	1	nucleolus (1e-07)	0.006	10		
protein_40_YLR197W	2	SIE1: Essential evolutionary-conserved nucleic acid binding protein	[NHUD]G[PTP]	55			WD40	1.E-02	1.7	nucleolus (1e-28)	0.010	10		
yeast-Tc2_GO-0016797			[GEIJK][TWKQLA] I[GOL]G[ISH]QF	55		Motif for covalent cholesterol	P	1.E-34	2.7	GTPase activity (1e-35)	0.013	10		
protein_40_YLLO21C	2	MAK11: Protein involved in an early nucleic acid processing step	[L]F[KHF][LMH] [ASGIC]C[IRQ]	55	LFG	Protease Papain substrate, a	DEAD	1.E-02	2.7	nucleolus (1e-07)	0.006	10		
protein_40_YLLO08W	2	DRS1: Nuclear DEAD-box protein required for cell-cycle regulation	[ED[EAK][DEG]	55	C.C.	Motif on TIM mitochondrial tr	Pkinase	1.E-04	3.3	protein kinase activity (0.001)	Y	0.006	9	
protein_40_YJR066W	2	TOR1: PIK-related protein kinase and rapamycin target	[EVA][ERD]...GDE	55	SEDEE	CXII kinase phosphorylation	GATA	1.E-06	7	regulation of nitrogen utilization (1e-07)	0.006	10		
yeast-324_GO-0030528	2	transcription regulator activity	[L]Q[WGL][LT[E]LK]	55	RGD	CXII kinase phosphorylation	Zn_clus	1.E-36	20.7	transcription regulator activity (1e-33)	0.012	10		
yeast-322_GO-0005654	2	nucleoplasm	[KHY][VKDP]JKV	55		LG_RGDLL_RGD				nucleoplasm (1e-10)	Y	0.012	10	
protein_40_YPR161C	2	SGV1: Cyclin (Bur2p)-dependent protein kinase	[VP]	55						SWI/SNF complex (1e-05)	0.006	9		
protein_40_YPR034W	2	ARP7: Component of both the SWI/SNF and Paf1 complexes	[RPG][VQ]	55		Interleukin converting enzym					0.006	10		
protein_40_YPL204W	2	HRR25: Protein kinase involved in regulating cell cycle and apoptosis	[PGI][GSICIGA]A	55						DNA integrity checkpoint (0.001)	Y	0.006	9	
protein_40_YPL153C	2	RADS1: Protein kinase, required for cell-cycle regulation	[KR[KR]R]	55		ALPHA 2 MACROGLOBUL					Y	0.006	8	
protein_40_YLR193C	2	RAS1: Ras GTPase-activating protein	[KR[KR]K][KEAR]	55	KR	CLV_PCSK_CK2E2_1				cytoplasm organization and biogenesis (1e-30)	0.011	10		
protein_40_YPL093W	2	DOG1: Putative GTPase that associates with proteins	[DHWIK]K[DMMK]	55						cytoskeletal part (0.01)	0.006	8		
protein_40_YMLR117C	2	SPC24: Component of the evolutionarily conserved nucleolar pre-ribosome	[VVV]V[SEI]GHY	55	VEHD	Protease Caspase 6-stringer				cytosol (0.001)	0.005	9		
protein_40_YML073C	2	SPS1: Protein that forms a complex with Spt4	[DFD][E]DK	55						nuclear lumen (1e-10)	Y	0.010	10	
protein_40_YML010W	2	CRN1: Cronin, cortical actin cytoskeleton coat protein	[IDF][L]K[C]TJL	55							Y	0.006	10	
protein_40_YLR429W	2	CRN1: Cronin, cortical actin cytoskeleton coat protein	[IDF][L]K[A]WTJL	55							Y	0.006	9	
protein_40_YLR180W	2	SAM1: S-adenosylmethionine synthetase, catalyzes methylation of proteins	[NPO][EQL]...RLK	55							microtubule cytoskeleton (0.001)	0.006	8	
protein_40_YLR144W	2	TID3: Component of the evolutionarily conserved nucleolar pre-ribosome	[L][H][I]...S	55	S...	WD40 binding motif, Ser resi	rRNA export from nucleus (0.001)					Y	0.006	9
protein_40_YGR218W	2	CRM1: Major karyopherin, involved in nuclear protein import	[RGG][FNO][RFA]	55	GGRRG	Arginine methyl transferase	Pkinase	1.E-04	-4.8	replication factor (sensu Eukaryota) (0.01)	Y	0.011	10	
protein_40_YGR088C	2	PIL1: Primary component of esosomes, white protein	N[N]SEN	54						cell cycle (10)	Y	0.007	10	
protein_40_YLR077C	2	BRX1: Basic helix-loop-helix (bHLH) transcript factor	[KK][SVR][KEG]	54	RKK[ST]	ZTIP kinase phosphorylation n	RNN_R1	1.E-07	-2.8	RNA binding (1e-09)	0.006	9		
protein_40_YOL118C	2	AD24: Transcriptional cooperator, component of the nucleolus	L[L]S[Q]O	54	LSOE	ATM kinase substrate motif					0.005	10		
protein_40_YDR448W	2	AD42: Transcriptional cooperator, component of the nucleolus	[KK][SVR][KEH]	54	RKK[ST]	ZTIP kinase phosphorylation n	Pkinase	1.E-04	-1.4	cell cycle (1e-25)	Y	0.011	10	
protein_40_YCR009C	2	RVN161: Amylophylase-like lipid raft protein; a member of the SNF2 family	N[N]NT[TFN]	54						cytoskeleton organization and biogenesis (1e-26)	0.010	10		
protein_40_YOL198W	2	AKL1: Ser-Thr protein kinase, member (with) of the SNF2 family	[SVS][DS][WH]	54	S.D.	CAMKII phosphorylation site				DEAD binding (1e-19)	Y	0.011	10	
protein_40_YAR007C	2	RFA1: Subunit of heterochromatin Replication Factor	[PFEK][P]V[PTL]	54	LVRPG	Protease Thrombin				chromosome organization and biogenesis (1e-3L)	Y	0.011	10	
yeast-340_GO-0007049	2	cell cycle	[SIV]...S	54	WD40	WD40 binding motif, Ser resi				ribosomal large subunit assembly and maintenance	Y	0.006	9	
oshei_mitochondrion	2	RNA binding	[RGG][FNO][RFA]	54						actin cortical patch (1e-05)	Y	0.006	9	
protein_40_YOL077C	2	oshei_mitochondrion	N[N]SEN	54						actin filament (1e-12)	Y	0.006	10	
protein_40_YOL070C	2	BRX1: Nuclear protein, constituent of 6S rRNA	[KK][SVR][KEG]	54						RNA helicase activity (1e-10)	0.006	10		
protein_40_YOL07409	2	cell cycle	L[L]S[Q]O	54						0.005	10			
protein_40_YOL07409	2	BRX1: Nuclear protein required for the normal assembly of the nucleolus	[KK][SVR][KEH]	54						translation elongation factor activity (1e-08)	0.006	9		
protein_40_YOL07409	2	cell organization and biogenesis	N[N]NT[TFN]	54						actin cytoskeleton organization and biogenesis (1e-09)	0.006	10		
protein_40_YOL020C	2	NOC3: Protein that forms a nuclear complex with RPS28A	[RVT][AJAG]R	54	AG[IR]	Protein matriphate protease				barrier septum (1e-89)	Y	0.013	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[DVA][ACG]TRP	54	DVAD	Protease Caspase 2-stringe				0.005	8			
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	A[P]P...P	54		SH3 domain ligand				transcription factor TFIID complex (1e-07)	0.006	10		
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	L[Q]D[EPI]	54	LSOE	ATM kinase substrate motif				spindle pole body (1e-04)	Y	0.006	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[TR][J]GER[J]K	54	FRTG	Phosphoinositide binding mo	GTP_EFTU_D2	1.E-08	-0.8	protein kinase activity (1e-10)	Y	0.006	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[S]D[Q]R[YAD]S	54	KR	CLV_PCSK_PCE1E2_1				RNA helicase activity (1e-10)	0.006	10		
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[S]D[Q]R[YAD]S	54	SP	PROK_C02_ANHYDRASE				0.005	8			
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[N]P[K]P...RPP	54		ERK1, ERK2 Kinase substra				actin cytoskeleton organization and biogenesis (1e-15)	Y	0.006	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	A[F]G[LA]	54						carboxylic acid metabolism (1e-15)	Y	0.011	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	V[ST]A[G]	54						carboxylic acid metabolism (1e-15)	Y	0.011	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	V[ST]A[G]	54						transcription factor TFIID complex (1e-07)	Y	0.006	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[Y]L[E]LMV][LV]M	54	Y[L]	SH2 ligand for PLCoamma1				proline-rich region (1e-06)	Y	0.006	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[R]T[L]R[RG]V[J]G	54	RGG	Alternative interein binding si				protein kinase activity (1e-07)	0.007	10		
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	K[I]H[R]J[V]P]H	54	KR	CLV_PCSK_PCE1E2_1				0.005	10			
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[P]M[P]K[H]G]WD	54	PWDLW	WD40				ATP-dependent RNA helicase activity (1e-06)	Y	0.007	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[G]K[R]KAA[F]MS	54						ATP-dependent RNA helicase activity (1e-18)	Y	0.006	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[D]D[P]K1[S]Q[M]J	54	DDDD...S	ZIPL domain				protein kinase activity (1e-17)	Y	0.008	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[T]W[D]SKR]Y	54						amino acid activation (1e-15)	Y	0.009	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[D]E[D]J[E]DE[K]	54						transcription elongation factor complex (1e-04)	Y	0.008	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]G[Q]P[E]D[E]	54						cytosolic large ribosomal subunit (sensu Eukaryo)	Y	0.006	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[Y]D[E]P[D]V	54						small nuclear ribonucleoprotein complex (1e-01)	Y	0.006	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[S]D[Q]R[YAD]S	54						snoRNA binding (1e-08)	Y	0.006	7	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[P]T[D]P[Q]R	54						rRNA processing (1e-11)	Y	0.005	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]H[R]G[CLT]	53						small nuclear ribonucleoprotein complex (1e-005)	Y	0.006	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[K]L[SE]	53	NKLY	ZIPL domain in enigma bind				snoRNA binding (1e-08)	Y	0.006	7	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53	RKK[ST]	ZIP kinase phosphorylation n				0.005	9			
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						ATP-dependent RNA helicase activity (1e-15)	Y	0.011	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						ATP-dependent RNA helicase activity (1e-53)	Y	0.012	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						RNA helicase activity (1e-19)	Y	0.006	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						transcription, DNA-dependent (1e-13)	Y	0.011	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						cellular morphogenesis (1e-13)	Y	0.011	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						protein kinase activity (1e-13)	Y	0.008	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						transporter activity (1e-13)	Y	0.010	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						small nuclear ribonucleoprotein complex (1e-1)	Y	0.006	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						ribosome biogenesis (1e-17)	Y	0.007	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						ribosome biogenesis (1e-19)	Y	0.011	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						endoplasmic reticulum (1e-22)	Y	0.012	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						transferase activity, transferring phosphorus-con	Y	0.007	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						snRNP protein import into nucleus (1e-09)	Y	0.007	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						pyrophosphatase activity (1e-07)	Y	0.007	8	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						plasma membrane (1e-86)	Y	0.011	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						rRNA export from nucleus (1e-12)	Y	0.011	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						cellular morphogenesis (1e-13)	Y	0.009	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						DNA damage response, signal transduction (0.01)	Y	0.010	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						regulation of gene expression, epigenetic (0.001)	Y	0.010	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						cytosolic ribosome (sensu Eukaryota) (1e-07)	Y	0.006	9	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						nucleolus (1e-13)	Y	0.010	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						cellular morphogenesis (0.01)	Y	0.006	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						bud (1e-27)	Y	0.007	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						proteasome core complex, alpha-subunit comple	Y	0.010	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						RNA processing (1e-11)	Y	0.011	10	
protein_40_YOL198W	2	RRP8: Protein component of the large 60S ribosomal subunit	[L]P[K]R[KEG]	53						establishment and/or maintenance of chromatin	Y</td			

yeast-376_GO-0012919	2 regulation of nucleobase, nucleoside, nucleotide metabolism	N_L[DETD]	52 NK.D	Motif for specificity of quanini	PUF_Helicase_C	1.E-02	-0.2	regulation of nucleobase, nucleoside, nucleotide metabolism	0.011	10
protein_40_YPL131W	2 RPL5: Protein component of the large (60S) ribosomal subunit	[NGKIK[KIN]KP]	52 P.[ST]PKK.KK	Cdc2 like protein kinase sub	MFS_1	1.E-02	0.3	cytoplasm organization and biogenesis (1e-17)	0.010	10
yeast-629_GO-0005234	2 translational elongation	LV.[UUTFLHMLV]	52 KEN	LIG_APCC_KENbox_2	Ribosomal_60s	1.E-08	0.4	translational elongation (1e-12)	0.011	10
yeast-312_GO-0005414	2 translational elongation	[AIES].[KEIHEI]	52 KEN		Histone	1.E-04	1.6	establishment and/or maintenance of chromatin	0.006	10
protein_40_YNL031C	2 HHT2: One of two identical histone H3 protein	L.E.[GRJA]NIIJA	52 KEN		PALP	1.E-05	1.7	amino acid and derivative metabolism (1e-13)	0.011	10
yeast-200_GO-0006519	2 amino acid and derivative metabolism	[GACJ]L...G	52 KEN		Mito_carr	1.E-31	1.8	transporter activity (1e-16)	0.011	10
yeast-413_GO-0005215	2 transporter activity	EG.[AGAS]L[FVW]	52 KEN		Mito_carr	1.E-23	1.9	envelope (1e-17)	0.011	10
yeast-379_GO-0031975	2 envelope	[DKP]I[VTC]KTR	52 KEN		Mito_carr	1.E-23	2	envelope (1e-17)	0.011	10
yeast-379_GO-0031967	2 organelle envelope	[DKP]I[VTC]KTR	52 KEN		Mito_carr	1.E-46	2.2	transporter activity (1e-22)	0.012	10
yeast-413_GO-0005215	2 transporter activity	[LFID].[KTVFJ]	52 KEN		PKinase	1.E-05	2.2	DNA metabolism (1e-65)	0.011	10
yeast-1547_GO-0043283	2 biopolymer metabolism	V.[ELJK]	52 P.V.L	Shadow-Chromo domain bin	ABC_tran	1.E-19	2.5	hydrolase activity, acting on acid anhydrides (1e-16)	0.011	10
protein_40_YLR057B	2 hydrolytic enzyme	G.[IAWV]AD]	52 Y.L	Motif for down regulation of tfl	PtN	1.E-19	3.1	protein catabolic activity (1e-19)	0.009	10
yeast-341_CO-0045449	2 ARID1A: Protein that binds RNA and methionine	KR.[KGKE]	52 KR	CLV_PCSK_PC1ET2_1	Zn_clus	1.E-08	3.1	regulation of transcription (1e-19)	0.011	10
protein_40_YDR498C	2 PUF6: Pumilio-homology domain protein that	[GVSK]AA[FSG]	52 KR		DEAD	1.E-03	3.1	nucleolus (1e-07)	0.006	8
protein_40_YER006W	2 NUG1: GTPase that associates with nuclear I	DEAD[RAIR]RLS	52 KR		DEAD	1.E-02	3.2	ribosome biogenesis (1e-05)	0.005	8
protein_40_YML010W	2 SPTS: Protein that forms a complex with Spt4/Spt5	[TRIV]G[GKTY]	52 KR		DEAD	1.E-04	3.4	ATP-dependent RNA helicase activity (1e-05)	0.006	8
protein_40_YLL008W	2 DRS1: Nuclear DEAD-box protein required	[PTD]T[ES]REL	52 KR		DEAD	1.E-09	3.4	ribosomal large subunit assembly and maintenan	0.006	10
protein_40_YOL127W	2 RPL25: Primary RNA-binding ribosomal prot	F.[GK]PQHJA	52 QIMLV[IGD].CLV_TASPACE1		RNA helicase activity (1e-09)		3.4	RNA helicase activity (1e-09)	0.005	10
yeast-468_GO-0051276	2 chromosome organization and biogenesis	[AGEF]PSFG	52 F.F					chromosome organization and biogenesis (1e-12)	0.011	10
yeast-234_GO-0006605	2 structural molecule activity	L.[CIC]C	52 F.F					snRNP protein import into nucleus (1e-09)	0.007	9
protein_40_YPR119W	2 protein targeting	[LIC]C	52 F.F					fRNP export from nucleus (1e-15)	0.006	10
protein_40_YOL120C	2 CLB2: B-type cyclin involved in cell cycle pro	[LIC]C	52 F.F					cell cycle (1e-07)	0.006	10
protein_40_YOL120C	2 RPL25: Primary RNA-binding ribosomal prot	NOP6: Protein involved in pre-mRNA process	52 [ST]P					small nucleolar ribonucleoprotein complex (1e-1)	0.006	9
protein_40_YNL118C	2 NOP1: Constituent of 60S pre-ribosomal pa	[TENY]EVFJ	52 [ST]P					cytoplasm organization and biogenesis (0.001)	0.006	10
protein_40_YNL110C	2 NOP15: Constituent of 60S pre-ribosomal pa	[LSDT].[EIEF]	52 [ST].E					nucleolus (1e-13)	0.007	10
protein_40_YNL002C	2 RPL7: Nuclear protein with similarity to larg	SIDS[WL].[ELES]	52 QPS_E	Phosphorylation motif in alpha				nucleolus (0.001)	0.005	9
protein_40_YMR049C	2 ERBI: Protein required for maturation of the small (40S) ribosomal subunit	E.[EAS].[ENL]	52 [AG]R	Protease matriphate protease				ribonucleoprotein complex (0.001)	0.006	10
protein_40_YJL190C	2 RPS2A: Protein component of the small (40S) ribosomal subunit	[DQCI]R[DYS]	52 R.L						0.005	8
protein_40_YHR152W	2 B2B1: SH3 domain protein implicated in the r	[LFRIT]MGL	52 G[KR]I[KR]							
protein_40_YHR144W	2 RPL25: N-terminally acetylated protein comp	[LFRIT]MGL	52 R.L							
protein_40_YGR191W	2 CSE1: Belongs to a family of amino acid	[LFRIT]MGL	52 R.L							
protein_40_YDR459W	2 RPS18: Protein component of the small (40S) ribosomal subunit	[LFRIT]MGL	52 R.L							
protein_40_YDR382W	2 RPL25: Ribosomal protein P2 beta, a compo	[LFRIT]MGL	52 R.L							
protein_40_YDR145W	2 TAF12: Subunit (6.6 kDa) of TFIID and SAI	[SVLPEV]KING	52 LPKY	WW motif (non-conventional						
protein_40_YDL005C	2 PSA1: GDP-mannose pyrophosphorylase (m	[FARQ]PQJQD	52 D.D	Protease moiety of UDP and m						
protein_40_YDL014W	2 NOP1: Nuclear protein, component of the s	[SEAJD]NSEN	52 LFG	Protease Papain substrate, a						
protein_40_YBR017C	2 CAP194: Transprin, cytosolic karyopherin b	LFN[NAC]NKF	52 [ST]Q..NNTJN							
oshea_nuclear_periphery	2 oshea_nuclear_periphery	[FYLQ].[SWTT]	52 RE..E							
oshea_mitochondrion	2 oshea_mitochondrion	[EN].[KOL]	52 E.[P]							
genetic_YLR262C	2 YPT6: GTPase, Ras-like GTP binding protein	[TACR]P	52 AGIR	Protease matriphate protease	DEAD	1.E-14	-1.3	ATP-dependent RNA helicase activity (1e-18)	0.017	10
yeast-217_GO-0007746	2 ribosome biogenesis	R[DI]DAG[DP]	51 RGD	LIG_RDDG_RDD	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	10
protein_40_YMR099W	2 NUD1: Putative GTPase that associates with	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	10
protein_40_YCL111W	2 NUD1: Putative GTPase that associates with	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YHR052W	2 RPL25: N-terminally acetylated protein comp	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YDR498C	2 C1C1: Essential protein that interacts with pro	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YNL061W	2 NOP2: Probable RNA m6C/methyltransfera	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
yeast-215_GO-00077010	2 nucleobase, nucleoside, nucleotide and nucleic acid metabolism	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
yeast-1433_GO-0006139	2 chromosome organization and biogenesis (see	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YOL002C	2 transporter activity	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YPR202W	2 membrane	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR085C	2 TUB1: Alpha tubulin; associates with beta-tub	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YGR191W	2 RPL25: N-terminally acetylated protein comp	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YOL002C	2 RPL25: N-terminally acetylated protein comp	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 RPL25: N-terminally acetylated protein comp	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
yeast-256_GO-0006142	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
yeast-256_GO-0006142	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
yeast-256_GO-0006142	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006	9
protein_40_YMR222C	2 response to endogenous stimulus	R[DI]DAG[DP]	51 RGD	Cyclin A motif that binds cdk2	DEAD	1.E-08	-1.3	ATP-dependent RNA helicase activity (1e-08)	0.006</td	



protein_40_YLR180W	2	SAM1: S-adenosylmethionine synthetase, cat	EAE[EFITGN] EE.[EDWIEKXM]	48	EED	Ankyrin B C-terminal motif th	Y		Y	0.009	10
protein_40_YLR200W	2	RPL24: Essential protein with sensitivity to Rpl	[ATCIPR]	48	[AG]R	Protease matriptase protease			Y	0.009	10
protein_40_YLL04PC	2	ERB1: Nucleolar protein required for the mat	KR	48	CLV_PCSK_FC1ET2_1					0.005	10
protein_40_YKL014C	2	TOR1: PIK-related protein kinase and rapam								0.005	9
protein_40_YIL019W	2	FAF1: Protein required for pre-rRNA processing	[AFVIKISWRDJE] [FLMLN...NL.RVIG]	48						0.005	9
protein_40_YGL200C	2	EMP24: Integral membrane component of the sr	[LNFI5...I[KFV]LG]	48						0.007	9
protein_40_YFR052W	2	RPN12: Subunit of the 19S regulatory particle	[AQI][AIL].YG	48						0.005	10
protein_40_YFR028C	2	CDC4: Protein phosphatase required for mit	[LPNDIL][EFD]	48						0.005	9
protein_40_YFL037W	2	TUB2: Beta-tubulin; associates with alpha-tub	RK.SLKL[K]EPR]	48	R.RK,[ST]	Zip kinase phosphorylation n	Y			0.005	8
protein_40_YDR429C	2	RPN9: Non-ATPase regulatory subunit of the	E[TRNR]K[EGELJK]	48						0.005	8
protein_40_YDR429W	2	UTP10: Nucleolar protein, constituent of the sr	LA.[GLR]GDRGE	48						0.007	10
protein_40_YDR174W	2	U2AF2: One of two subunits of the SRP	[SIVG]E[FGV]K]	48	[ED]GS[G][DE]	Glycosaminoglycan attachment				0.005	8
protein_40_YDR145W	2	HMO1: Chaperone associated high mobility gr	E[EVG]I[EVG]E	48	EISTII[A]REAI	RIBOSOMAL S28E PATTIE				0.005	8
protein_40_YCR031C	2	SUP35: Translation termination factor eIF3- <i>f</i>	KNSGCL.NDVYVS	48	R.GSF	PKCdelta kinase phosphoryl	Y			0.006	10
protein_40_YLC059C	2	KRR1: Essential nuclear protein required for	VIL[H]K[GEJS]	48						0.005	10
matsuyama_ cytosol	2	matsuyama_ cytosol	E[ALP]K[I]EH[AJ]	48	[KR]JR	CLV_PCSK_KEX2_1				0.005	7
genetic_YNL153C	2	GIM3: Subunit of the heterotrimeric coacchar	[SOT]L[DPT]JAT	48	L.PTG	C-terminal sorting signal whi				0.005	10
protein_40_YBR093W	2	NOG1: Putative GTPase that associates with	[SVH]L[D]L[SP]	48	L.FDLM	Binding motif in Cln1 for clath				0.011	10
yeast-261_GO_0016491	2	2 oxidoreductase activity	N..[DMT]K	48						0.009	10
osher_cytoplasm	2	2 esterase activity	L..[ILM]K	48						0.009	10
matsuyama_ Golgi	2	2 mutasyma_ Golgi	[ODVY].[ETP]LP	48	[ED]YJY	TC-PTP phosphatase substn				0.006	10
yeast-413_GO_0005215	2	2 transporter activity	GC[K]P[ASR]K	48	KTP40	GSK-3, ERK1, ERK2, CDK5	Y	Histone	1.E-13	-3	nuclear nucleosome (1e-08)
protein_40_YOL133W	2	2 HRT1: RING finger containing subunit of Skp	R.[R]R[K]	48				DEAD	1.E-10	-1.8	nucleus (1e-24)
protein_40_YAR019C	2	2 CDC16: Protein kinase of the Mitotic Exit Net	HT.[EOS]PK[MP]	47				zfc2H2	1.E-18	-1.4	transcription regulator activity (1e-13)
protein_40_YDR145C	2	2 HRT2: One of two identical histone H3 protein	T.[MD]P	47				Zn_clus	1.E-11	-1.3	transcription (1e-20)
yeast-22_GO_0009298	2	2 transcription	[T]D[R]A[ASL]R	47	[AG]R	Protease matriptase protease	Y	DEAD	1.E-07	-1.3	ribosomal large subunit assembly and maintena
protein_40_YJR002W	2	2 PP1: Component of the SSU ribosomal	G[P]LYI[G]VJL	47	GP	Protease T1P cleavage site		Ferric_reduct	1.E-05	-0.9	oxidoreductase activity (1e-52)
yeast-261_GO_0016491	2	2 oxidoreductase activity	PQ[QEH]	47	HPQ	Biotin binding motif in strepti			1.E-05	-0.9	regulation of metabolism (1e-06)
osher_cytoplasm	2	2 biopolymer modification	Y.[LG]Y	47				MFS_1	1.E-03	-0.9	Golgi apparatus (1e-09)
matsuyama_ Golgi	2	2 nucleoside-triphosphatase activity	[P]F[P]Y[G]AVW]	47				MFS_1	1.E-02	-0.9	transporter activity (1e-54)
yeast-240_GO_0005215	2	2 development	SPTS: Protein that forms a complex with Spt	47				Pkinase	1.E-02	-0.4	cullin-RING ubiquitin ligase complex (1e-04)
protein_40_YML010W	2	2 nitrogen compound metabolism	[ASIGG].[APG]D	47				F-box	1.E-02	-0.4	protein amino acid phosphorylation (0.01)
protein_40_YAR019C	2	2 structural constituent of ribosome	[KEG]K[IA]LA	47				Pkinase	1.E-02	-0.2	nutrient catabolic process
protein_40_YDR496C	2	2 H2R2: Protein kinase involved in regulating	[AGRS]G[S]VLF	47				Hbox	1.E-04	-0.4	amine metabolism (1e-61)
protein_40_YJR006W	2	2 transferase activity	[P]T[GLR]R[E]FQ	47	[AG]R	Protease matriptase protease	Y	PA[P]L	1.E-03	-0.5	small nuclear ribonucleoprotein complex (1e-0)
protein_40_YJR006W	2	2 TOR1: PIK-related protein kinase and rapam	[ILV]G.[ST]AJ	47				WD40	1.E-06	-0.5	oxidoreductase activity (1e-60)
protein_40_YPR103W	2	2 TIF2: Translation initiation factor eIF4A, ident	[T]P[NP].[R]FQ	47	P.R.KP	SH3 binding motif for GRB2		ADH_N	1.E-03	-0.5	proteasome complex (sensu Eukaryota) (1e-16)
protein_40_YPR103W	2	2 biopolymer modification	[K]P[L]L[D]M[G]	47	R.GG	Alternative interdomain binding si	Y	Proteasome	1.E-13	-1.8	proteasome core complex (sensu Eukaryota) (1e-16)
protein_40_YPR103W	2	2 nucleoside-triphosphatase activity	[H]U[K]L[G]P	47	C.O.	Motif on TIM-microchondrial tr		Proteasome	1.E-20	-1.8	proteasome core complex (sensu Eukaryota) (1e-16)
protein_40_YPR103W	2	2 physiological process	[A]P[H].[P]S[P]	47				DEAD	1.E-05	-1.8	nuclear lumen (1e-11)
protein_40_YPR103W	2	2 development	[S]T[P].[P]S[P]	47				Pkinase	1.E-05	-2.6	protein kinase activity (0.01)
protein_40_YPR103W	2	2 nitrogen compound metabolism	A.[I]EV[...]	47				D	1.E-07	-3.6	ribosome assembly (1e-09)
protein_40_YPR103W	2	2 structural constituent of ribosome	P.[P]S[O]	47				Pkinase	1.E-28	-4.8	protein kinase activity (1e-28)
protein_40_YPR110C	2	2 R2P40: RNA polymerase subunit, common	T[LF]AL[NG][KC]	47				GATA	1.E-02	-5.3	regulation of nitrogen utilization (1e-05)
protein_40_YPL204W	2	2 H2R2: Protein kinase involved in regulating	S[V]G[G].[P]L[Q]N	47				Pkinase	1.E-39	-5.5	protein amino acid phosphorylation (1e-45)
protein_40_YPL076W	2	2 GPI2: Protein involved in the synthesis of N-a	[V]A[J]G.[I]Q[NT]	47					11.6	-0.5	nucleoside-triphosphatase activity (1e-42)
protein_40_YOR326W	2	2 M0Y2: One of two type V myosin motors (ale	[R]E[J]R[WF]NL	47						-0.5	regulation of cellular metabolism (1e-18)
protein_40_YOR326W	2	2 M0Y2: One of two type V myosin motors (ale	[L]OR[L]V[...]	47						-0.5	multicellular organismal development (1e-38)
protein_40_YOR326W	2	2 nucleoside-triphosphatase activity	[V]V[G]I	47						-0.5	nitrogen compound metabolism (1e-17)
protein_40_YBL026W	2	2 LHF1: One of two identical histone H4 protein	T[LF]AL[NG][KC]	47						-0.5	
protein_40_YAR009C	2	2 IRE1: Serine-threonine kinase and endoribon	S[V]G[G].[P]L[Q]N	47						-0.5	
protein_40_YGR218W	2	2 PRK1: Serine-threonine kinase and endoribon	[T]D[AKT]L[TAI]	47						-0.5	
protein_40_YLR180W	2	2 EMG1: Protein required for the maturation of	[K]N[R]K [D]REI	47						-0.5	
protein_40_YLR180W	2	2 SAM1: S-adenosylmethionine synthetase, cat	[I]K[R]I [L]IMIK D	47						-0.5	
protein_40_YLR180W	2	2 essential evolutionarily-conserved nucl	[D]P[LI]V[T]V[...]	47						-0.5	
protein_40_YLR180W	2	2 cell cycle	[V]D[K]G	47						-0.5	
protein_40_YLR180W	2	2 nucleoside-triphosphatase activity	[D]K[E]D [K]E[O]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: Probable membrane protein, involve	[P]L[P]R [P]V[P]	47						-0.5	
protein_40_YLR180W	2	2 U2b: U2-like spliceosome of the SSU ribosomal	[I]R[K]S[P]R  P R	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	Cdc4	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[A]P[H].[C]D	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[R]D [P]R [Q]P ATT	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	S[N].T[NQ][K]G[P]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[V]A[D]S[N]D[D]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	D[P]L[Q]V[T]V[...]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[V]D[K]G	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[D]K[E]D [K]E[O]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[P]L[P]R [P]V[P]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[I]R[K]S[P]R  P R	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	Cdc4	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[A]P[H].[C]D	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[R]D [P]R [Q]P ATT	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	S[N].T[NQ][K]G[P]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	D[P]L[Q]V[T]V[...]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[V]D[K]G	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[D]K[E]D [K]E[O]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[P]L[P]R [P]V[P]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[I]R[K]S[P]R  P R	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	Cdc4	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[A]P[H].[C]D	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[R]D [P]R [Q]P ATT	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	S[N].T[NQ][K]G[P]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	D[P]L[Q]V[T]V[...]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[V]D[K]G	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[D]K[E]D [K]E[O]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[P]L[P]R [P]V[P]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[I]R[K]S[P]R  P R	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	Cdc4	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[A]P[H].[C]D	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[R]D [P]R [Q]P ATT	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	S[N].T[NQ][K]G[P]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	D[P]L[Q]V[T]V[...]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[V]D[K]G	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[D]K[E]D [K]E[O]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[P]L[P]R [P]V[P]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[I]R[K]S[P]R  P R	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	Cdc4	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[A]P[H].[C]D	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[R]D [P]R [Q]P ATT	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	S[N].T[NQ][K]G[P]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	D[P]L[Q]V[T]V[...]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[V]D[K]G	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[D]K[E]D [K]E[O]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[P]L[P]R [P]V[P]	47						-0.5	
protein_40_YLR180W	2	2 R2P40: U2-like spliceosome of the SSU ribosomal	[I]R[K]S[P]R  P R								



protein_40_YOR206W	2	NOC2: Protein that forms a nucleolar complex	[E K0]_E_E	44	SEDEE	Cdk1 kinase phosphorylation	Brix	1.E-02	-1.1	nucleolus (1e-26)	Y	0.009	10
protein_40_YGL111W	2	NSA1: Constituent of 66S pre-ribosomal parti	[G Y R]_H[T]A[R]	44	[AGR]	Protease matriphase proteas	DEAD	1.E-05	-1.1	ATP-dependent RNA helicase activity (1e-05)	Y	0.005	9
protein_40_YDU152O	2	S2H1: Constituent of 66S pre-ribosomal parti	[D Y K]_R[S]L[A]E	44	[KTR]	OLV_PCSK_KEX2_1	Phosphatase	1.E-04	-1.1	protein serine/threonine kinase activity (0.001)	Y	0.005	10
protein_40_YAR019C	2	CDC15: Protein kinase of the Mitotic Exit Net	[H KHT]_S[SHN]	44	[S1T]	MDC1 BRCT domain binding	Pin kinase	1.E-10	-1.1	protein kinase activity (1e-09)		0.007	10
protein_40_YPL153C	2	RAD51: Protein kinase, required for cell-cycle	N_K[T]ARY	44	KR	CLV_PCSK_P_C1ET2_1	Ank	1.E-02	-0.8		Y	0.008	10
protein_40_YNL186W	2	UBP10: Ubiquitin-specific protease that deub	Q_A[QW]I[S]YF]	44			Pin kinase	1.E-02	-0.7		Y	0.005	8
protein_40_YKR081C	2	RPF2: Essential protein involved in the proce	T[TRM]G_[GM]S[KT]	44	S...[ST]	Casein Kinase I consensus c	Helicase_C	1.E-08	-0.7	ribosome biogenesis (1e-07)		0.005	10
yeast-251_GO-0005886	2	plasma membrane	S...[N]L[P]	44	I...[EK]A[R]	CLV_PCSK_KEX2_1	MFS_1	1.E-05	-0.6	plasma membrane (1e-15)		0.009	10
yeast-244_GO-0000279	2	M phase	L[LC]Q[F]V[A]G	44	FIGQY	Ankyrin G binding motif in ne	Mut5_III	1.E-03	-0.6	M phase (1e-16)		0.009	10
yeast-1433_GO-0006139	2	NOC4: Nuclear protein, forms a complex wi	O_A[QW]I[S]YF]	44	KR	CLV_PCSK_P_C1ET2_1	WD40	1.E-02	-0.2	DNA metabolism (1e-62)		0.009	10
protein_40_YPR144C	2	protein, required for cell-cycle	T[AGC]...[ET]P]	44	S.D.	Pyruvate dehydrogenase kin	WD40	1.E-03	-0.2	snoRNA binding (1e-07)	Y	0.005	8
protein_40_YGL123W	2	DIF2: Nuclear protein, specifically associate	E[YQF]_Q[GQ]D	44	[IVI]DS/[G]IC	ALKALINE PHOSPHATASE	WD40	1.E-02	-0.2	cytoplasm organization and biogenesis (1e-15)		0.009	10
protein_40_YGR224Z	2	nucleobase, nucleoside, nucleotide and nucle	F...[AVW]Y	44	G...G.G	Phosphate, FAD, NADH, bin	zfc-C2H2	1.E-02	-0.2	cytoplasm organization and biogenesis (1e-15)		0.009	10
protein_40_CO-00028	2	cytoskeleton organization and biogenesis	G...[GNL]V	44		Histone	DEAD	1.E-02	-0.2	M phase (1e-16)		0.009	10
protein_40_YPL153C	2	M phase	V[LQW]E[YRQ]	44			ABC_Iran	1.E-13	-0.5	cell cycle (1e-16)		0.008	10
protein_40_YPR119W	2	half-life_beetle quantile 3	T[AGC]...[ET]P	44			DEAD	1.E-02	-0.2	chromosome assembly or disassembly (0.001)		0.010	10
protein_40_YPR119W	2	CLB2: B-type cyclin involved in cell cycle pro	E[YFW]...[G]GYI	44			MFS_1	1.E-02	-0.6	chromosome organization and biogenesis (sensi		0.010	10
protein_40_YNL002W	2	plasma membrane	D[EIN]P[D]RPL	44			WD40	1.E-05	-0.5	chromosome organization and biogenesis (sensi		0.009	10
protein_40_YBL020W	2	organelle organization and biogenesis	[D]T[C]P[D]I[C]	44			Ras	1.E-12	-2	protoplasts activity (1e-42)		0.010	10
protein_40_YGL016W	2	HTB2: One of two identifed (see HTB1)	V[F]W]I[KR]P[W]	44			Pkinase	1.E-09	-0.5	protein kinase activity (1e-11)		0.007	10
protein_40_YGL111W	2	pyrophosphatase activity	T[VLT]FIC	44			DEAD	1.E-03	-0.5	protein kinase activity (0.001)		0.005	7
protein_40_YGL111W	2	NSA1: Constituent of 66S pre-ribosomal parti	G...[GNL]V	44			DEAD	1.E-02	-0.5	nucleolus (1e-17)		0.009	10
protein_40_YGL111W	2	transferase activity, transferring phosphorus-c	V[VWT]FIC	44			DEAD	1.E-02	-0.5	nucleotide-triphosphatase activity (1e-68)		0.010	10
protein_40_YGL111W	2	transferase activity, transferring phosphorus-con	T[VLT]FIC	44			DEAD	1.E-04	-0.5	RNA helicase activity (1e-04)		0.005	9
protein_40_YGL111W	2	transferase activity	E[I]S[T]A[E]R[A]	44			DEAD	1.E-08	-0.5	cytoplasm organization and biogenesis (1e-06)		0.009	10
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	R[B]O[D]I[C]	44			DEAD	1.E-08	-0.5	nucleolus (1e-20)		0.009	10
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[F]W]I[KR]P[W]	44			DEAD	1.E-10	-0.5	ribosome biogenesis (1e-14)		0.008	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	G...[GNL]V	44			DEAD	1.E-03	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[VWT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	E[I]S[T]A[E]R[A]	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	R[B]O[D]I[C]	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[F]W]I[KR]P[W]	44			DEAD	1.E-03	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	G...[GNL]V	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[VWT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	E[I]S[T]A[E]R[A]	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	R[B]O[D]I[C]	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[F]W]I[KR]P[W]	44			DEAD	1.E-03	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	G...[GNL]V	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[VWT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	E[I]S[T]A[E]R[A]	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	R[B]O[D]I[C]	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[F]W]I[KR]P[W]	44			DEAD	1.E-03	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	G...[GNL]V	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[VWT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	E[I]S[T]A[E]R[A]	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	R[B]O[D]I[C]	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[F]W]I[KR]P[W]	44			DEAD	1.E-03	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	G...[GNL]V	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[VWT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	E[I]S[T]A[E]R[A]	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	R[B]O[D]I[C]	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[F]W]I[KR]P[W]	44			DEAD	1.E-03	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	G...[GNL]V	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[VWT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	E[I]S[T]A[E]R[A]	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	R[B]O[D]I[C]	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[F]W]I[KR]P[W]	44			DEAD	1.E-03	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	G...[GNL]V	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[VWT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	E[I]S[T]A[E]R[A]	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	R[B]O[D]I[C]	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[F]W]I[KR]P[W]	44			DEAD	1.E-03	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	G...[GNL]V	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[VWT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	E[I]S[T]A[E]R[A]	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	R[B]O[D]I[C]	44			DEAD	1.E-08	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	V[F]W]I[KR]P[W]	44			DEAD	1.E-03	-0.5	ATP-dependent RNA helicase activity (1e-08)		0.005	9
protein_40_YGL111W	2	transferase activity, transfering phosphorus-con	T[VLT]FIC	44			DEAD	1.E-02	-0.5	ATP-dependent RNA helicase activity (1e-08)</td			





protein_40_YOR181W	2	LAS17: Actin assembly factor, activates the A	[PMNIE..[RAMTY]	41		Y	endocytosis (0.01)	Y	0.005	7
protein_40_YOR093W	2	CKB2: Beta' regulatory subunit of casein kinase II	[SN[CG]QINHHQ]	41		Y	establishment and/or maintenance of chromatin		0.005	8
protein_40_YOL016C	2	LRRK1: LRRK1 kinase domain containing protein I	[HVGCVQPEV]	41	[YW]EV	Y			0.005	9
protein_40_YNL209W	2	SSBP2: Cytosolic ATPase that is a ribosome	[AFPIS.KAJIDV]	41		Y			0.004	7
protein_40_YMR154C	2	YCK2: Palmitoylated, plasma membrane-bound	[PPPHNPKPN]	41	[DE]FPPP	Y	cytoplasm organization and biogenesis (1e-28)		0.004	8
protein_40_YMR229C	2	HAS1: ATP-dependent RNA helicase; localizes	[DKQD]EGKQE	41		Y	transcription factor complex (1e-14)		0.008	10
protein_40_YMR236W	2	TAF9: Subunit (17 kDa) of TFIID and SAGA complex	[EMVIDEEDVNIE]	41	S [DE]  DE	Y			0.006	9
protein_40_YMR139W	2	RIM11: Protein kinase required for signal transduction	[EKTIL[LHNIN]	41		Y			0.005	7
protein_40_YMR012W	2	TUB1: Alpha-tubulin; associates with beta-tubulin	[R[ETP].IQGIP]	41	GP	Y			0.006	8
protein_40_YLR429W	2	CLU1:elf3 component of unknown function;	[SS..[LENJN]KWKQ]	41	S [ST]	Y	Y		0.004	7
protein_40_CRN1	2	CORNI: Cortical actin cytoskeleton core protein	[SS..[KJL]LPN]	41	S [ST]	Y	actin cytoskeleton organization and biogenesis (i)		0.004	8
protein_40_YLR429W	2	YOL102C: Component of the yeast nuclear co	[IVS[G]GL[AF]	41	SG.G	Y	proteasome complex (sensu Eukaryota) (0.001)		0.005	10
protein_40_YLR347C	2	KAP95: Karyopherin beta, forms a dimeric co	[GQGK]QIPIV	41	GGO	Y			0.005	7
protein_40_YLR347C	2	YOL102C: Component of the yeast nuclear co	[LTEL..[LIP]EOI]	41		Y	protein import into nucleus (1e-05)		0.004	7
protein_40_YKL203C	2	TOR2: PKC-related protein kinase and regulator	[R[QY]M[LOGI]	41	YM	Y	actin cytoskeleton organization and biogenesis (i)		0.004	8
protein_40_YKL148W	2	RPTF1: One of six ATPasases of the 19S regulat	[TIVV]AVMLA	41	DALDL	Y	proteasome complex (sensu Eukaryota) (0.001)		0.005	10
protein_40_YJL130C	2	URA2: Bifunctional carbamoylphosphate synthetase	[ED[ARI]DKA]	41	D.D	Y			0.005	7
protein_40_YJL130C	2	URA2: Bifunctional carbamoylphosphate synthetase	[K[QLO]..NFAVFT]	41		Y	establishment and/or maintenance of chromatin		0.005	9
protein_40_YJL081C	2	ARP4: Nuclear actin-related protein involved	[EDDV]EMI]	41		Y	nucleolus (1e-24)		0.007	10
protein_40_YJL074C	2	SMC3: Subunit of the multiprotein cohesion complex	[ESDQ]..[EGEP]	41		Y			0.008	10
protein_40_YJL010C	2	NOP8: Essential component of the 40S ribosomal subunit	[EMP1]..[FHIV]	41		Y			0.005	7
protein_40_YJL094C	2	YLS12: Homo-isocitrate dehydrogenase, an $\alpha$ -ketoglutarate dehydrogenase complex component	[SYT]YADA	41	[LNJ]R ITY	Y	Y		0.004	7
protein_40_YJL094C	2	YLS12: Homo-isocitrate dehydrogenase, an $\alpha$ -ketoglutarate dehydrogenase complex component	[AIK]K..[EREG]	41		Y	PDGFR kinase substrate mo		0.005	9
protein_40_YJL198W	2	YPR167: Alpha-protein component of the 19S nucleolar ribosomal subunit	[TINL]DDYI	41		Y			0.005	10
protein_40_YHR148W	2	IMP3: Component of the SRS1 processing complex	[RWEH]..[FHIV]	41		Y	DDDK[KACDEF] Protease Enterokinase		0.005	7
protein_40_YHR135C	2	YCK1: Palmitoylated, plasma membrane-bound	[KTGK]S	41		Y			0.006	10
protein_40_YHR088W	2	RPTF1: Nuclear protein involved in the assembly of the 19S nucleolar ribosomal subunit	[IYFIPS]AGMSI	41		Y	SH2 ligand for Vari1 (group II		0.005	10
protein_40_YGR252W	2	CIC1: Essential protein that interacts with one or more proteins involved in the assembly of the 19S nucleolar ribosomal subunit	[PEFK..GTP]	41		Y	14-3-3 binding motif in ExoS		0.005	10
protein_40_YGR216W	2	GCNS: Histone acetyltransferase, acetyltransferase	[L[QH]W].[OCIA]	41		Y	ribosome (0.01)		0.005	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[EE..[KLA]S]SLK]	41	EADAY	Y	cytoplasm organization and biogenesis (0.01)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[GNTF]..[NTKN]	41	EED	Y	ribosome biogenesis (0.001)		0.005	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[L..[QH]P]	41		Y	SAGA complex (0.01)		0.005	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[D[ER]..[E]GEE]	41		Y	snRNP protein import into nucleus (1e-08)		0.006	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[K[WT]K]..[KPRO]	41		Y	rRNA export from nucleus (1e-05)		0.007	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E[DE]..[D]GM]	41	KR	Y	cytoplasm organization and biogenesis (i)		0.004	8
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[SD]DYE[V]EHQ]	41	CLV_PCSK_PCIET2_1	Y	proteasome complex (sensu Eukaryota) (0.001)		0.005	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[K[QPR]BSLVE]	41	S.D.	Y			0.007	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[S]D[D]Y[V]EHQ]	41		Y	RNA processing (1e-19)		0.005	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[L[QH]W].[OCIA]	41		Y			0.005	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[L[QH]W].[OCIA]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.007	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[R[QK]L]SKR]	41	KR	Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.005	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[P]R[OS]K]	41	[ST]E	Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.005	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[Q[DWM]..[DISDP]	41	P.Q.D	Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.005	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[SC]N[L]EJP	41	SP	Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.005	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[IKA]S..[F]SQY]	41	S.F	Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.005	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[R..VAK]P]	41	[K]R R	Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.005	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[N]VYF]..[SD]VVA	41	YE	Y	ribonucleoprotein complex (1e-32)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[L[A]M..[R]AVK]	41		Y	nucleolus (1e-06)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[L[N]GK]..[V]NQK]	41	P ST PKK.KK	Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[G]F[P]..[VITMN]	41	KR	Y	nucleolus (1e-06)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[L[GVI]K..[TEMPL]	41	K..[ST]	Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.005	8
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[T[KD]P]K[SP]IG]	41		Y	ribosomal large subunit biogenesis (1e-04)		0.005	7
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[I[GDI]..[CAP]C]	41	[AG]R	Y	response to osmotic stress (0.001)		0.008	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[HTE]L..[SEVIT]	41	L..[LM]E	Y	mRNA cleavage and polyadenylation specificity i		0.008	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[L..[QH]P]..[VFT]	41		Y	nucleolus (0.01)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V]	41		Y	cytoplasm organization and biogenesis (i)		0.004	7
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cell cortex (1e-04)		0.007	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y			0.005	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	ribonucleoprotein complex (1e-32)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	nucleolus (1e-06)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	nucleolus (1e-06)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	9
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	41		Y	cytosolic ribosome (sensu Eukaryota) (1e-15)		0.004	10
protein_40_YGR216W	2	CRM1: Major karyopherin, involved in export	[E]P[D]V ..[V]P]	4						





yeast-144_GO-0016538	2	protein metabolism	K[LYL][DFLFT][G NS,ILM,VIN[KEG]	38	Pkinase	1.E-46	6.7	protein amino acid phosphorylation (1e-50)	0.008	10	
yeast-589_GO-0053898	2	response to stimulus	L[LMV][P]	38				response to stress (1e-37)	0.008	10	
yeast-513_GO-0005259	2	protein-protein complex	GTC[CDV[S]LY]	38	S[ST]			protein binding (1e-04)	0.005	9	
yeast-470_GO-0006259	2	protein binding	K[STGQ][TIR]	38	MDC1_BRCT domain bindinc			DNA metabolism (1e-75)	Y	0.008	10
yeast-410_GO-0007049	2	DNA metabolism	L[ERI][EMH][D	38			cell cycle (1e-58)	0.008	10		
yeast-410_GO-0007049	2	cell cycle	T[LSF][KMAP]	38			cell cycle (1e-54)	0.008	10		
yeast-388_GO-0007275	2	development	L[SNP].[KNTC]	38			multicellular organismal development (1e-76)	0.008	10		
yeast-320_GO-0006355	2	regulation of transcription, DNA-dependent	DD,[IQY][EDGR]	38	DD, Y	Shb PTB domain binding mo		regulation of transcription, DNA-dependent (1e-1)	0.008	10	
yeast-284_GO-0005740	2	mitochondrial envelope	E.[DSH][S]	38	[LIVMA].EGID[ TOPoisomerase II PATTI				0.008	10	
yeast-284_GO-0005740	2	mitochondrial envelope	KRK[HV]	38	KR	CLV_PCSK_C1E2_1			0.008	10	
yeast-255_GO-0042544	2	integral to membrane	[AGPS].[S][FL]	38	S,F	LIG_BRCT_BRCA1_1			0.008	10	
yeast-255_GO-0007028	2	cytoskeleton organization and biogenesis	P.[QNR][P]	38			Integral to membrane (1e-12)	0.008	10		
yeast-249_GO-0043285	2	biopolymer catabolism	[LSR][TNT][Q]	38			rRNA processing (1e-07)	0.005	8		
yeast-244_GO-0002797	2	M phase	L[TSN][III][P]	38			rRNA processing (1e-07)	0.005	8		
yeast-235_GO-0006563	2	morphogenesis	P.[QNR][P]	38			biopolymer catabolism (1e-07)	0.005	7		
yeast-235_GO-0006092	2	cellular morphogenesis	T[KS][A][NQK]	38			M phase (1e-90)	0.008	10		
yeast-215_GO-0007010	2	cytoskeleton organization and biogenesis	[ILG][QEAJ[E]	38			cellular morphogenesis (1e-65)	0.008	10		
yeast-207_GO-0006974	2	response to DNA damage stimulus	L[SEC][T][Q]	38			cellular morphogenesis (1e-65)	0.008	10		
yeast-1547_GO-0043283	2	biopolymer metabolism	DD, Y	38			cytoskeleton organization and biogenesis (1e-46)	0.008	10		
protein_40_YPR120C	2	CLBS: B-type cyclin involved in DNA replicati	[LIVMA].EGID[ TOPoisomerase II PATTI	38			response to DNA damage stimulus (1e-60)	0.008	10		
protein_40_YPR1680W	2	TET2: Translational regulator of Eif-1 al	E.[DSH][S]	38			protein modification (1e-09)	0.008	10		
protein_40_YPL140C	2	protein involved in rRNA processing	KRK[HV]	38				0.008	10		
protein_40_YPL141C	2	F1FK1: Putative protein kinase similar to F1	[AGPS].[S][FL]	38				0.008	10		
protein_40_YPL093W	2	NOG1: Putative GTPase that associates with protein	[LSR][TNT][Q]	38				0.008	10		
protein_40_YOR294W	2	RSS1: Essential protein that binds ribosomal protein	P.[QNR][P]	38				0.008	10		
protein_40_YOR133W	2	EFT1: Elongation factor 2 (EF-2), also encod	T[KS][A][NQK]	38				0.008	10		
protein_40_YOL133W	2	HRT1: RING finger containing subunit of Skp	[ILG][QEAJ[E]	38				0.008	10		
protein_40_YOL086C	2	A1H1: Alcohol dehydrogenase, fission yeast	D[QDQ][V]	38				0.008	10		
protein_40_YOL004W	2	SIR1: Component of the Sln3-Rpd3 histone deacetylase complex	[VWV][H]	38				0.008	10		
protein_40_YNR054C	2	ESF2: Essential nucleolar protein involved in rRNA processing	C[QDQ][V]	38				0.008	10		
protein_40_YNL298W	2	CL4A: Cdc42 activated signal transduc	[LJL][CSD]	38				0.008	10		
protein_40_YLR118C	2	PDC2: Cdc42-activated cyclin of the Pdc2-like subfam	[PCK][W]	38				0.008	10		
protein_40_YMR194W	2	DRP3A: N-terminal acetylated protein deacetylase	D[QDQ][V]	38				0.008	10		
protein_40_YMR139W	2	RIM1: Protein kinase required for signal trans	D[QDQ][V]	38				0.008	10		
protein_40_YMP116C	2	ASC1: G-protein beta subunit and caspase-11	A.[VGR][K]	38				0.008	10		
protein_40_YMR001C	2	CD25: Poly-L-proline kinase with similarity to Xenc	[NKA][NDLS]	38	N.KD	Motif for specificity of quanini		macromolecule catabolism (1e-04)	Y	0.007	10
protein_40_YML063W	2	RPS18: Ribosomal protein 10 (rp10) of the small ribosomal subunit	[KLN][M][GKS]	38			histone deacetylase complex (1e-08)	Y	0.005	7	
protein_40_YLR448W	2	RPB8: Protein component of the large (60S)	[NKA][NDLS]	38			nucleolus (1e-14)	Y	0.007	10	
protein_40_YLR429W	2	CRN1: Cytomatric actin cytoskeletal col	[D].[RIP][GDK]	38			cytosolic ribosome (sensu Eukaryota) (1e-30)	Y	0.008	10	
protein_40_YLR180W	2	SAM1: S-adenosylmethionine synthetase, catalyzes the transfer of methyl group to SAM	[D].[RIP][GDK]	38				0.007	10		
protein_40_YLR029C	2	RPL1A: Protein component of the large (60S)	[D].[RIP][GDK]	38				0.007	10		
protein_40_YLR002C	2	NOC3: Protein that forms a nuclear complex	[E][E][AG][E][W]	38	R.DD.	S Casein kinase 1 phosphoryla		cytosolic ribosome (sensu Eukaryota) (1e-29)	Y	0.007	10
protein_40_YLR021C	2	RPB1: Protein involved in early nucleolar	[R].[E][E]	38			cytosolic ribosome (sensu Eukaryota) (1e-27)	Y	0.006	8	
protein_40_YLR019C	2	RPB1: Protein involved in early nucleolar	[R].[E][E]	38				0.006	8		
protein_40_YLR007C	2	RPB1: Protein component of the large (60S)	[R].[E][E]	38				0.006	8		
protein_40_YFR052W	2	RPB12: Subunit of the 19S regulatory particle	[R].[E][E]	38				0.006	8		
protein_40_YFR034C	2	RPB14: Basic helix-loop-helix (bHLH) transcri	[V].[T][L][K]	38				0.006	8		
protein_40_YFR031C-A	2	RPB12A: Protein component of the large (60S)	K[KS][A][KVR]	38				0.006	8		
protein_40_YFR031C-W	2	RPB12A: Protein component of the large (60S)	D[N][D][P]	38				0.006	8		
protein_40_YGR218W	2	CRM1: Major karyopherin involved in export	A.[VGR][K]	38				0.006	8		
protein_40_YGR218W	2	CRM1: Major karyopherin involved in import	I[ESR][AYR][E]	38				0.006	8		
protein_40_YGR060W	2	ERG23: C-4 methyl sterol oxidase, catalyzes	A.[G][R][VWP]	38				0.006	8		
protein_40_YGL105W	2	ARC1: Protein that binds RNA and methionyl	R.[A][P][A][K]	38				0.006	8		
protein_40_YGL076C	2	RPL7A: Protein component of the large (60S)	E[Q][E][AG][E][W]	38				0.006	8		
protein_40_YFR076C	2	RPL7A: Protein component of the large (60S)	R.[V][W][F]	38				0.006	8		
protein_40_YFR052W	2	RPB12: Subunit of the 19S regulatory particle	R.[V][W][F]	38				0.006	8		
protein_40_YFR034C	2	RPB14: Basic helix-loop-helix (bHLH) transcri	K[KS][A][KVR]	38				0.006	8		
protein_40_YFR031C-A	2	RPB12A: Protein component of the large (60S)	D[N][D][P]	38				0.006	8		
protein_40_YLR190W	2	B2M1: Beta-2 microglobulin, major isoform, controls protein folding	[G][G...K]	38				0.006	8		
protein_40_YLR149W	2	B2M1: Beta-2 microglobulin, minor isoform, controls protein folding	S.[S][W][G]	38				0.006	8		
protein_40_YLR128W	2	CRM1: Major karyopherin involved in import	[S][N][L][N][G]	38				0.006	8		
protein_40_YDR388W	2	RPS2: Ubiquitin-protein ligase involved in cell	[YFG][VCTP][DT]	38				0.006	8		
protein_40_YDR145W	2	TAF12: Subunit (0.163 kDa) of TFIID and SAI	A[TAP][T]	38				0.006	8		
protein_40_YDL213C	2	NOP8: Putative RNA-binding protein implicated in pre-mRNA splicing	[PSI][PSI]	38				0.006	8		
protein_40_YDL140C	2	RPB42: Protein required for pre-mRNA splicing	K[KEP][SL][IFN]	38				0.006	8		
protein_40_YDL055C	2	PSA1: GDP-mannose pyrophosphorylase (m	[LMR][SK][DS][L]	38				0.006	8		
protein_40_YDL055C	2	PSA1: GDP-mannose pyrophosphorylase (m	[SWH][D][AS][FL]	38				0.006	8		
protein_40_YDL055C	2	PSA1: GDP-mannose pyrophosphorylase (m	G[G][GOY]	38	RGG	Alternative integrin binding si		ribosome assembly (0.01)	Y	0.007	10
protein_40_YDL055C	2	PSA1: GDP-mannose pyrophosphorylase (m	R..[EV][E]	38	YE	TPK-IIIB/P38y kinase phos		nucleolus (0.01)	Y	0.007	10
protein_40_YDL055C	2	PSA1: GDP-mannose pyrophosphorylase (m	D[PW][R][PFD]	38	R..L	LIG_APCC_Dbox_1		proteasome complex (sensu Eukaryota) (0.01)	Y	0.007	10
protein_40_YLR190W	2	SIT1: Type 2A-related serine/threonine phospho	[P][V][P]	38				cytosolic ribosome (sensu Eukaryota) (1e-18)	Y	0.007	10
protein_40_YBR181C	2	CRM1: Major karyopherin involved in import of some mRNAs	S.[S][T][S]	38				cytosolic ribosome (sensu Eukaryota) (1e-16)	Y	0.007	10
protein_40_YBL227W	2	RPL1B: Ribosomal protein, large subunit B	R.[R][M]	38				rRNA export from nucleus (1e-06)	Y	0.007	10
protein_40_YAL032C	2	PRP46: Protein required for pre-mRNA splicing	[R][S][M]	38				rRNA export from nucleus (1e-06)	Y	0.007	10
matsumuya_Nucleus	2	YKE2: Subunit of the heterohexameric Gim1/pr	E[DF][Y][E]	38					0.007	10	
matsumuya_Nucleus	2	YKE2: Catalytic subunit of the main cell cycle	[ED][FRE][KTR]	38					0.007	10	
matsumuya_Nuclear_envelope	2	YKE2: Subunit 4 of the 20S proteasome	[SKLD][N][QE]	38					0.007	10	
matsumuya_Cytosol	2	YKE2: Subunit of the heterohexameric Gim1/pr	[ST][S][P]	37					0.007	10	
genetic_YLR262C	2	YPT6: GTPase, Ras-like GTP-binding protein	[G][IY][V][K]	37					0.007	10	
genetic_YLR200W	2	YPT6: GTPase, Ras-like GTP-binding protein	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Protein component of the large (60S)	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[S][W][I][A]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[G][IY][V][K]	37					0.007	10	
protein_40_YER012W	2	RPB1: Conserved ribosomal protein PO simili	[I][C][P][M]	37					0.007	10	
protein_40_YER012											

protein_40_YNL188W	2	UBP10: Ubiquitin-specific protease that deub	A[PO]E	37	A[E A EEY FV ] FGFR kinase substrate motif	Y	Kinase	1.E-17	4	protein kinase activity (e-17)	Y	0.007	10
yeast-601_GO-0006454	2	protein modification	W S Q V L F G C	37		Y	Kinase	1.E-19	4.3	protein modification (e-27)	Y	0.008	10
yeast-602_GO-0002924	2	kinase activity	K P N I V L T A K I	37		Y	Kinase	1.E-59	6.5	protein kinase activity (e-56)	Y	0.008	10
yeast-601_GO-0005829	2	cysteine	[R PG AA R K G]	37						cysteol (e-47)		0.008	10
yeast-470_GO-0006259	2	DNA metabolism	[T L D S E F Q C ]	37	[P L I M I L D E] ATM kinase substrate motif	Y				DNA metabolism (e-86)		0.008	10
yeast-470_GO-0006259	2	DNA metabolism	T T P G _K K D R	37	KR CLV_PCSK_PC1ET2_1	Y			DNA metabolism (e-64)		0.008	10	
yeast-410_GO-0007049	2	cell cycle	E . . K S N I N R	37	T. [S A] FHA of KAPP binding motif, 1				cell cycle (e-76)		0.008	10	
yeast-388_GO-0007275	2	development	[T R Q S T T E W C]	37					multicellular organismal development (e-09)	Y	0.007	7	
yeast-343_GO-0005198	2	structural molecule activity	[G P Q Q G F M G ]	37					snRNP protein import into nucleus (e-07)		0.005	8	
yeast-301_GO-0044451	2	nucleoplasm part	[L V A J N N D M G ]	37	KEN LiG_APCC_KENbox_2				nucleoplasm part (e-11)		0.007	10	
yeast-301_GO-0044451	2	nucleoplasm part	D.. D D G	37					nucleoplasm part (e-17)	Y	0.008	10	
yeast-299_GO-0001224	2	nucleoplasm part	A P S F R . . . .	37					integrin-linked kinase (e-11)		0.005	10	
yeast-244_GO-00079	2	membrane	M P S F P L I L	37					M phase (e-49)		0.005	10	
yeast-238_CO-0017111	2	nucleoside-triphosphatase activity	N S P T P A P H I	37					nucleoside-triphosphatase activity (e-09)	Y	0.005	7	
yeast-238_CO-0017111	2	nucleoside-triphosphatase activity	[H D E V . . H T C O C ]	37					nucleoside-triphosphatase activity (e-15)		0.006	9	
yeast-235_GO-0009653	2	morphogenesis	[I S V L E I E L U G ]	37					cellular morphogenesis (e-37)		0.008	10	
yeast-235_GO-0009092	2	cellular morphogenesis	T G [TP MI TP ]	37	TGY ERK6/SAPK3 activation sites	Y			cellular morphogenesis (e-37)		0.008	10	
yeast-223_GO-0003735	2	structural constituent of ribosome	T G [TP MI TP ]	37	TGY ERK6/SAPK3 activation sites				cellular morphogenesis (e-37)		0.008	10	
yeast-220_GO-0044255	2	cellular lipid metabolism	E.. G V N F	37					cellular lipid metabolism (e-15)		0.008	10	
yeast-205_GO-0005858	2	cytoskeleton	L . [L V R T ]	37	PLARTLSVAG Calmodulin-dependent protei	Y			cytoskeleton (e-18)		0.008	10	
yeast-1493_GO-0043234	2	protein complex	L Q E N E	37					cytoskeletal part (e-10)	Y	0.005	9	
yeast-1493_GO-0043234	2	nucleoside, nucleotide, nucleotide and nucle	T L D N M D Q	37	LFDLIM Binding motif in Clint for clat				endoplasmic reticulum (e-07)		0.003	9	
protein_40_YPR140C	2	protein forms a complex w/	F L S W F	37	F.FP LIG_MAPK_2LIG_MAPK_2				transcription, DNA-dependent (e-28)		0.004	9	
protein_40_YPR140C	2	RNA polymerase subunit, common to	S I D P K N D	37					RNA polymerase complex (e-09)		0.007	10	
protein_40_YPR140C	2	HSP28: Heat shock protein required for sheroes	[S I D P K N D ]	37	IEPD Protease Granzyme B				RNA polymerase complex (sensu Eukaryota) (0.001)		0.006	10	
protein_40_YPL240C	2	HSP28: Heat shock protein required for sheroes	D.. T R L	37					cytoplasm organization and biogenesis (0.001)	Y	0.007	9	
protein_40_YPL240C	2	HSP28: Heat shock protein required for sheroes	A [K E B D E D ]	37	AEVD Protease Caspase 10				rRNA metabolism (e-04)		0.004	8	
protein_40_YPL240C	2	HSP28: Heat shock protein required for sheroes	O.. Q E P N	37	VP Interleukin converting enzym				nucleolus (e-34)		0.006	9	
protein_40_YPL240C	2	HSP28: Heat shock protein required for sheroes	T L D N E Q J L V A	37	PTLPL RAF1 kinase substrate motif				nucleolus (e-21)		0.004	9	
protein_40_YPL153C	2	RAD53: Protein kinase, required for cell-cycle	A N L A E C O M	37					carboxylic acid metabolism (0.01)		0.007	10	
protein_40_YPL153C	2	RAD53: Protein kinase, required for cell-cycle	Q Q K S L L P L P K	37	EED Ankyrin B C-terminal motif th	Y			proteasome complex (sensu Eukaryota) (0.001)	Y	0.007	9	
protein_40_YPL153C	2	NOP4: Nuclear protein, forms a complex w/	E.. V E G D I E K P E	37					cytoplasm organization and biogenesis (0.001)	Y	0.004	7	
protein_40_YPL153C	2	NOP4: Nuclear protein, forms a complex w/	N E S D M J K E S	37					rRNA metabolism (e-04)		0.004	8	
protein_40_YPL153C	2	RNA polymerase II subunit, common to	S I D P K N D	37					nucleolus (e-34)		0.004	8	
protein_40_YPL153C	2	RNA polymerase II subunit, common to	D.. T R L	37					nucleolus (e-21)		0.004	9	
protein_40_YPL153C	2	EFT1: Elongator factor 2 (EF-2), also encod	A [K E B D E D ]	37					condensed nuclear chromosome (0.001)		0.007	10	
protein_40_YPL153C	2	EFT1: Elongator factor 2 (EF-2), also encod	T R Q G . V E G A	37					SWR1 complex (e-06)		0.004	10	
protein_40_YPL153C	2	T-RNA: One of six tRNAs of the 19S rRNA	T L K A J F V S L	37					small nucleolar ribonucleoprotein complex (e-11)		0.007	10	
protein_40_YOL120C	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					snRNP protein import into nucleus (e-08)		0.005	8	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					RNA processing (0.001)		0.007	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					nuclear pore (e-16)		0.004	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					nuclear mRNA splicing, via spliceosome (e-07)		0.004	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					endoplasmic reticulum (0.001)		0.004	9	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					nucleolus (0.01)		0.005	9	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-15)	Y	0.004	7	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-15)	Y	0.007	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					RNA processing (e-14)		0.007	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-12)	Y	0.004	9	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	S I P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	P P D P N P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	Q P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.005	10	
protein_40_YOL069W	2	RPL18A: Protein component of the large (60S	K P H P I P P P	37					cytosolic ribosome (sensu Eukaryota) (e-16)	Y	0.00		





protein_40_YPL128W	2	NAN1_U3 snoRNP protein, component of the regulation of cellular process	[D GKS ][VDT JK	35		WD40	1.E-08	2.4	small nuclear ribonucleoprotein complex (1e-2: regulation of cellular metabolism (1e-57)	Y	0.007	10	
protein_40_YLR145C	2	Cdc14p, component of the small IADS	[P AKT V	35	R_K	G98 bindins motif for GADS	1.E-02	2.5	regulation of nucleoprotein complex (1e-18)	Y	0.008	10	
protein_40_YNL008W	2	DRS1_Nuclear DEAD-box protein required	[T SD DF GRY	35	D_F,DF	EF hand in gamma-synergin	1.E-11	3.2	protein kinase activity (1e-10)	Y	0.006	10	
protein_40_YNL002C	2	RLP7_Nuclear protein with similarity to larg	[R E K J L IEA	35	M R DE [IL]	TUBULIN_B AUTOREG PAI	1.E-03	3.3	cytoplasm organization and biogenesis (1e-19)	Y	0.007	10	
yeast-335_GO-0016772	2	transferase activity, transferring phosphorus-c	[V Y L K Y PAV]	35	Y L L	SH2 ligand for PLCoamma1	1.E-14	3.4	cytoplasm organization and biogenesis (1e-19)	Y	0.007	10	
yeast-244_GO-0000279	2	M phase	[L S LN Q	35	L S LN Q	ATM kinase substrate motif	1.E-05	3.5	M phase (1e-18)	Y	0.008	9	
protein_40_YGL111W	2	NSA1_Constituent of 66S pre-ribosomal parti	[L F M SA	35	WLN	Lipid binding motif in C-terminal	1.E-05	3.5	cytoplasm organization and biogenesis (1e-17)	Y	0.004	8	
protein_40_YDR060W	2	MAK21_Constituent of 66S pre-ribosomal parti	[RE W E LD Y A	35	EAD Y	Abl kinase substrate motif	1.E-07	3.5	ATP-dependent RNA helicase activity (1e-15)	Y	0.006	10	
protein_299_GO-0005730	2	nucleolus	[PT G T SD JREL	35	RE..E	Iron binding motif in ferritin L-	1.E-13	3.8	ATP-dependent RNA helicase activity (1e-15)	Y	0.006	10	
Oshea_mcl	13	Oshea_mcl	[K K P K J	35	K K R J K	Nuclear localization motif	Zn_clus	1.E-07	4.1	nuclear lumen (1e-52)	Y	0.035	10
yeast-335_GO-0016772	2	transferase activity, transferring phosphorus-c	[L U L P Q	35	L U L P Q	Protein phosphatase 1	1.E-27	4.9	transmembrane receptor phosphorus-con	Y	0.007	9	
yeast-648_GO-0005794	2	protein modification	[K W K V K W R	35	D L U K P K	FKPY	TLA binding motif in Brinker t	1.E-26	5.2	protein modification (1e-57)	Y	0.007	9
yeast-238_GO-0017111	2	nucleotide-triphosphatase activity	[R T V W P Q T	35	R T V W P Q T	Motif on TIM mitochondrial tr	Y	1.E-24	5.6	protein amino acid phosphorylation (1e-47)	Y	0.008	10
yeast-1547_GO-004283	2	bisphosphotriester metabolism	[W D H P P N D	35	C..C	Motif on TIM mitochondrial tr	Y	1.E-15	5.8	nucleotide-triphosphatase activity (1e-43)	Y	0.008	10
yeast-207_GO-0003677	2	DNA binding	[A H H C C P P	35	KEN	Zn_clus	1.E-15	13.8	protein amino acid phosphorylation (1e-29)	Y	0.008	10	
yeast-460_GO-0006351	2	transcription, DNA-dependent	[A T G C P P	35	F..C	Motif on TIM mitochondrial tr	Y	1.E-19	16.9	transcription, DNA-dependent (1e-21)	Y	0.008	10
yeast-856_GO-0009059	2	macromolecule biosynthesis	[A T G C K A T	35		Zn_clus			macromolecule biosynthetic process (1e-77)	Y	0.008	10	
yeast-752_GO-0016787	2	hydrolase activity	[D A E H .. F C R	35		Protease	1.E-27	4.9	hydrolase activity, acting on ester bonds (1e-07)	Y	0.007	10	
yeast-648_GO-0050791	2	regulation of biological process	[E I G D .. T F N H	35		Phosphatase	1.E-26	5.2	regulation of metabolism (1e-28)	Y	0.007	10	
yeast-648_GO-0050791	2	regulation of physiological process	[E I G D .. T F N H	35		Protein kinase	1.E-39	5.6	regulation of metabolism (1e-29)	Y	0.007	10	
yeast-544_GO-0016770	2	RNA metabolism	[D P A T P T N L Q	35	S ST	MDC1 BRCT domain binding			regulation of metabolism (1e-72)	Y	0.007	10	
yeast-462_GO-0019222	2	regulation of metabolism	[E N M D .. E N C	35					RNA metabolism (1e-29)	Y	0.007	10	
yeast-388_GO-0007275	2	development	[S L G S .. R P Q E	35	S.R	PKC phosphorylation motif			regulation of metabolism (1e-56)	Y	0.008	10	
yeast-341_GO-0045449	2	regulation of transcription	[L V A E J N D M G	35	KEN	LIG_APCC_KENbox_2			multicellular organismal development (1e-57)	Y	0.007	10	
yeast-322_GO-0005654	2	nucleoplasm	[R K A E .. Q K W K	35					regulation of transcription (1e-14)	Y	0.008	10	
yeast-248_GO-0016072	2	rRNA metabolism	[L E N D .. D L V M K	35	D..D	Ribose moiety of UDP and n-			nucleoplasm (part 1e-11)	Y	0.007	9	
yeast-244_GO-0000279	2	M phase	[S P Q Q .. S K M R	35	SQ	ATM kinase substrate motif			rRNA processing (1e-28)	Y	0.008	10	
yeast-244_GO-0000279	2	M phase	[S P N R H D S K	35	SP	ERK1, ERK2 Kinase substra			M phase (1e-15)	Y	0.007	10	
yeast-233_GO-0006624	2	mitotic cell cycle	[A H F I F Q C Y	35	F..I..	PTPRJ phosphatase substra			M phase (1e-66)	Y	0.008	10	
yeast-233_GO-0006735	2	lipid metabolism	[L K A P .. L K W K	35	F..L..K..K..R..	Phosphotyrosine binding n			mitotic cell cycle (1e-51)	Y	0.008	9	
yeast-216_GO-0009255	2	structural constituent of ribosome	[A F I Q E Q L	35					lipid metabolism (1e-22)	Y	0.008	10	
yeast-216_GO-0009255	2	chromatin and/or maintenance of chromatin	[A F I Q E Q L	35					establishment and/or maintenance of chromatin	Y	0.006	9	
yeast-216_GO-0009255	2	chromosome	[A F I Q E Q L	35					establishment and/or maintenance of chromatin	Y	0.006	9	
yeast-207_GO-0009274	2	response to DNA damage stimulus	[R P V L Q I G Q	35	LLKL	AP-2 binding motif in CXCR2			chromosome (1e-26)	Y	0.008	10	
yeast-207_GO-0009274	2	bisphosphotriester metabolism	[R P V L Q I G Q	35	LLKL	AP-2 binding motif in CXCR2			response to DNA damage stimulus (1e-41)	Y	0.008	10	
yeast-1547_GO-004283	2	proteins involved in pre-rRNA processing	[Y D N G .. I E E I S	35	Q MLV D G .. D C V	MDC1 BRCT domain binding			DNA metabolism (1e-16)	Y	0.007	10	
protein_40_YPR182W	2	SMX3_Core Sm protein Sm F; part of hetero	[S P Q I .. S K M R	35	Q MLV D G .. D C V	MDC1 BRCT domain binding			U2-dependent spliceosome (1e-04)	Y	0.007	10	
protein_40_YPR161C	2	SGV1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K			nucleolus (1e-10)	Y	0.007	10		
protein_40_YPR120C	2	CLB5_B-type cyclin involved in DNA replication	[S P N R H D S K	35	SP N R H D S K			chromatin remodeling complex (1e-08)	Y	0.006	10		
protein_40_YPR080W	2	TEF1_B-type cyclin involved in cell cycle pro	[S P N R H D S K	35	SP N R H D S K			chromatin remodeling complex (0.001)	Y	0.005	9		
protein_40_YPR043W	2	ARP1_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR031C	2	ARP2_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR182W	2	TOP1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR161C	2	SGV1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR120C	2	CLB5_B-type cyclin involved in DNA replication	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR080W	2	TEF1_B-type cyclin involved in cell cycle pro	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR043W	2	ARP1_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR031C	2	ARP2_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR182W	2	TOP1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR161C	2	SGV1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR120C	2	CLB5_B-type cyclin involved in DNA replication	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR080W	2	TEF1_B-type cyclin involved in cell cycle pro	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR043W	2	ARP1_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR031C	2	ARP2_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR182W	2	TOP1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR161C	2	SGV1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR120C	2	CLB5_B-type cyclin involved in DNA replication	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR080W	2	TEF1_B-type cyclin involved in cell cycle pro	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR043W	2	ARP1_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR031C	2	ARP2_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR182W	2	TOP1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR161C	2	SGV1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR120C	2	CLB5_B-type cyclin involved in DNA replication	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR080W	2	TEF1_B-type cyclin involved in cell cycle pro	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR043W	2	ARP1_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR031C	2	ARP2_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR182W	2	TOP1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR161C	2	SGV1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR120C	2	CLB5_B-type cyclin involved in DNA replication	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR080W	2	TEF1_B-type cyclin involved in cell cycle pro	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR043W	2	ARP1_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR031C	2	ARP2_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR182W	2	TOP1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR161C	2	SGV1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR120C	2	CLB5_B-type cyclin involved in DNA replication	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR080W	2	TEF1_B-type cyclin involved in cell cycle pro	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR043W	2	ARP1_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR031C	2	ARP2_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR182W	2	TOP1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR161C	2	SGV1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR120C	2	CLB5_B-type cyclin involved in DNA replication	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR080W	2	TEF1_B-type cyclin involved in cell cycle pro	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR043W	2	ARP1_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR031C	2	ARP2_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR182W	2	TOP1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR161C	2	SGV1_Cyclin (Bur2p)-dependent protein kinase	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR120C	2	CLB5_B-type cyclin involved in DNA replication	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR080W	2	TEF1_B-type cyclin involved in cell cycle pro	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR043W	2	ARP1_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R H D S K								
protein_40_YPR031C	2	ARP2_Component of both the SWI5/SNF and	[S P N R H D S K	35	SP N R								





protein_40_YBR159W	2	IFAI38. Microsomal beta-keto-reductase; contd	L[PAI][ITVJA	33	TP1 PATTERN	MFS_1	1.E-02	-0.3	transporter activity (1e-07)	0.006	10	
protein_40_YOR272W	2	YTR18. Constituent of 6S pre-ribosomal part	K[JARWK]	33	SKRKYRK	Brix	1.E-02	-0.2	cytosol organization and biogenesis (1e-32)	0.006	10	
protein_40_YUL074C	2	SMC3. Subunit of the multiprotein cohesin complex	[KLT][MCJ][E	33	[STJE]	Sec24pSe24pSe24p	Y	0.1	nuclear chromosome part (0.001)	0.006	9	
protein_40_YUL074C	2	SMC3. Subunit of the multiprotein cohesin complex	Q[JLDY]	33	L[LME]	cohesin complex (0.01)	Y	0.2	cohesin complex (0.01)	0.007	10	
yeast-215_GO-0005694	2	chromosome	V[SKQ][KOPJ]	33	GIQVD	ovine kith chain LC8 interai	Y	0.3	chromosome (1e-97)	0.007	10	
yeast-470_GO-0006259	2	DNA metabolism	[KDAJK][KRJREAD]	33	KR	CLV_PCSK_PCIET2_1	MFS_1	0.4	DNA metabolism (1e-48)	0.007	10	
yeast-335_GO-0016772	2	transferase activity, transferring phosphorus-con	IF[VIV]	33	F[YTFP]	DEF motif for ERK docking	MFS_1	0.5	Golgi apparatus (1e-35)	0.030	10	
matsuyma_K_G15	15	matsuyma_K_G15	T[RINR]	33	[KJR][R]	CLV_PCSK_KEX2_1	Zn_clus	0.6	regulation of metabolism (1e-76)	0.007	10	
yeast-631_GO-0050794	2	regulation of cellular process	[NEAJT..][VPIY]	33	VP	Interleukin converting enzym	Y	0.6	actin cortical patch (1e-07)	0.005	9	
protein_40_YDL14W	2	NOP1. Nuclear protein, component of the A	V[KNJD]	33	WD40	nucleolus (1e-34)	Y	0.6	nucleolus (1e-34)	0.006	10	
protein_40_YLR374W	2	protein_40_YLR374W	I..[LWV][G]	33	Sugar_Ir	integrin to membrane (0.01)	Y	0.8	integrin to membrane (0.01)	0.007	10	
protein_40_YLR374W	2	2. SUR4. Elongase, involved in fatty acid and st	[LWV][G]	33	LLG	cytosol organization and biogenesis (sensi	Y	0.8	cytosol organization and biogenesis (sensi	0.005	9	
yeast-457_CO-0007001	2	2. UGA. Essential light chain of the 20S proteasome	[MCJ][DANT]	33	WD40	chromosome organization and biogenesis (1e-97)	Y	0.9	chromosome organization and biogenesis (1e-97)	0.007	10	
yeast-255_GO-0042254	2	2. cytosol organization and biogenesis (see	[TAQ][IAANM]	33	WD40	cytosol organization and biogenesis (1e-12)	Y	0.9	cytosol organization and biogenesis (1e-12)	0.007	10	
yeast-255_GO-0007028	2	2. cytosol organization and biogenesis	G..[ENGK]	33	WD40	cytosol organization and biogenesis (1e-12)	Y	0.9	cytosol organization and biogenesis (1e-12)	0.007	10	
yeast-143_GO-0006139	2	2. nucleic acid, nucleotide and nucleic	L[LAVN]	33	HLVNK	actin cortical patch (1e-07)	Y	0.9	actin cortical patch (1e-07)	0.005	9	
protein_40_YNL189W	2	SRP1. Karveophilin alpha homolog, forms a c	[KROQ][LYRYA]	33	EEEYF	nucleolus (1e-34)	Y	0.9	nucleolus (1e-34)	0.006	10	
protein_40_YMR047C	2	UTP15. Nuclear protein, component of the t	R[NMIS][LEFJEE]	33	EGFR kinase phosphorylato	RNase_Ph_C	1.E-02	1	rRNA processing (1e-23)	0.005	9	
protein_40_YMR047C	2	UP11P. Subunit of the nuclear pore complex	Q..[ONR]	33		WD40	rnasecyploplasmic transport (1e-24)	Y	1	nucleocytoplasmic transport (1e-24)	0.006	10
protein_40_YBR159W	2	UTP18. Microsomal beta-keto-reductase; contd	L[LWV][G]	33		IBN_N	1.E-05	1.1	rRNA processing (1e-23)	0.005	9	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	LLT[PLP]	33		MFS_1	1.E-02	1.1	transporter activity (1e-09)	0.006	10	
protein_40_YML007W	2	gene regulator	S..[R]	33		Bromodomain	1.E-03	1.3	proteins (1e-13)	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	L..[VIV]	33		Kinesin	1.E-02	1.3	cell cycle (1e-07)	0.007	10	
protein_40_YML007W	2	gene regulator	G..[FWF]	33		MFS_1	1.E-04	1.4	integral membrane protein (1e-75)	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[FIOK][FWFV]	33		WD40	macromolecular catalysis (1e-08)	Y	1	macromolecular catalysis (1e-08)	0.005	7
protein_40_YML007W	2	gene regulator	DL..[SPQJ][EMI]	33	STG	PKC phosphorylation motif	Y	1.0	small nuclear ribonucleoprotein complex (1e-1)	0.006	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	I..[FLV]	33	DLL	EH(3) EF hand domain bindi	Pkinase	1.E-03	1.6	protein kinase activity (0.01)	0.006	10
protein_40_YML007W	2	gene regulator	[LOVY][RTW][G]	33	YIGPY	G protein receptor k	Kinesin	1.E-03	1.6	microtubule cytoskeleton (1e-35)	0.007	10
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[KTSQ][S][FED]	33	DSG..S	beta2-Integrin binding motif	MFS_1	1.E-11	1.6	endoplasmic reticulum (1e-39)	0.034	10
protein_40_YML007W	2	gene regulator	R..[FWV]	33	WD40	transporter activity (1e-20)	Y	1.7	transporter activity (1e-20)	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[PEYV][HIVM]	33		Pkinase	1.E-11	1.7	protein kinase activity (1e-10)	0.007	10	
protein_40_YML007W	2	gene regulator	[T][GIV][HIVM]	33		UQ_cnn	1.E-16	1.7	protein modification (1e-26)	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[IL][NP..Y]	33		WD40	ubiquitin ligase complex (1e-11)	Y	1.8	ubiquitin ligase complex (1e-11)	0.006	9
protein_40_YML007W	2	gene regulator	[DGMG][KVYN]	33		SNF2_N	1.E-02	1.8	rRNA processing (1e-14)	0.006	9	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	R..[QD]	33		ATPase activity (0.001)	2.3	ATPase activity (0.001)	0.004	7		
protein_40_YML007W	2	gene regulator	[R][QD][FGSN]	33		DPF	2.5	snoRNA binding (1e-16)	0.006	9		
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[RHC][VFC][QSR]	33		AP2 binding motif in Synaptc	AP2	2.7	ATP binding (1e-11)	0.008	10	
protein_40_YML007W	2	gene regulator	[G][WJS][FCDFG]	33		Helicase_C	1.E-04	2.7	protein modification (10)	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[VQVQ][WVNWJ]	33		R.GSF	1.E-10	2.9	protein kinase activity (1e-10)	0.005	10	
protein_40_YML007W	2	gene regulator	[LFR][DEAKD]	33		Pkinase	1.E-10	2.9	chromosome organization and biogenesis (sensi	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[SISWQ][F][GTM]	33		WD40	1.E-10	3.1	chromosome organization and biogenesis (sensi	0.007	10	
protein_40_YML007W	2	gene regulator	[KQAJK..][KRV]	33		DEAD	1.E-07	3.3	rRNA helicase activity (1e-07)	0.004	7	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	G[GEY][TNP][TS]	33		Pkinase	1.E-24	3.4	cytosol organization and biogenesis (1e-16)	0.007	10	
protein_40_YML007W	2	gene regulator	[F][QINJ]	33		DEAD	1.E-03	3.4	protein kinase activity (1e-22)	0.007	9	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[Q][DN][TNY]	33		PRM1	1.E-05	3.9	ribonucleoprotein complex (0.001)	0.006	10	
protein_40_YML007W	2	gene regulator	[S][KFO][R][KSQ]	33		Pkinase	1.E-15	4.0	cell cycle (1e-19)	0.008	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[V][S][A]	33		QDQQTQKQI	4.0	cell cycle (1e-19)	0.007	10		
protein_40_YML007W	2	gene regulator	[IAYM][SVF][JNG]	33		4D POSTSYNAPTIC PA		4.2	rRNA processing (1e-10)	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	IL..[LCW][VALP]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VNR][EESPM]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	L..[VNR][EESPM]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[YHW][DIA][SYN]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[D][SGV][KWIWS]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	SA..[ER][CINOH]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[EYPT][IKWAJ]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][CIPQ][AMK]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[DT][MWV][KLJN]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][LWW][EGJH]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	AR..[ART]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[IGR][GE]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	YAP1. Basic leucine zipper (BZIP) transcription	[L][VDE][L][ML]	33				4.2	regulation of nucleic acid, nucleoside, nucleotide	0.007	10	
protein_40_YML007W	2	gene regulator</										







yeast-842_GO-0043228	2	non-membrane-bound organelle	WV[SYA]	31	PWY[ST]  STIR SRP1_TIP1 PATTERN		0.007	10
yeast-921_GO-0008310	2	transport	[TKGIC].[PRE]GN	31	[DGH  IVSAQ]" TRANSALDOLASE 1 PATT		0.007	10
yeast-792_GO-0005412	2	organic acid biosynthesis	E [EFS].[EID G6W]	31	F.E DNA binding motif in MutS		0.007	10
yeast-610_GO-0031090	2	organic acid biosynthesis	Q.[LOFIS]	31		Y	0.007	10
yeast-548_GO-0051641	2	cellular localization	[KAG S EIM S]	31			0.007	10
yeast-470_GO-0006259	2	DNA metabolism	[KAJ R].[ENH EE]	31	[KR R]R CLV_PCSK_KEX2_1		0.007	10
yeast-468_GO-0051276	2	chromosome organization and biogenesis	[SLO S R].[LOPI E	31	S.R PKC phosphorylation motif		0.007	10
yeast-436_GO-0031323	2	regulation of cellular metabolism	D.D [EKV ]	31	D.D Ribose moiety of UDP and n		0.007	10
yeast-424_GO-0006950	2	response to stress	E [LEW].[NDK L]	31			0.006	10
yeast-424_GO-0006950	2	response to stress	R..[JEAT	31			0.006	10
yeast-410_GO-0007049	2	cell cycle	[KOD R].[ESM ]	31		Y	0.007	10
yeast-304_GO-0019162	2	regulation of transcription	[PHI P].[PIT AM]	31	IP IV  Crystallin motif for dimerizati		0.007	10
yeast-304_GO-0006082	2	carboxylic acid metabolism	PIT AM	31	IP IV  Crystallin motif for dimerizati		0.007	10
yeast-267_GO-0044265	2	cellular macromolecule catabolism	C..[ATC ]	31			0.005	8
yeast-251_GO-0005886	2	plasma membrane	D [AR J].[OH S]	31			0.007	10
yeast-238_GO-0017111	2	nucleoside-triphosphatase activity	E..[IRV K]	31	YE IV  SH2 ligand for Fees (Tyr must		0.007	9
yeast-238_GO-0017111	2	nucleoside-triphosphatase activity	K..[DL P Q]	31			0.006	9
yeast-235_GO-0000278	2	mitotic cell cycle	A [IAS ]	31	F MLV Y PTRRJ phosphatase substra		0.007	10
yeast-233_GO-0006629	2	lipid metabolism	T [SQ].[EK VP D]	31	[ST].E Casien kinase II consensus :		0.007	10
yeast-222_GO-0009309	2	amine metabolism	[V Q].[Q Q P ]	31			0.007	10
yeast-216_GO-0006325	2	establishment and/or maintenance of chromatin	L LT T [M P Q ]	31	LLG Beta2-Integrin binding motif		0.007	10
yeast-216_GO-0006325	2	establishment and/or maintenance of chromatin	V [Q Q].[Q P ]	31			0.007	10
yeast-216_GO-0006323	2	DNA packaging	L LT T [M P Q ]	31	LLG Beta2-Integrin binding motif		0.007	10
yeast-216_GO-0006323	2	DNA packaging	[ADCP PS V P]	31	P [ST P  Erk p44 MAP kinase phospho	Y	0.007	10
yeast-215_GO-0007010	2	cytoskeleton organization and biogenesis	Q..[E L P ]	31			0.007	10
yeast-215_GO-0007010	2	cytoskeleton organization and biogenesis	K [REV L N DF N	31	KR CLV_PCSK_PC1ET2_1		0.007	10
yeast-205_GO-0005868	2	cytoskeleton	[SMPL S FC S ]	31			0.006	10
yeast-193_GO-0043234	2	protein complex	[LE K..G L N T	31			0.007	10
protein_40_YPR144C	2	Nucleolar protein, forms a complex w/	I [DSA].[LD K Q Y]	31	VP Interleukin converting enzym		0.005	9
protein_40_YPR119W	2	CLB2: B-type cyclin involved in cell cycle pro	[ER V N AP Q ]	31			0.005	10
protein_40_YPR110C	2	R2C4: RNA polymerase subunit, common w/	K..[D F T V ]	31			0.005	10
protein_40_YPL217C	2	BMS1: Essential conserves nucleolar TBP-bl	[EV D P T V ]	31			0.005	10
protein_40_YPL217C	2	proteins involved in rRNA processing for 60S ribo	N P F P	31			0.005	10
protein_40_YPL193C	2	2SL1: Autophagy receptor involved in rRNA pro	S [R G P ].[R G K ]	31	K K R K  KR Nuclear localization motif		0.007	10
protein_40_YPL204W	2	HHR25: Protein kinase involved in regulating	D D C V [P S V P ]	31	Y D Q D V  SH2 ligand for Blink (Tyr mus		0.006	10
protein_40_YPL153C	2	RAD51: Protein kinase, required for cell-cycle	N A Y O].[E U Q ]	31			0.006	10
protein_40_YPL128W	2	NAN1: U3 snoRNP protein, component of the	[K A P F].[T M Q O J]	31	[K R R  CLV_PCSK_KEX2_1		0.007	10
protein_40_YPL121W	2	R2P12: Protein required for the synthesis of the	E K S Y Y K A T	31			0.007	10
protein_40_YPL004C	2	LSP1: Primary component of esosomes, whi	G Q S Q].[S I R F ]	31	S..S Casien kinase I phosphoriat	Y	0.005	9
protein_40_YOR308C	2	SNU8: Component of the U4/U6 snRNP	R I R H G].[K V R	31	KR CLV_PCSK_PC1ET2_1		0.005	10
protein_40_YOR174W	2	MED4: Subunit of the RNA polymerase II 3' end	[Q M C D L R S ]	31			0.005	7
protein_40_YOR174W	2	MED4: Subunit of the RNA polymerase II 3' end	P Q P H Y [V W ]	31	N.P.Y LIG_PTB_IIG_PTB_1		0.005	8
protein_40_YOR168W	2	C2KA: Beta catalytic subunit of casen kinase	R G S W [H K W T ]	31	RGD LIG_RGD_LIG_RGD		0.004	8
protein_40_YOR168W	2	C2KB: Beta regulatory subunit of casen kinase	[T O A J].[A E Y ]	31	KP..[Q K  LIG_SH4_4LIG_SH4_4		0.004	8
protein_40_YOR133W	2	HRT1: RING finger containing subunit of Skp	R T Q [A P H ]	31			0.005	9
protein_40_YOR133W	2	HRT1: RING finger containing subunit of Skp	F..[P A K H P ]	31	FTY mTOR kinase substrate moti		0.006	10
protein_40_YOL133W	2	HRT1: RING finger containing subunit of Skp	[I RE T K S L P E ]	31	[ST E] G protein-coupled receptor k		0.006	10
protein_40_YLN289W	2	POL1: Phos8 cytin of the Prt1-like subunit	T N D O F	31			0.006	10
protein_40_YLN244C	2	SU11: Translation initiation factor elf-1 compo	F..[E G I A ]	31	GFRGE [AG J  DNA MISMATCH REPAIR		0.006	10
protein_40_YLN175C	2	NOP13: Protein of unknown function, localiz	D D S H E [E O C ]	31	SDE Casein kinase II substrate mi		0.006	10
protein_40_YLN118C	2	D2C2: Catalytic subunit of the Dcp1-Dcp2p	K I N W S [S M H ]	31	S I S  MDCC1 BRCT domain binding		0.006	10
protein_40_YMR242C	2	R2P2A: Protein component of the leucine (60S	A..[G A K I ]	31	VPGKARKKSS Calmodulin-dependent protei		0.006	10
protein_40_YMR242C	2	R2P2A: Protein component of the leucine (60S	R..[G A K J ]	31	R G A K  Protease ItpA proteolytic site		0.006	9
protein_40_YMR236W	2	TAF9: Subunit (17 KDa) of TFIID and SAGA c	L T [Q L N Q ]	31	LT Q L N Q  WD40 domain of Cdc4 bindi		0.006	10
protein_40_YMR222C	2	R2P5: Protein required for the synthesis of the	E [P A K W K L ]	31	FGF VVA Zyxin motif that binds alpha-		0.006	10
protein_40_YMR186W	2	HSP10: Chaperone involved in assembly of import	E..[E N D P ]	31	LPKY Zyxin motif that binds alpha-		0.006	10
protein_40_YLR372W	2	PKC1: Tyrosine kinase of the Rho GTPases	P K V W [H V Y ]	31	LPKY Zyxin motif that binds alpha-		0.006	8
protein_40_YLR246W	2	PKC2: Tyrosine kinase of the Rho GTPases	[L V D P Y ].[S I R Y ]	31	LPKY WW motif (non-conventional		0.006	9
protein_40_YLR129W	2	D2P2: Nuclear protein, specifically associated	S..[P S V L N E L ]	31	S I E F  G protein-coupled receptor k		0.004	7
protein_40_YLR111W	2	SOF1: Essential protein required for biogenet	R..[E K H I S A D ]	31	R K R K  ZIP kinase phosphorylation n		0.005	9
protein_40_YMR106C	2	T2R2: RIK-pinked protein kinase and rapam	R T D Y C [G D K ]	31	L T D Y C [G D K  WD40 domain of Cdc4 bindi		0.006	10
protein_40_YMR106C	2	T2R1: RIK-pinked protein kinase and rapam	S Q [F D E V ]	31	E D Y  EGFR kinase substrate moti		0.006	10
protein_40_YMR093W	2	UTP15: Nucleolar protein, component of the	N K T N [F C T ]	31	R K K  ZIP kinase phosphorylation n		0.006	10
protein_40_YMR001C	2	CD55: Polo-like kinase, similarity to Xer	[E K P K S I R K E ]	31	RKK S T  ZIP kinase phosphorylation n		0.006	10
protein_40_YML010W	2	CD56: Polo-like kinase with similarity to Xer	F P P P ].[K D I Q ]	31			0.006	10
protein_40_YML010W	2	SPT5: Protein that forms a complex with Sptd	[K Q Q ].[A E Y D ]	31			0.006	10
protein_40_YML010C	2	SPT5: Protein that forms a complex with Sptd	E T C D I P W	31	E S T D  Ankyrin G binding motif in K		0.006	10
protein_40_YML010C	2	SPT5: Protein that forms a complex with Sptd	D I D C D I P W	31			0.006	10
protein_40_YLR246W	2	SRS2: Translational elongation factor 3, align	S I S F P	31	S..F..K LIG_BRCT_BRCA1_2		0.006	10
protein_40_YLR129C	2	D2P2: Nuclear protein, specifically associated	R J D O S	31			0.006	10
protein_40_YLR074C	2	SRS2: DNA helicase involved in DNA repair	D Y D R I G L G Y	31	D E J  EGFR kinase substrate moti		0.006	10
protein_40_YLR074C	2	SRS2: DNA helicase involved in DNA repair	R D S I S F P	31	F..R..S F I M P N  PKC zeta kinase substrate m		0.006	10
protein_40_YLR061C	2	SRS2: Subunit of the multiprotein cohesin co	S I S F P Y	31			0.006	10
protein_40_YLR035C	2	SRS2: Subunit of the multiprotein cohesin co	[S D Y I N S ]	31	Y..N LIG_SH2_GRB2		0.006	9
protein_40_YHR197W	2	CKA1: Alpha catalytic subunit of casein kinase	A E G J R	31	[A G J R  Protease matrmatase protease		0.004	7
protein_40_YHR165C	2	PRPB: Component of the U4/U6 snRNP	L E S L ].[E A S ]	31	Y..P  CPV Heme binding site in mitoch		0.006	10
protein_40_YHR135C	2	YCK1: Polyimido, plasma membrane-bou	P Y	31			0.006	10
protein_40_YHR092C	2	YCK2: Nonessential catalytic serine/threonine	V..[Y D W K ]	31			0.006	9
protein_40_YLR074C	2	YCK2: Nonessential catalytic serine/threonine	K..[G W N G ]	31			0.006	10
protein_40_YHR053W	2	G101: Essential component of the Rsk1 comp	E..[D N G C Y C ]	31	EED Ankyrin B C-terminal motif th		0.006	9
protein_40_YHL007C	2	STE20: Signal transducing kinase of the PMK	E [D T W T V ]	31			0.006	10
protein_40_YHL001W	2	YOS1: Tyrosine kinase involved in the Rsk1 (60S	N A E S O C	31	SDE Casein kinase II substrate mi		0.005	9
protein_40_YGR218W	2	CRM1: Major karyopherin, involved in export	[P N E R ].[K A V A ]	31			0.006	9
protein_40_YGR103W	2	NOP7: Nucleolar protein involved in RNA pro	S Q [E G F I P N K ]	31			0.006	10
protein_40_YGR086C	2	PIL1: Primary component of esosomes, whi	K..[E V F V ]	31			0.006	10
protein_40_YGR040W	2	KSS1: Mitogen-activated protein kinase (MAP	[K H W T ].[F L R Y ]	31			0.006	8
protein_40_YGR040W	2	KSS1: Mitogen-activated protein kinase (MAP	A [S T A ].[N E T ]	31			0.006	10
protein_40_YGR040W	2	KSS1: Mitogen-activated protein kinase (MAP	T..[E D Y ].[G C F ]	31			0.006	10
protein_40_YGR040W	2	KSS1: Mitogen-activated protein kinase (MAP	C P L P T E ].[S T ]	31			0.006	10
protein_40_YGR040W	2	T053: Protein kinase, related to and function	G E F Q K	31			0.006	9
protein_40_YGL179C	2	T053: Protein kinase, related to and function	D P W W I P Q	31			0.006	9
protein_40_YGL120C	2	PRP4: RNA helicase in the DEAH-box fami	K..[D Q W Q ]	31			0.006	10
protein_40_YGL106W	2	MCL1: Essential light chain for Myo1, light c	R S L R P N Y	31			0.006	10
protein_40_YGL030W	2	PRL40: Protein component of the large (60S	[T F N W J A ]	31			0.006	10
protein_40_YFR034C	2	PH04: Basic helix-loop-helix (bHLH) transcri	E..[E S F D K ]	31			0.006	10
protein_40_YFR039C	2	ACT1: Actin structural protein involved in el	[D T V J ].[E L T G ]	31			0.006	10
protein_40_YFL037W	2	TUB2: Beta-tubulin; associates with elpha-tub	R..[Q L G T ]	31			0.006	10
protein_40_YER177W	2	B1H1: 14-3-3 protein, major isoform; control	[R S L W ].[N D L ]	31			0.006	10
protein_40_YER082C	2	UP7P: Nuclear protein, component of the sr	I D D H I K D N	31			0.006	10
protein_40_YER082C	2	ATPase of the ATP-binding cassette (ABC)	D P W W I P Q	31			0.006	10
protein_40_YER082C	2	protein_40_YER082C: Component of the SLMO1 fan	[T P T P I M E Q ]	31			0.006	10
protein_40_YDR515W	2	ADA2: Transcription coactivator, component	R..[Q L G T ]	31			0.006	10
protein_40_YDR448W	2	ADA2: Transcription coactivator, component	R S L R P N Y	31			0.006	10
protein_40_YDR448W	2	ADA2: Transcription coactivator, component	[T F N W J A ]	31			0.006	10
protein_40_YDR448W	2	ADA2: Transcription coactivator, component	E..[E S F D K ]	31			0.006	10
protein_40_YDR448W	2	ERD1: Predicted membrane protein required	[D T V J ].[E L T G ]	31			0.006	10
protein_40_YDR365C	2	ESF1: Nuclear protein involved in pre-rRNA	I D D H I K D N	31			0.006	10
protein_40_YDR324C	2	UTP4: Nuclear protein, component of the sr	[D T V J ].[E L T G ]	31			0.006	10
protein_40_YDR303C	2	R3C3: Component of the RSK1 chromatin ren	R..[Q L G T ]	31			0.006	10
protein_40_YDR225W	2	HTA1: One of two nearly identical (see also H	[D T V J ].[E L T G ]	31			0.006	10
protein_40_YDR135W	2	TAF12: Subunit (16/18 KDa) of TFIID and SA	R..[Q L G T ]	31			0.006	10
protein_40_YDR093W	2	TFIIB: Subunit (16/18 KDa) of TFIID and SA	R..[Q L G T ]	31			0.006	10
protein_40_YDR093W	2	TFIIE: Subunit (16/18 KDa) of TFIID and SA	R..[Q L G T ]	31			0.006	10
protein_40_YDR048W	2	TFIIE: Subunit (16/18 KDa) of TFIID and SA	R..[Q L G T ]	31			0.006	10
protein_40_YDL213C	2	NOP8: Putative RNA-binding protein implicated	[G F P ].[A A Q P ]	31				

protein_40_YBR142W	2	MAKS: Essential nucleolar protein, putative D protein	2	[A GRPIK][K KIPFEN]	31	I.YA.P	c-Abl kinase phosphorylation	nucleolus (1e-13)	0.006	10	
protein_40_YBR109C	2	CMLB: Calmodulin/Ca++ binding protein that binds to the C-terminal histone H3 protein	2	[T NPKL][R KQJS]	31			regulation of nucleobase, nucleoside, nucleotide	0.006	10	
protein_40_YBR019W	2	RPL37: Protein component of the large (60S)	2	[N ADIK][L ONL]	31	S.D	CAMKII phosphorylation site	nuclear mRNA splicing, via spliceosome (1e-08)	0.006	9	
protein_40_YAL032C	2	PRP45: Protein required for pre-mRNA splicing	2	L [SPQJ][DIFER]	31	F MLV Y	PTPRJ phosphatase substrate	mRNA processing (1e-08)	0.006	10	
protein_40_YAL032C	2	PRP45: Protein required for pre-mRNA splicing	2	[F STF][L GEIM]	31	DRY	Binding motif for interaction c	storage vacuole (1e-16)	0.006	10	
oshea_vacuole	2	oshea_vacuole	2	[F STF][GDL][KP]	31	FKPY	TLA binding motif in Brinker t	microtubule cytoskeleton (1e-12)	0.005	10	
oshea_spindle_pole	2	oshea_spindle_pole	2	A [NQJS]	31	RPVSSAAASVY	14-3-3 domain binding motif	vesicle-mediated transport (1e-05)	0.006	10	
oshea_punctate_composite	2	oshea_punctate_composite	2	F G[PA][L ASF]	31			nuclear pore (1e-16)	0.007	10	
oshea_nuclear_periphery	2	oshea_nuclear_periphery	2	V [FMI][W FGW]	31			nucleoplasm (1e-24)	0.005	9	
oshea_nuclear_periphery	2	oshea_nuclear_periphery	2	V [FMI][W FGW]	31	E EEEVVF	PDGFR kinase substrate mo	plasma membrane (1e-15)	0.005	10	
oshea_cell_periphery	2	oshea_cell_periphery	2	P O VNO]	31	L FDLM	Binding motif in Clint for clat	plasma membrane (1e-15)	0.007	10	
oshea_cell_periphery	2	oshea_cell_periphery	2	K H[EK]	31	[ST].E	Casien kinase II consensus :	plasma membrane (1e-15)	0.006	10	
oshea_bud_neck	2	oshea_bud_neck	2	R K[RSN]	31	III Q.C...K.R.	Mysin light chain binding mi	site of polarized growth (1e-26)	0.006	10	
matsuyama_Spindle or SPI	2	matsuyama_Spindle or SPI	2	I [EMC].[EH]E	31			spindle (1e-15)	Y	0.008	9
matsuyama_Spindle or SPI	2	matsuyama_Spindle or SPI	2	A [PSQI]	31	[ST]Q	ATM kinase phosphorylation	spindle (1e-10)	Y	0.008	10
matsuyama_periphery	2	matsuyama_periphery	2	E [T]L5 K	31	ESIRKIFYIYLIS	LIQ_WH1LIG_WH1	barrier septum (1e-13)	Y	0.008	10
matsuyama_nuclear_envelope	2	matsuyama_nuclear_envelope or dots	2	A [QAK][KLDJ]	31			nuclear pore (1e-13)	Y	0.008	10
matsuyama_nuclear_envelope	2	matsuyama_nuclear_envelope or dots	2	D L Q[D]	31	[K R]R	CLV_PCSK_KEX2_1	nuclear envelope (1e-28)	Y	0.008	9
matsuyama_ER	2	matsuyama_ER	2	R H W CV	31	H.R.G	Motif for cell cycle arrest in S	nuclear envelope (1e-10)	Y	0.007	10
matsuyama_Cyttoplasmic_dots	2	matsuyama_Cyttoplasmic_dots	2	P O VNO]	31	KP Q[K]	LIQ_SH2_ALG_SH2_4	vesicle-mediated transport (1e-04)	Y	0.008	10
genetic_YPL020C	2	LGE1: Protein of unknown function; null muta	2	K H[EK]	31	[RK]I R[K ST].	Akt kinase substrate motif	chromosome organization and biogenesis (sensi)	0.006	10	
genetic_YPL020C	2	LGE1: Protein of unknown function; null muta	2	R K[RSN]	31	R.K.	SH3 binding motif for GADS	chromosome organization and biogenesis (sensi)	0.006	10	
genetic_YNL153C	2	GIM3: Subunit of the heterotrimeric cooch	2	P T QH S	31	NPKI[S]TISAG	PROK_SULFATE BIND 2 P.	cytoskeleton organization and biogenesis (1e-06)	Y	0.006	10
genetic_YNL153C	2	GIM3: Subunit of the heterotrimeric cooch	2	Q G D V S	31	[PT]GKHG_AK	IF5A_HYPUSINE PATTERN	asexual reproduction (0.001)	Y	0.006	10
genetic_YLR200W	2	YKE2: Subunit of the heterotrimeric Gim3p	2	[F NL]AK	31			cell cycle (1e-09)	Y	0.006	10
genetic_YLR200W	2	YKE2: Subunit of the heterotrimeric Gim3p	2	K [HDM]Q	31	[ST]Q	ATM kinase phosphorylation	cytoskeleton organization and biogenesis (0.001)	Y	0.005	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	E S V YE	31			chromosome organization and biogenesis (sensi)	0.006	10	
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	L P TQ E EPN]	31			chromosome organization and biogenesis (sensi)	0.006	10	
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	Q L D S J	31			chromosome organization and biogenesis (sensi)	0.006	10	
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	D L D L	31	L PDEL	Motif in CBP for interaction w	chromosome organization and biogenesis (sensi)	0.006	10	
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T D KQ J	31	P T.. D	FHA binding motif	chromosome organization and biogenesis (sensi)	0.006	10	
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	R..E	31	E RE..	Iron binding motif in ferritin L	chromosome organization and biogenesis (sensi)	0.006	10	
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	L Q K K D N L D V	31			cell cycle (1e-11)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	D L Q P N	31	SIL WL D DEIE	TRG_LysEnd_GGAACLL_2	chromosome organization and biogenesis (sensi)	0.006	9	
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	K N T S P	31	C K..N T F	RNASE PANCREATIC PATI	chromosome organization and biogenesis (sensi)	0.006	9	
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A L . AR L	31	T .. L L	FHA binding motif, Thr mus	cell cycle (1e-11)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T J ED H	31	F H2A	FHA binding motif, Thr mus	site of polarized growth (1e-10)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	V F V MF L	31	Y MF.. 3	FHA binding motif, Ser resi	mitotic cell cycle (1e-13)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	E P P R E	31	P K N A E	FHA binding motif, Ser resi	endoplasmic reticulum (1e-08)	Y	0.006	9
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	P K N A E	FHA binding motif, Ser resi	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	T .. S A	FHA binding motif, Ser resi	protein kinase activity (0.01)	Y	0.006	9
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	S .. S..	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	T P S L J N	31	[K R]R	CLV_PCSK_KEX2_1	protein kinase activity (0.01)	Y	0.006	10
genetic_YLR058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), inv	2	A K F E R	3						

yeast-513_GO-0005615	2	protein binding	E..L[RAK]	30	IBN_N	1.E-04	2.6	protein binding (1e-25)	Y	0.006	10			
protein_40_YKR081C	2	RPP1: Essential protein involved in the proce	RIEKQ[LILQA	30	MR[DE][IL]	TUBULIN_B AUTOREG PAI	DEAD	1.E-05	2.8	nucleolus (1e-15)	0.006	10		
protein_40_YCN1203	2	Lpp1: Major protein required for export o	VKQIL[IVWPR]	30	UD40	1.E-05	2.8	mRNA binding (1e-12)	Y	0.005	10			
yeast-217_GO-0007046	2	ribosome biogenesis	AIDII[JIRQL]	30	DALDL	14-3-3 binding motif in ExoS	DEAD	1.E-06	2.9	ribosome biogenesis (1e-62)	0.006	8		
protein_40_YHR030C	2	SLT2: Serine/threonine MAP kinase involved	E[YRP].G[GRS]	30	GIFLIPGER.G.LIG_IBS_.LIG_IBS_1	Pkinase	1.E-03	3.2	kinase activity (0.001)	0.005	8			
yeast-685_GO-0016740	2	transferrase activity	[FYFG][GYTIV]	30	FRGGT	Phosphonositide binding mo	Pkinase	1.E-10	3.3	transferase activity, transferring phosphorus-con	0.007	10		
protein_40_YBL007C	2	SLA1: Cytoskeletal protein binding protein re	DF[G]LIMI	30			Pkinase	1.E-10	3.3	protein kinase activity (1e-10)	0.004	8		
yeast-706_GO-0043412	2	bipolymer modification	Y[RMC][AKH]P	30			Pkinase	1.E-14	3.4	protein modification (1e-19)	0.007	10		
protein_40_YOR272W	2	TPK3: cAMP-dependent protein kinase catal	A[TH].GRF	30	[AG]JR	Protease matriphase protease	Y	DEAD	1.E-04	3.4	ATP-dependent RNA helicase activity (0.001)	0.004	8	
protein_40_YKL166C	2	YMT1: Constituent of 68S pre-ribosomal parti	R[DFW].K[PI]C	30			Pkinase	1.E-22	4	protein amino acid phosphorylation (1e-10)	0.006	10		
yeast-565_GO-0005646	2	protein modification	[MRTAP]EMI	30	P[TJS]AP	LIG_PTAPLIG_PTAP	Pkinase	1.E-05	4	protein amino acid phosphorylation (1e-10)	0.007	9		
yeast-565_GO-0005672	2	transferrase activity, transferring phosphorus-c	[D[KDS]JN]	30	SI(ST)	TRG_LysEnd_GOAALL_2	Pkinase	1.E-05	4	protein amino acid phosphorylation (1e-10)	0.007	9		
yeast-642_GO-004232	2	non-membrane-bound organelle	[TNDD]GCGTQIK	30	SI(ST)	MDC1 BRCT domain binding	Y	DEAD	1.E-06	5.1	RNA helicase activity (1e-17)	0.007	10	
yeast-1389_GO-0044262	2	cellular macromolecule metabolism	[TNDD]GCGTQIK	30	SI(ST)	MDC1 BRCT domain binding	Y	DEAD	1.E-14	5.2	RNA helicase activity (1e-17)	0.007	10	
yeast-1340_GO-0044267	2	cellular protein metabolism	K[PTQ].N[ILKIL]	30			Pkinase	1.E-33	5.6	protein amino acid phosphorylation (1e-43)	0.007	10		
yeast-324_GO-0030528	2	transcription regulator activity	K[P][NLL][FLMD]	30			Pkinase	1.E-43	5.7	protein amino acid phosphorylation (1e-49)	0.006	9		
yeast-324_GO-0030528	2	transcription regulator activity	FSRSR[SH]HDYN	30	RR.SR	SRPK2 kinase phosphorylat	Y	zfc-C2H2	1.E-14	6.4	transcription regulator activity (1e-11)	0.006	9	
yeast-1974_GO-0005634	2	nucleus	L..[ROT]H	30	C..C	Motif on TIM mitochondrial tr.	Y	zfc-C2H2	1.E-33	9.5	transcription regulator activity (1e-09)	0.006	9	
yeast-939_GO-005123	2	establishment of localization	C..[NIV]C	30	TG.Y	ERK5/GAPK3 activation sites	Y	Zn_clus	1.E-12	16.4	transcription (1e-16)	0.006	9	
yeast-856_GO-0009059	2	macromolecule biosynthesis	TG.[VLA]EMS]	30	Y.D.NHKE	PMU_I_1 PATTERN					cellular localization (1e-18)	0.007	10	
yeast-856_GO-0009059	2	macromolecule biosynthesis	SIPNLJ	30	PTL	Motif for proteosome c						0.006	10	
yeast-559_GO-0050896	2	hydrolyase activity	SIVFH[AVKII]	30							hydrolase activity, acting on ester bonds (1e-11)	0.006	10	
yeast-559_GO-0050896	2	membrane	IG..[GIVV]DAI	30							integral to membrane (1e-12)	0.007	9	
yeast-559_GO-0050896	2	transporter activity	D..[LRM]C	30	D..G	Motif that binds phosphate in					response to stress (1e-90)	0.006	10	
yeast-513_GO-0005515	2	protein binding	[RATL].F[FTK]	30							protein binding (1e-44)	0.006	9	
yeast-513_GO-0005515	2	protein binding	PP[PMD]IPGQJA	30	PPR	LIG_WW_3LIG_WW_3					protein binding (1e-11)	0.006	8	
yeast-504_GO-0008350	2	transcription	A[QVS].A[QGPJA	30							transcription (1e-14)	0.007	9	
yeast-470_GO-0006259	2	DNA metabolism	Q[EDF][NGW]JK	30							DNA metabolism (1e-08)	0.006	9	
yeast-457_GO-0007001	2	chromosome organization and biogenesis (se	L[LTK].[OHM]Q	30							chromosome organization and biogenesis (sensi	0.006	10	
yeast-424_GO-0006950	2	response to stress	[PLD]P[KMG]	30	KR	CLV_PCSK_PC1ET2_1					response to stress (1e-38)	0.007	10	
yeast-413_GO-0005215	2	transporter activity	N..[K]RK	30							multicellular organismal development (1e-44)	0.006	10	
yeast-388_GO-0007275	2	development	K[TKTM].[TQG]G	30							regulation of nucleobase, nucleoside, nucleotide	0.007	9	
yeast-388_GO-0007219	2	regulation of nucleobase, nucleoside, nucleo	K[TKTM].[TQG]G	30							catalysis (1e-36)	0.006	10	
yeast-371_GO-0009056	2	cellular catalysis	[ASPA].[GIFT]F	30							cellular catalysis (1e-41)	0.006	9	
yeast-358_GO-0044248	2	cellular catalysis	[LCVCE]ISOV	30							DNA processing (1e-11)	0.006	10	
yeast-345_GO-0005396	2	RNA processing	KN..[LSD]G[MY]	30							RNA processing (1e-11)	0.006	10	
yeast-284_GO-0005740	2	mitochondrial envelope	L[LQFQ]I	30	IY	cFGR and Csk kinase phosph					reproduction (1e-53)	0.007	10	
yeast-267_GO-0000003	2	reproduction	[LNTL]LUTLN	30	DLL	Binding motif for clathrin hea					intrinsic to membrane (1e-96)	0.006	9	
yeast-262_GO-0031224	2	intrinsic to membrane	YFYNF	30	D..SII	SH2 ligand for Grb2					M phase (1e-48)	Y	0.007	9
yeast-244_GO-0000279	2	M phase	[LASI]R[MP]F	30	YVE	Ck1 delta kinase phosphor	Y				M phase (1e-32)	0.007	10	
yeast-244_GO-0000279	2	M phase	[QTQ]L[VPH]	30	DLL	cP55 ES kinase phosphor					M phase (1e-25)	0.007	10	
yeast-238_GO-0017111	2	nucleotide-triphosphatase activity	T[L]CMQ[FGM]	30	PTL	Motif in Fos for proteosome c					nucleotide-triphosphatase activity (1e-45)	0.007	10	
yeast-238_GO-0017111	2	ribosome biogenesis	[GAQ]LIT[GT]	30	DLL	Binding motif for clathrin hea					ribosome biogenesis (1e-15)	0.006	9	
yeast-238_GO-0017111	2	ribosome organization and biogenesis	[EKQ]LIT[GT]DT	30	Y..L	Motif for down regulation of tI					cytosolic ribosome organization and biogenesis (1e-11)	0.006	10	
yeast-213_CO-0007119	2	cytosolic ribosome organization and biogenesis	YNYMO[ESQ]JA	30							response to endogenous stimulus (1e-25)	0.007	10	
yeast-212_GO-0045045	2	secretory pathway	[ESCN]K[SLD]	30	D..SII	SH2 ligand for Grb2					secretory pathway (1e-12)	Y	0.005	9
yeast-207_GO-0006974	2	response to DNA damage stimulus	[LEAD]D[RNL]	30	D..LL	Di-Leu motif for receptor end					response to DNA damage stimulus (1e-57)	Y	0.006	10
yeast-203_GO-0005975	2	carbohydrate metabolism	F..[TY]G	30							carbohydrate metabolism (1e-87)	0.006	10	
yeast-201_GO-0050876	2	reproductive physiological process	VN..[RVIA]NLT	30							reproductive physiological process (1e-42)	0.007	10	
yeast-201_GO-0048610	2	reproductive cellular physiological process	VN..[RVIA]NLT	30	RGD	LIG_RGDLIG_RGD					reproductive physiological process (1e-42)	0.004	7	
protein_40_YPR144C	2	NOC4: Nucleolar protein, forms a complex wi	R[PL04]C	30	[PSAT].[QE]J	LIG_TRAF2_1					RNA polymerase complex (1e-07)	Y	0.005	10
protein_40_YPR120C	2	CLB5: B-type cyclin involved in DNA replicati	R[PL04]C	30	RA[F]E[FE]EL						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPR110C	2	CLB4: RNA polymerase I subunit, common to	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPR010C	2	RPA35: RNA polymerase I subunit A135	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPR010C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005	10	
protein_40_YPL240C	2	HSP26: Heat shock chaperone required for pher	R[PL04]C	30	N..L						RNA polymerase complex (1e-07)	0.005</		



yeast-235_GO-0009663	2	morphogenesis	T_Q[EQJII]	29	Ras	1.E-03	1.3	cellular morphogenesis (1e-10)	0.006	9
yeast-235_GO-0009662	2	cellular morphogenesis	T_Q[EQJII]	29	Ras	1.E-03	1.3	cellular morphogenesis (1e-10)	0.006	9
protein_40_YGL1200	2	Protein involved in the DEAH-box family	D[IKAI]_V[ETM]	29	Dixi	1.E-03	1.3	nucleus (fe-10)	0.006	10
protein_40_YLR239W	2	RUB1: Essential protein involved in transcript	D_I[ERAVI]	29	Actin	1.E-04	1.4	chromatin remodeling complex (1e-05)	0.006	10
protein_40_YKR048C	2	NAP1: Protein that interacts with mitotic cycl	[PVA]R_Q[LTK]	29	Casein kinase II substrate m:	1.E-04	1.4	nuclear chromatin (1e-07)	0.006	10
yeast-235_GO-0009653	2	morphogenesis	[TPMA]Q[SNQ]	29	[AGJR]	1.E-06	1.5	cellular morphogenesis (1e-33)	0.007	10
yeast-216_GO-0006325	2	establishment and/or maintenance of chromat	[VK]I[LEY][LGC]	29	ATM kinase phosphorylation	1.E-04	1.5	establishment and/or maintenance of chromatin	0.005	9
protein_40_YDR224C	2	DNA packaging	[YV]L[TFC]	29	Histone	1.E-04	1.5	establishment and/or maintenance of chromatin	0.005	9
protein_40_YDL153C	2	HTB1: One of two nearly identical (see HTB2	[YV]L[TFC]	29	Histone	1.E-02	1.5	nuclear chromatin (1e-04)	0.005	10
protein_40_YNL00902	2	SAS10: Component of the small (ribosomal) :	[LD]Q[LT]EJA	29	Pkinase	1.E-02	1.5	protein amino acid phosphorylation (0.01)	0.003	7
yeast-235_GO-0009267	2	cellular morphogenesis	TRWRY	29	Ras	1.E-06	1.6	cellular morphogenesis (1e-33)	0.007	10
protein_40_YMR229C	2	cellular morphogenesis required for the synthesis of ta	[TPMA]Q[SNQ]	29	[STIQ]	1.E-06	1.6	ubiquitin conjugating enzyme activity (1e-11)	0.005	10
protein_40_YLR228W	2	HTA1: One of two nearly identical (see also H	[GLK]P[IVYL]	29	LIG_WW_ALIG_WW_4	1.E-01	1.6	nucleolus (1e-39)	0.005	10
protein_40_YLR106W	2	PHOB: Probable membrane protein, involve	R_A[PAIDG]	29	PAP	1.E-07	1.7	protein carboxyl activity (1e-04)	0.005	10
protein_40_YML010W	2	SPTS: Protein that forms a complex with Spk4	D_I[GFL]	29	LIG_TNKBLMLG_TNKBM	1.E-02	1.7	protein carboxyl activity (1e-04)	0.005	10
yeast-205_GO-0005898	2	cytokinesis	[MFVF]_V[YML]	29	F.D.F	1.E-02	1.7	protein carboxyl activity (1e-04)	0.005	10
yeast-921_GO-0006810	2	transport	O_(NEGIV)	29	[S]T[ST]	1.E-03	1.7	nuclear lumen (1e-12)	0.005	10
matsuyma_Spindle_or_Spi	2	matsuyma_Spindle_or_SPB	[LYFGIV]	29	LLG	1.E-03	1.7	cytoskeletal part (1e-18)	0.006	10
protein_40_YFR010W	2	UBP6: Ubiquitin-specific protease situated in	[IHLT]_LN[RK]	29	Beta2-Integrin binding motif	1.E-03	1.7	intracellular transport (7e-78)	0.006	9
protein_40_YNL272C	2	SEC2: Guanyl-nucleotide exchange factor for	[RDW]D_K[PEQ]	29	[T]R[D]P[YI]F[YI]HEMCOCAN 2 PATTERN	1.E-03	1.7	spindle (1e-43)	0.007	10
protein_40_YGL111W	2	regulation of cellular function	M_Y[CM]	29	YM	1.E-03	1.7	protein kinase activity (1e-04)	0.006	8
protein_40_YAR019C	2	DRS1: Nuclear DEAD-box protein required	[RA]AK[N]Q[OPT]	29	SH2 ligand for Vav1 (group II	1.E-03	1.7	protein kinase activity (1e-06)	0.003	9
protein_40_YNL186W	2	CDC13: Protein kinase of the Mitotic Exit Net	V[A]P[TF]K[RK]	29	DVAD	1.E-04	1.7	regulation of metabolism (1e-20)	0.006	10
protein_40_YLR175C	2	UBP10: Ubiquitin-specific protease that deub	A_P[PTP]	29	APAP	1.E-04	1.7	protein kinase activity (1e-07)	0.005	10
protein_40_YLR249W	2	NOP13: Protein of unknown function, localiz	D_E[EVK]	29	Motif for hydroxylation of Pro	1.E-04	1.7	protein serine/threonine kinase activity (1e-04)	0.005	10
protein_40_YGR128C	2	UTP6: Nuclear protein required for export o	[AYVIT]_Y[MRID]	29	WD40	1.E-03	1.7	processing of 25 pre-rRNA (1e-31)	0.005	9
protein_40_YDR449C	2	UTP6: Nuclear protein, component of the st	T_P[VHL]M[JID]	29	WD40	1.E-03	1.7	snoRNA binding (1e-13)	0.004	9
yeast-593_GO-0031981	2	nuclear lumen	D_K[PK]	29	[ST]P	1.E-06	1.7	nuclear lumen (1e-07)	0.006	8
protein_40_YLL008W	2	DRS1: Nuclear DEAD-box protein required	[K]R[KQSA]DEI_ER	29	SH2 ligand for Vav1 (group II	1.E-03	1.7	cytoplasm organization and biogenesis (1e-20)	0.005	8
protein_40_YGL111W	2	NSA1: Constituent of 66S pre-ribosomal part	[REFQ]E[QW]JLA	29	DEAD	1.E-03	1.7	cytoplasm organization and biogenesis (1e-12)	0.005	10
protein_40_YAR019C	2	UBP10: Ubiquitin-specific protease that deub	[YLMH]H	29	Pkinase	1.E-19	1.7	protein kinase activity (1e-19)	0.006	10
protein_40_YNL186W	2	NOP13: Protein of unknown function, localiz	[IFV]_HR	29	Pkinase	1.E-22	1.7	protein kinase activity (1e-19)	0.006	9
protein_40_YLR175C	2	UBP10: Ubiquitin-specific protease that deub	[ML]L[SA]T[IT]	29	Y	1.E-22	1.7	protein kinase activity (1e-19)	0.006	9
protein_40_YLR249W	2	NOP13: Protein of unknown function, localiz	T_D[SAP]K[PKA]	29	[K]R[K]	1.E-03	1.7	protein kinase activity (1e-05)	0.004	7
protein_40_YGR128C	2	UTP6: Nuclear protein required for export o	R_E[CK]P[TF]	29	CLV_PCSK_KEX2_1	1.E-03	1.7	protein kinase activity (1e-08)	0.006	9
protein_40_YLR249W	2	UTP6: Nuclear protein required for export o	[MRA]A[P]P[TR]	29	FQ...RG...R...[F] Myosin light chain binding mi	1.E-07	1.7	cell septum (1e-49)	0.007	10
protein_40_YMR049C	2	UBP10: Ubiquitin-specific protease that deub	DEAD[DNP]K[PK]	29	[P]T[ST]P	1.E-07	1.7	intracellular transport (1e-42)	0.006	10
yeast-792_GO-0006412	2	regulation of biological process	[I]V[L]M[F]I[L]V[M]	29	ILVMFILVMF DEAD ATP HELICASE PAT	1.E-13	1.7	protein kinase activity (1e-13)	0.005	9
yeast-792_GO-0006412	2	establishment of localization	[L]V[L]M[F]I[L]V[M]	29	[K]R[K]	1.E-13	1.7	protein kinase activity (1e-12)	0.006	8
yeast-792_GO-0006412	2	regulation of biological process	[I]V[L]M[F]I[L]V[M]	29	DEAD	1.E-13	1.7	cytoplasm organization and biogenesis (1e-11)	0.006	10
yeast-792_GO-0006412	2	regulation of biological process	[I]V[L]M[F]I[L]V[M]	29	Pkinase	1.E-13	1.7	cytoskeleton organization and biogenesis (1e-11)	0.006	10
yeast-792_GO-0006412	2	regulation of biological process	[I]V[L]M[F]I[L]V[M]	29	DEAD	1.E-13	1.7	DNA metabolism (1e-11)	0.006	10
yeast-792_GO-0006412	2	regulation of biological process	[I]V[L]M[F]I[L]V[M]	29	Pkinase	1.E-13	1.7	chromosome organization and biogenesis (sensi	0.006	10
yeast-792_GO-0006412	2	regulation of biological process	[I]V[L]M[F]I[L]V[M]	29	DEAD	1.E-13	1.7	chromosome organization and biogenesis (1e-8t)	0.006	10
yeast-379_GO-0031975	2	cell envelope	[L]V[H]T[T]J	29	Pkinase	1.E-19	1.7	cell cycle (1e-19)	0.007	10
yeast-379_GO-0031967	2	organelle envelope	[L]V[H]T[T]J	29	Pkinase	1.E-19	1.7	regulation of metabolism (1e-27)	0.006	10
yeast-379_GO-0031967	2	cell envelope	S_D[GNN]	29	S.D	1.E-19	1.7	nucleic acid binding (1e-29)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[FTCT]_T[NDYK]	29	T.D	1.E-19	1.7	establishment of cellular localization (1e-48)	0.006	10
yeast-379_GO-0031967	2	cell envelope	G[QD]H[Q]I[D]P[IR]	29	FH41 bindina motif, Thr mus	1.E-19	1.7	protein binding (1e-29)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[G]P[IR]P[IR]	29	[K]R[K]	1.E-19	1.7	intracellular transport (1e-60)	0.006	10
yeast-379_GO-0031967	2	cell envelope	E[Q]G[Q]I[S]AM	29	SH3 binding motif for GADS	1.E-19	1.7	DNA metabolism (1e-11)	0.006	10
yeast-379_GO-0031967	2	cell envelope	I_K[KT]P[IS]	29	R.GG	1.E-19	1.7	chromosome organization and biogenesis (sensi	0.006	10
yeast-379_GO-0031967	2	cell envelope	L_I[LP]I[SE]A[J]	29	Alternative integrin binding si	1.E-19	1.7	chromosome organization and biogenesis (1e-8t)	0.006	10
yeast-379_GO-0031967	2	cell envelope	R_A[RQL]	29	R.[ST]	1.E-07	1.7	establishment of cellular localization (1e-28)	0.006	10
yeast-379_GO-0031967	2	cell envelope	E_E[LOC]	29	Y.E.E	1.E-06	1.7	cell cycle (1e-19)	0.007	10
yeast-379_GO-0031967	2	cell envelope	E_E[LOC]	29	Y.E.E	1.E-06	1.7	catabolism (1e-50)	0.006	9
yeast-379_GO-0031967	2	cell envelope	[AQD]Q[TE]A[J]	29	Src phosphorylation site	1.E-06	1.7	endoplasmic reticulum (1e-14)	0.006	10
yeast-379_GO-0031967	2	cell envelope	V[A]L[E]	29	Src phosphorylation site	1.E-06	1.7	regulation of transcription, DNA-dependent (1e-4)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[DNH]G[EMV]K	29	GQQ	1.E-06	1.7	ribosome (1e-22)	0.007	10
yeast-379_GO-0031967	2	cell envelope	F[J]L[RN]	29	N-methylation motif in E. coli	1.E-06	1.7	integral to membrane (1e-26)	0.007	10
yeast-379_GO-0031967	2	cell envelope	[EKV]I[A]V[E]AA[K]	29	P	1.E-06	1.7	intrinsic to membrane (1e-09)	0.006	9
yeast-379_GO-0031967	2	cell envelope	F[EGQ]I[S]AM	29	[ST]P	1.E-06	1.7	cytoplasm organization and biogenesis (1e-11)	0.006	10
yeast-379_GO-0031967	2	cell envelope	I_V[A]V[F]	29	GP	1.E-06	1.7	plasma membrane (1e-34)	0.006	10
yeast-379_GO-0031967	2	cell envelope	R_A[RQL]	29	Protease TTP cleavage site	1.E-06	1.7	plasma membrane (1e-34)	0.006	10
yeast-379_GO-0031967	2	cell envelope	R_A[RQL]	29	Y	1.E-06	1.7	biopolymer catabolism (1e-07)	0.004	7
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	PTL	1.E-06	1.7	nucleic acid-triphosphatase activity (1e-95)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Motif in Fos for proteosom e	1.E-06	1.7	aminobase (1e-27)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	GQQ	1.E-06	1.7	amine metabolism (1e-40)	0.007	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	N-methylation motif in E. coli	1.E-06	1.7	secretory pathway (1e-12)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	FH41 bindina motif, Thr mus	1.E-06	1.7	cytoskeleton organization and biogenesis (1e-21)	0.007	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	[CD]2	1.E-06	1.7	cytoskeleton organization and biogenesis (1e-55)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	[CD]2	1.E-06	1.7	cytoskeleton organization and biogenesis (1e-12)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	[CD]2	1.E-06	1.7	carbohydrate metabolism (1e-14)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	[CD]2	1.E-06	1.7	DNA metabolism (0.001)	0.005	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	ribosome biogenesis (0.01)	0.005	8
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	nuclear mRNA splicing, via spliceosome (1e-08)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	rRNA metabolism (1e-10)	0.005	8
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	nucleolus (1e-28)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	nucleolus (1e-24)	0.005	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	ribosome biogenesis (1e-10)	0.005	9
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	cytoplasm organization and biogenesis (1e-09)	0.005	9
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	nucleolus (1e-13)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	general RNA polymerase II transcription factor a	0.006	9
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	translation elongation factor activity (0.001)	0.005	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	catabolism (0.001)	0.005	8
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	catabolism (0.001)	0.004	7
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	catabolism (0.001)	0.005	8
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	catabolism (0.001)	0.005	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	RNA elongation from RNA polymerase II promot	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	cytosolic ribosome (sensu Eukaryota) (1e-14)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	cytosolic ribosome (sensu Eukaryota) (1e-21)	0.006	10
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	small nuclear ribonucleoprotein complex (1e-1'	0.005	9
yeast-379_GO-0031967	2	cell envelope	[S]D[GNN]	29	Y	1.E-06	1.7	rRNA processing (1e-12)	0.005	9

protein_40_YLR180W	2 SAM1: S-adenosylmethionine synthetase, cs	D_RDRP	29		carboxylic acid metabolism (0.01)	Y	0.005	9
protein_40_YLR180W	2 ADRP: Adrenoleptin receptor, membrane, cs	NLL_NLRSRJK	29			Y	0.003	8
protein_40_YLR168C	2 SEC10: Sec10p: 100Da subunit of the vesicle	E[KEAJA EKT]	29			Y	0.006	10
protein_40_YLR129W	2 DIP2: Nuclear protein, specifically associated	[KPFID.. TGAJK]	29	D..G	motif binds phosphate in		0.006	9
protein_40_YLR129W	2 DIP2: Nuclear protein, specifically associated	K[QVAJ.. LJQG]	29			Y	0.006	10
protein_40_YLR106C	2 MDN1: Huveo-related AAA-type ATPas	AG[NSV TAW]	29			Y	0.005	9
protein_40_YLR096W	2 KIN2: Serine/threonine protein kinase involved	[SDR TDI DWI SL]	29			Y	0.005	10
protein_40_YLR074C	2 BUD26: Protein involved in bud-site selection	A[IWJ ITRV]	29			Y	0.005	9
protein_40_YLR074C	2 BUD26: Protein involved in bud-site selection	R[AEN APQIR	29	[AG R]	Protease matriptase proteasi	Y	0.005	9
protein_40_YLL045C	2 RPL28: Ribosomal protein L4 of the large (6S)	A.. VIAED]	29			Y	0.003	8
protein_40_YKR026C	2 GCN3: Alpha subunit of the translation initiation	G[SAH NKY IV]	29			Y	0.006	10
protein_40_YKL203C	2 TOR2: PIK-related protein kinase and rapam	G[IMAJ.. LMJD S]	29			Y	0.006	9
protein_40_YKL197W	2 TOR2: PIK-related protein kinase and rapam	L[LMR ]	29			Y	0.006	10
protein_40_YKL172W	2 EPP1: Essential kinase required for the assembly	E[EPP D ECE]	29			Y	0.005	8
protein_40_YKL104C	2 YET1: Endoplasmic reticulum transmembrane	D.. LRAQ	29			Y	0.005	9
protein_40_YKL085C	2 YET1: Endoplasmic reticulum transmembrane	[GWMIL.. LPC]	29	[LV IDEI LM LIG_PXL LIG_PXL		Y	0.005	10
protein_40_YJR123W	2 RPS26: Protein component of the small (40S)	A.. HETJS	29	[IVAIPI IIIA..EIS	Ankryin G binding motif in vol	Y	0.005	10
protein_40_YJR059W	2 PTK2: Putative serine/threonine protein kinase	K[KRPJA]	29	KR	CLV_PCSK_PCE1T2_1	Y	0.005	8
protein_40_YJL190C	2 RPS22A: Protein component of the small (40S)	A[AMJ EV YVL]	29	AEVD	Protease Caspase 10	Y	0.006	9
protein_40_YJL092W	2 BCK1: Mitogen-activated protein (MAP) kinase	S[SER I VN WIE]	29			Y	0.006	10
protein_40_YJL074C	2 SMC3: Subunit of the multiprotein cohesin complex	V[DCK Q ALTY	29			Y	0.005	10
protein_40_YJL144W	2 TID3: Component of the evolutionarily conserved	Q[LOQE.. LYAE]	29	YE	TPK-IIIB/P38Syk kinase phos		0.005	10
protein_40_YIL133C	2 RPL16A: N-terminal acetylated protein component	[AHK G V ..RG	29			Y	0.005	10
protein_40_YIL061C	2 RPS28B: Subunit of the 60S ribosomal subunit	A T[KM D .. D]	29			Y	0.005	10
protein_40_YIL061C	2 RPS28B: Subunit of the 60S ribosomal subunit	R[GEMM K V U]	29	LEVD	Protease Caspase 4-stringer		0.005	9
protein_40_YHR203C	2 RPS4B: Protein component of the small (40S)	Y RDC E	29	FRY CEG	REL_1 PATTERN	Y	0.005	10
protein_40_YHR197W	2 RIX1: Essential component of the Rix1 complex	R.. IVAR	29	[AGR	Protease matriptase proteasi	Y	0.005	8
protein_40_YHR196W	2 UTP29: Nuclear protein, component of the sr	K[VPKJ.. SKAJ]	29	K.. [ST]	PKA kinase substrate motif	Y	0.006	9
protein_40_YHR196W	2 UTP29: Nuclear protein, component of the sr	O[QYGI.. KILG	29	K LECD	Motif for binding quanine nuc	Y	0.005	10
protein_40_YHR082C	2 KSP1: Nonessential putative serine/threonine	VT[NDW J DF S]	29	[NT K D]		Y	0.005	10
protein_40_YHR079C	2 IRE1: Serine/threonine kinase and endoribonuclease	S.. R GH P]	29	R.. [ST].R	CLK1 kinase substrate motif	Y	0.006	10
protein_40_YHR064C	2 SSZ1: Hsp70 protein that interacts with Zus1:	D N P G	29			Y	0.005	9
protein_40_YHR030C	2 SLT2: Serine/threonine MAP kinase homolog	[ST D TM J D K]	29	S ST	MDC1 BRCT domain bindin		0.005	10
protein_40_YHR030C	2 S2P1: Putative RNA binding protein; involved in rRNA processing	[RDP N K EJA	29			Y	0.006	10
protein_40_YHR030C	2 TAF17: Component of the large (40S) ribosomal subunit	E KTR S P	29	IEPD	Protease Granzyme B		0.005	10
protein_40_YHR030C	2 TAF17: Major亮氨酸-rich protein in ribosomes	[KAT V .. AVIK	29			Y	0.006	10
protein_40_YHR030C	2 CRM1: Major karyopherin involved in export	Q.. QCV E	29			Y	0.005	10
protein_40_YHR030C	2 UTP22: Putative 3D snRNP protein involved in rRNA processing	V G T S TR R	29			Y	0.003	7
protein_40_YHR030C	2 RPL11B: Protein component of the large (60S)	A.. P G H G RD	29	GGRRGG	Arginine methyl transferase		0.005	10
protein_40_YHR030C	2 RPL11B: Protein component of the large (60S)	[AA.. ARC IE HA	29			Y	0.005	10
protein_40_YHR040W	2 KSS1: Mitogen-activated protein kinase (MAP kinase)	A[N STR I]	29			Y	0.005	10
protein_40_YGR040W	2 KSS1: Mitogen-activated protein kinase (MAP kinase)	K[KGP J.. L SDE	29			Y	0.005	10
protein_40_YGL195W	2 GCN1: Positive regulator of the Gcn2p kinase	G LVC .. NK YV	29			Y	0.005	10
protein_40_YGR085C	2 SEC13: Essential beta' coat protein of the DEAH-box family	D.. P	29	DLPPP	EVH1 binding motif		0.005	10
protein_40_YGL180W	2 RPL21B: Protein component of the large (60S)	[SRHD Q DN QNR	29			Y	0.005	10
protein_40_YGL180W	2 RPL21B: Protein component of the large (60S)	[ET S IS G L .. D]	29	CLILVIA_ALVF	CASEIN ALPHA BETA PAT	Y	0.003	7
protein_40_YGL180W	2 RPL21B: Protein component of the large (60S)	L EFD P Q D Q D Y	29			Y	0.005	8
protein_40_YGL076C	2 RSC8: Component of the RSC chromatin rem	E FKP K OPE	29	FKPY	TIA binding motif in Brinker t		0.005	9
protein_40_YGL076C	2 RSC8: Component of the RSC chromatin rem	R.. E G A .. EIS	29	EISTID	Ankyrin G binding motif in K		0.005	9
protein_40_YFR037C	2 RSC8: Component of the RSC chromatin rem	R.. R AKC	29	R.. RK R	CLV_PCSK_FUR_1		0.005	10
protein_40_YFR037C	2 RSC8: Component of the RSC chromatin rem	E.. IKTR	29	[K R R	CLV_PCSK_KEX2_1		0.005	10
protein_40_YFL037W	2 TUB2: Beta-tubulin; associates with alpha-tub	[IQM N.. IQT Q	29	[ST Q]	ATM kinase phosphorylation	Y	0.005	10
protein_40_YFL037W	2 TUB2: Beta-tubulin; associates with alpha-tub	[RQA ACG.. NK	29	G S AIJLNK	GDP-mannose binding motif	Y	0.004	8
protein_40_YER133W	2 GLCT: Catalytic subunit of type 1 serine/threonine	[TAJ W.. N RDA	29	L KE AD A R Z	TROPOMYOSIN PATTERN	Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[S D W D I F S]	29	SILWILDIDE	TRG_LysEng_GGA4L_2	Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	E KPF K ER	29	KR	CLV_PCSK_PCE1T2_1	Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	D D N P S Q N Q	29			Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	P V K G A V Y	29	AGYGSTT	ICE_NUCLEATION PATTER	Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	I L T Y .. C T	29			Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	M P Y D	29	DMQQD	Protease Caspase 3 -stringe	Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	DL N L V F R S	29			Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	P S .. Y K E AL K	29	[P ST]	DNA dependent Protein kin	Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[D TP K .. G TN R	29	[AG R]	Protease matriptase proteasi	Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	L K E W .. AT M N	29			Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	I P T R D F W J	29			Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	I T V K E T	29			Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	M L T R G K	29			Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[E R C .R T	29	LRT	LKB1 Kinase substrate motif	Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	L N S A P F H E	29			Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[L K R N .. H Y G	29			Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	S J Q D T	29			Y	0.005	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	G T E A	29	EDAIY	Abl kinase substrate motif	Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	K Q K E J C H	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	I A T R H G K A	29	D.G.T.. K.I	Pyrophosphate binding motif	Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	W V A C H K S P	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	A A MK .. V D H A	29	H LV N K	Motif for targeting CD44 to bi	Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	K K Q A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	F D K M .. N E Q	29	RKK ST	ZIP kinase phosphorylation	Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	G S .. K H J A H E	29	S.. E .	Casein kinase II substrate mi	Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	V K T J D W J	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[K C A E D D P J	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	G T C E A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	K V A F V A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[A T W H J .. D ]	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	Q H W I .. D Q W J	29	Q MLV J D .. D	CLV_TASPASE1	Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	M L R G K	29	LRT	LKB1 Kinase substrate motif	Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[E R C .R T	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	L N S A P F H E	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[L K R N .. H Y G	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	S J Q D T	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	G T E A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	K Q K E J C H	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	I A T R H G K A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	W V A C H K S P	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	A A MK .. V D H A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	K K Q A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	F D K M .. N E Q	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	G S .. K H J A H E	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	V K T J D W J	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[K C A E D D P J	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	G T C E A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	K V A F V A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[A T W H J .. D ]	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	Q H W I .. D Q W J	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	M L R G K	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[E R C .R T	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	L N S A P F H E	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[L K R N .. H Y G	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	S J Q D T	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	G T E A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	K Q K E J C H	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	I A T R H G K A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	W V A C H K S P	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	A A MK .. V D H A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	K K Q A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	F D K M .. N E Q	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	G S .. K H J A H E	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	V K T J D W J	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[K C A E D D P J	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	G T C E A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	K V A F V A	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[A T W H J .. D ]	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	Q H W I .. D Q W J	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	M L R G K	29			Y	0.006	10
protein_40_YER082C	2 UTP27: Nuclear protein, component of the sr	[E R C .R T	29			Y	0.006	10
matsumaya_Spindle_or_SPI	2 matsumaya_Spindle or SPI	S T N K L	29			Y	0.006	10
matsumaya_Nucleus	2 matsumaya_Nucleus	S Q D S	29	R..S.P	14-3- binding motifs, Ser mi	Y	0.006	10

protein_40_YGR128C	2	UTP8: Nucleolar protein required for export o osheas_nucleus	[LTHL].[AHWJS]	28	I.KR JR	CLV_PCSK_KEX2_1	WD40	1.E-04	-1.3	rRNA processing (1e-19)	0.005	9	
yeast-1036_GO-0005739	2	cell organization and biogenesis	[A ALGK]	28	P.P.K	SH3 binding motif for Crk, ge	Helicase_C	1.E-03	-1.3	DNA metabolism (1e-24)	0.006	10	
yeast-1721_GO-0016043	2	cell organization and biogenesis	[N EVMI DQQT]	28	P.IPOVK	P	Helicase_C	1.E-02	-1.1	mitochondrial function (1e-60)	0.006	9	
protein_40_YJL010C	2	NOP9: Essential component of pre-40S ribos	L.[DQJ]	28	P MVLRWYIV	LIG_HP1_1LIG_HP1_1	MFS_1	1.E-03	-1.1	chromosome organization and biogenesis (1e-21)	Y	0.006	10
oshea_cell_periphery	2	oshea_cell_periphery	L.[DQJ]	28	I.Y	HEAT	BRCT	1.E-02	-1	plasma membrane (1e-24)	0.005	9	
yeast-207_GO-0006974	2	response to DNA damage stimulus	I.N [LSN]	28	GGRGG	Arginine methyl transferase	HEAT	1.E-02	-1	response to DNA damage stimulus (1e-16)	0.006	9	
yeast-1216_GO-0009058	2	biosynthesis	T[KS P G]GR	28	P TTS AP	LIG_PTAPLIG_PTAP	Zn_clus	1.E-06	-0.9	cell cycle (1e-09)	0.006	9	
matsuyama_nucleolus	2	matsuyama_nucleolus	T[APQ]	28	HATPase_c	HEAT	Zn_clus	1.E-06	-0.9	regulation of cellular metabolism (1e-14)	0.006	9	
yeast-436_GO-0031323	2	regulation of cellular metabolism	[NDPI Q PHC Y]	28	I.E	Arginine methyl transferase	Helicase_C	1.E-03	-0.9	transferase activity, transferring phosphorus-con	0.006	9	
yeast-335_GO-0016772	2	transf erase activity, transferring phosphorus-con	[TLYK N FH T]	28	P.L.	pyrophosphate activity (1e-37)	Helicase_C	1.E-06	-0.9	pyrophosphate activity (1e-37)	0.005	9	
yeast-401_GO-0006462	2	pyrophosphate activity	D[SD P F L K A E]	28	S DE  D E E	BARD1 BRCT domain bindin	DEAD	1.E-02	-0.9	pyrophosphate activity (1e-37)	0.004	8	
protein_40_YLR131W	2	Protein involved in the large ribosomal subunit	P LK R K	28	P.L.	Motif in C-Fos for protein kinase	F_box	1.E-07	-0.9	ubiquitin ligase complex (1e-10)	Y	0.006	10
protein_40_YLR293C	2	GSP1: GTP binding protein (mammalian Ran protein)	E.[KOP IA]	28	I.BN_N	IBN_N	IBN_N	1.E-09	-0.9	nucleoplasmic transport (1e-14)	0.005	9	
protein_40_YML085C	2	TUB1: Alpha-tubulin; associates with beta-tub	A [ADN A DNK]	28	I.Y	cGFR and Csk kinase phosph	HEAT	1.E-03	-0.8	nucleocytoplasmic transport (1e-14)	0.006	10	
protein_40_YML007W	2	YAP1: Basic leucine zipper (bZIP) transcrip	I.E	28	D. YE	HEAT	HEAT	1.E-02	-0.8	protein carrier activity (0.01)	0.006	10	
yeast-630_GO-0051244	2	regulation of cellular physiological process	[SRHJK KST]	28	D. YE	Lyn kinase phosphorylation s	Zn_clus	1.E-06	-0.7	nucleoplasm (1e-09)	0.006	10	
protein_40_YGL105W	2	ARC1: Protein that binds RNA and methiony	R IEVL LTJA	28	C SAIDS ILIV	PROK_C02 ANHYDRASE	Pkinase	1.E-07	-0.7	regulation of cellular metabolism (1e-14)	0.006	9	
protein_40_YER102W	2	RPB8: Protein component of the small (40S r	I.E	28	I.E	proteins of the large (60S r	Helicase_C	1.E-06	-0.7	ribonucleoprotein complex (1e-10)	0.006	9	
yeast-631_GO-0050794	2	regulation of cellular process	[TLYK N FH T]	28	D. YE	lymphocyte-specific phosphatase	Helicase_C	1.E-06	-0.6	regulation of cellular metabolism (10)	Y	0.006	10
protein_40_YOL139C	2	CD383: Cytoplasmic mRNA cap binding prot	N KDR JR	28	[K R JR]	CLV_PCSK_KEX2_1	Pkinase	1.E-03	-0.6	protein kinase activity (0.01)	0.005	10	
protein_40_YMR229C	2	RPP5: Protein required for the synthesis of tRNA	[F R F P AR]	28	I.G R	Protease matriptase protease	Helicase_C	1.E-02	-0.6	nucleoplasm (1e-10)	Y	0.005	10
protein_40_YER202C	2	chromosome organization and biogenesis	A V U L L P E	28	D DALD	14-3-3 binding motif in ExoS	Y	1.D-05	-0.6	ubiquitin ligase complex (1e-10)	0.005	9	
yeast-468_GO-0051276	2	response to endogenous stimulus	S K NC T P E	28	I.KR JR	ARKGSLRQ	ARKGSLRQ	1.E-05	-0.5	ubiquitin ligase complex (1e-15)	Y	0.006	10
protein_40_YIL094C	2	LYS12: Homo-isocitrate dehydrogenase, an h	L S R I P E	28	I.KR JR	PKC alpha kinase substrate i	Y	1.E-03	-0.5	chromosome organization and biogenesis (1e-8'	0.006	9	
protein_40_YHR052W	2	C1C1: Essential protein that interacts with pro	A [KAL N ATN]	28	I.KR JR	ARKGSLRQ	BRCT	1.E-05	-0.5	response to endogenous stimulus (1e-15)	Y	0.006	10
protein_40_YPR144C	2	NOC4: Nucleolar protein, forms a complex with pro	[DEN V AK RW]	28	I.KR JR	D F NGN	DEAD	1.E-04	-0.5	cytoplasm organization and biogenesis (1e-07)	0.005	9	
protein_40_YDR328C	2	SKI1: Evolutionarily conserved kinetochore s	D L V E L	28	WDL	Binding motif for AP-2 and cl	WD40	1.E-02	-0.5	small nucleolar ribonucleoprotein complex (1e-3	Y	0.005	9
protein_40_YDR224C	2	HTB1: One of two nearly identical (see HTB2	K KK D L	28	KKKKPLATGDY	Insulin receptor kinase subunit	F_box	1.E-17	-0.5	ubiquitin ligase complex (1e-15)	0.005	10	
protein_40_YLR222C	2	Nuclear protein, component of the t	G A P K N	28	G.RA	Protease tPA proteolytic site	Histone	1.E-06	-0.5	DNA metabolism (1e-05)	Y	0.005	10
protein_40_YLR129W	2	DIP2: Nuclear protein, specifically associate	K K R L C	28	KR	CLV_PCSK_C1E2_1	WD40	1.E-08	-0.5	ubiquitin ligase complex (1e-10)	0.005	9	
protein_40_YMR217W	2	SKI2: Evolutionarily-conserved nuc	R. F K H E F G	28	R..K	SH3 binding motif for GADS	WD40	1.E-03	-0.5	nucleoplasm (1e-19)	0.005	9	
protein_40_YOL089W	2	SKP2: Component of the evolutionarily cons	D O F N G	28	F.D.F	LIG_AP2alpha_1	SMC_N	1.E-03	-0.5	microtubule cytoskeleton (1e-08)	0.005	9	
protein_40_YMR117C	2	YAP1: Protein that binds RNA and methiony	D N K D L P E	28	DLL	Binding motif for clathrin hea	SMC_N	1.E-03	-0.5	condensed chromosome (0.01)	0.005	9	
protein_40_YMP117C	2	SPC24: Component of the evolutionarily cons	A A D E W D T	28	T.Y	MEK phosphorylation of MAP	E1-E2_ATPase	1.E-05	-0.5	pyrophosphatase activity (1e-43)	Y	0.006	10
yeast-939_GO-0051234	2	establishment of localization	T C V Y L	28	WD40	Binding motif for AP-2 and cl	E1-E2_ATPase	1.E-02	-0.5	establishment of cellular localization (1e-20)	0.006	9	
protein_40_YDR38BW	2	RVS167: Activin-associated protein, subunit of	[SN R A T G K F Q	28	I.KR JR	KKKKPLATGDY	Pkinase	1.E-02	-0.5	cell cortex part (0.01)	0.005	10	
yeast-207_GO-0006974	2	response to DNA damage stimulus	[N F G L E N M E	28	I.KR JR	Insulin receptor kinase subunit	WD40	1.E-08	-0.5	DNA damage (1e-05)	Y	0.006	10
yeast-341_GO-0045449	2	regulation of transcription	[D N G E K S Q	28	I.KR JR	Protease tPA proteolytic site	WD40	1.E-03	-0.5	nucleoplasm (1e-28)	Y	0.005	10
yeast-322_GO-0005654	2	nucleoplasm	L E Q D J N A T A	28	G.RA	QIMLV IDG_ID CLV_TASPASE1	Bromodomain	1.E-02	-0.5	ubiquitin ligase complex (1e-13)	0.005	9	
yeast-213_GO-0009719	2	response to endogenous stimulus	D F N G N	28	I.KR JR	D F N G N	BRCT	1.E-04	-0.5	response to endogenous stimulus (1e-11)	Y	0.006	10
yeast-212_GO-0007010	2	cytokinesis and organization	[D N K D L P E ]	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-03	-0.5	cytoskeleton organization and biogenesis (1e-73)	Y	0.006	9
protein_40_YOL084Z	2	pyrophosphatase activity	A A D E W D T	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	cytoskeleton organization and biogenesis (1e-73)	Y	0.006	9
protein_40_YOL272C	2	SPC24: Component of the evolutionarily cons	T C V Y L	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	cytoskeleton organization and biogenesis (1e-73)	Y	0.006	9
protein_40_YJL019W	2	osheas_bud_neck	[I L W V K N J L Y F	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	cytoskeleton organization and biogenesis (1e-73)	Y	0.006	9
yeast-295_GO-0016192	2	vesicle-mediated transport	[I L W V K N J L Y F	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	cytoskeleton organization and biogenesis (1e-73)	Y	0.006	9
yeast-1389_GO-0044260	2	cellular macromolecule metabolism	G P T S P V G V	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	cytoskeleton organization and biogenesis (1e-73)	Y	0.006	9
yeast-145_GO-0006058	2	DIP2: Nuclear protein, component of the	[A Y S T K J D K Q	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	cytoskeleton organization and biogenesis (1e-73)	Y	0.006	9
protein_40_YHR148W	2	component of the SRS1 complexosome, w	[P F G Y ]	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	macromolecular biosynthetic process (1e-60)	Y	0.006	10
yeast-1547_GO-0043282	2	bisulfite metabolism	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	macromolecular biosynthetic process (1e-60)	Y	0.006	10
protein_40_YMR125W	2	STO1: Large subunit of the nuclear RNA ca	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	DNA metabolism (1e-21)	Y	0.006	10
protein_40_YLR186W	2	EMG1: Protein involved for the pre-rRNA process	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	DNA processing (1e-28)	Y	0.005	10
protein_40_YPL148C	2	NOP93: Nucleolar protein; involved in biogen	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	proteasome complex (sens u Eukaryota) (1e-14)	Y	0.005	10
protein_40_YPL272C	2	SEC2: Guanyl-nucleotide exchange factor for	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	protein kinase activity (1e-16)	Y	0.005	10
yeast-388_GO-0007275	2	development	[R E N Y J L C T A]	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	protein kinase activity (1e-16)	Y	0.005	10
protein_40_YGL105W	2	ARC1: Protein that binds RNA and methiony	[D H V I Y GR ]	28	I.KR JR	SH3 binding motif for GADS	SMC_N	1.E-02	-0.5	GTPase activity (1e-11)	Y	0.005	8
protein_40_YMR128W	2	ECM1: Essential DEAH-box ATP-dependent	[P F G Y ]	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	ubiquitin conjugating enzyme activity (1e-18)	Y	0.005	9
protein_40_YMR229C	2	transcriptional regulator activity	[P F G Y ]	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	ubiquitin conjugating enzyme activity (1e-18)	Y	0.005	9
protein_40_YOR310C	2	transcriptase regulator activity	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	macromolecular biosynthetic process (1e-60)	Y	0.006	10
protein_40_YMR047C	2	RNA metabolism	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	DNA metabolism (1e-11)	Y	0.006	10
protein_40_YMR047C	2	response to stress	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR JR	SH3 binding motif for GADS	WD40	1.E-03	-0.5	protein kinase activity (1e-16)	Y	0.006	10
protein_40_YOR0273Z	2	catalog	G T S K I R P L S	28	I.KR								







protein,_YGL106W	2	MCL1, Essential light chain for Myo10, light c	[ECKFK[KRCY]	27	KR	CLV_PCSK_PC1ET2_1		Y	0.004	S
protein,_YGL106W	2	MCL1, Essential light chain for Myo10, light c	[FSVQK[L]DQ]	27					0.006	S
protein,_YGL106W	2	MCL1, Essential light chain for Myo10, light c	[EJKQW][V]GW	27	YE,[IV]	SH2 ligand for Fes (Tyr must			0.005	S
protein,_YGL106W	2	RPL28, Ribosomal protein of the large (60S)	AA,[ARW][EHA]	27					0.006	S
protein,_YGL048C	2	RPT6, One or six ATPasases of the 19S complex	[SAY][I][LIG]	27	YASI	SH2 phosphatase substrat	Y		0.005	S
protein,_YGL019W	2	CKB1, Beta regulatory subunit of casein kinase	VI[EKVK][V]KR	27	KR	CLV_PCSK_PC1ET2_1			0.005	S
protein,_YGL019W	2	TUB2, Beta-tubulin; associates with alpha-tub	V,[A]LRG	27					0.005	S
protein,_YER177W	2	BMH1, 14-3-3 protein, isoform: control	Q[QAR][O][N]I	27					0.005	S
protein,_YER177W	2	BR22, RNA-dependent RNA polymerase II, RNA	E[ITY][K][HII]	27	I[KR]R	CLV_PCSK_KEX2_1			0.005	S
protein,_YER177W	2	BR22, RNA-dependent RNA polymerase II, RNA	T[NPVE][F]EH	27				Y	0.005	S
protein,_YER165W	2	PAB1, Poly(A) binding protein, part of the e	O,T[GOS]	27					0.005	S
protein,_YER133W	2	GLC7, Catalytic subunit of type I serine/threonine	[KEN][IE]	27		EEEEEYIEE	cFPS/E kinase phosphory		0.005	S
protein,_YER133W	2	GLC7, Catalytic subunit of type I serine/threonine	AA,[IGNE][KTH]	27					0.005	S
protein,_YER133W	2	GLC7, Catalytic subunit of type I serine/threonine	AR, [TAH][HTL]V	27	[AG]R	Protease matri�ate proteas			0.005	S
protein,_YER112W	2	LSM4, Lsm-like Sm protein, part of hetero	[VGTJ][DQ][K]	27	HAVDI	N-Cadherin ligand			0.005	S
protein,_YER102W	2	RPS24A, Protein component of the small (40S	[HAFGL][FR]	27	[AG]R	Protease matri�ate proteas			0.005	S
protein,_YER074W	2	RPS24A, Protein component of the small (40S	K,[AR]K	27	I[KR]R	Nuclear localization motif			0.005	S
protein,_YER022W	2	RSP4, Subunit of the RNA polymerase II promoter	[EAT][IV][MF]	27				Y	0.004	S
protein,_YER018C	2	SPCA2, Component of the evolutionarily conserved	[M][QK][K]R	27	KR	CLV_PCSK_PC1ET2_1			0.004	S
protein,_YER018C	2	SPCA2, Component of the evolutionarily conserved	D,[LDT][AWM]	27					0.005	S
protein,_YEL037C	2	SPCA2, Component of the evolutionarily conserved	[PSK][PK],[VKM]A	27	[ST]P	LIG_WW_4LIG_WW_4			0.005	S
protein,_YDR448W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	K,[RQ]C	27				Y	0.005	S
protein,_YDR427W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	F,[YAI][Y]C	27					0.005	S
protein,_YDR361W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[GAK]	27	[AG]R	Protease matri�ate proteas			0.005	S
protein,_YDR356W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[DVC][D]ESP	27	D,D	Ribose moiety of UDP and m			0.005	S
protein,_YDR331W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	M,[ALU][EKA]	27				Y	0.005	S
protein,_YDR174W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,V[KD]C	27	YE,[IV]	SH2 ligand for Fes (Tyr must			0.005	S
protein,_YDR167W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	A[TEQ][K]LHV	27					0.005	S
protein,_YDR167W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	S,[A]PES	27		LKEADJAE_R2_TROPOMYOSIN PATTERN			0.005	S
protein,_YDR142W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[VATR][A]LAK	27	[AG]R	Protease matri�ate proteas			0.004	S
protein,_YDL213C	2	SPCP110, Inner plaque subunit of the Arp2/3 com	K,[L]KIS[P]	27	SP	ERK1 ERK2 Kinase substra			0.005	S
protein,_YDL185W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[R]GYV	27	R,[RK]R	CLV_PCSK_FUR_1			0.005	S
protein,_YDL148C	2	SPCP110, Inner plaque subunit of the Arp2/3 com	T[EFHH][EM]D	27					0.005	S
protein,_YDL140C	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[OK]Q,[AQKD]	27					0.005	S
protein,_YDL127W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[LHF][D]NVSQ	27					0.005	S
protein,_YDL127W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	I[P]R[G][SKA]	27	IP[IV]	Crystallin motif for dimerizati			0.005	S
protein,_YDL127W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,S,R,P	27	R,S,R,P	14-3-3 binding motifs, Ser mi			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	V[GPM]B	27	[IDE][DE]..V[P]I	LIG_COP1LIG_COP1	Y	0.005	S	
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[IGEG][A]P[A]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[YEG][OLG]H	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	K,RETIV	27	KR	CLV_PCSK_PC1ET2_1			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	L[LEF][F]I[F]V	27	LFG	Protease Papain substrate, a			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	K,[PKY][K]VAR	27	KR	CLV_PCSK_PC1ET2_1			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[G]E[EF]	27				Y	0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[RPH][E]L[H]F	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[VH][D]AGM][TL]	27	PTL	Motif in Fos for proteosom c			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[LIVI].[ILMIL]AA	27	[ILV].[ILMIL]AA	LIG_Sin_3_1LIG_Sin_3	Y	0.005	S	
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	K,[AEW][ER]F	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	A[GE][D]	27	G[KR]R	Amidation after cleavage site			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[DRL][E][TMW]	27				Y	0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,K[ETI]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[I]ESD,[EV]IA	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[ISJV]V[NH]SD	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[NAH]P[TD]A	27		NPK1STISG_A1 PROK SULFATE BIND 2 P			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[F]NV[J][SO]JS	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	P,[KS]MP	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	Q,[QR]DQ	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[D]R[LE][T]M[W]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[L]M[EL][K]PQAJ	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	T[Q]V[G]M[F]EW	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	L,[VLD]N	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[RGM][K]P[AR]	27	KP,[OK]	LIG_SH3_4LIG_SH3_4			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	L,[T]EQ[G]	27	[S]T Q	ATPase kinase phosphorylation			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	L,[N]DQ	27	[S]T O	ATP kinase phosphorylation	Y		0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	L,[R]I[EP]	27	RPL	VEGFR and neuropilin bindir			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	M,[P]NLT	27	[P]ST	DNA dependent Protein kina			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[L]OTJE	27	[S]T E	G protein-coupled receptor k			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[I]LYQW,[Y]QIN	27				Y	0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[Q]I[O][E]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	T[Q]V[V]I[Q]SE	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[T]Q[V]V[Q]I[Q]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[DFV][Q]FQJR	27	[AG]R	Protease matri�ate proteas			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[E]E[PI]	27	RE..E	Iron binding motif in ferritin L-	Y		0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[R]V[AF]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[A]S[P]J	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[GE]C[D],[T]FYP	27	[K]R R	CLV_PCSK_KEX2_1	Y		0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[N]H[J]R	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	N[P]V[P]H]R	27	E,[H][N]R	Binding motif for chlorophyll			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[S]T[R]N [Y]I[Y]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	T[Q]Y[Q]I[Q]E[Q]S	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[D]FV [Q]FQJR	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	T[Q]Y[Q]I[Q]E[Q]S	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[T]Q[V]V[Q]I[Q]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[DFV][Q]FQJR	27	[AG]R	Protease matri�ate proteas			0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[E]E[PI]	27	RE..E	Iron binding motif in ferritin L-	Y		0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[R]V[AF]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[A]S[P]J	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[GE]C[D],[T]FYP	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[C]Y[T]T	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[I]LYQW,[Y]QIN	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[Q]I[O][E]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	T[Q]V[V]I[Q]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[T]Q[V]V[Q]I[Q]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[DFV][Q]FQJR	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[E]E[PI]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[R]V[AF]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[A]S[P]J	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[GE]C[D],[T]FYP	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[C]Y[T]T	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[I]LYQW,[Y]QIN	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[Q]I[O][E]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	T[Q]V[V]I[Q]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[T]Q[V]V[Q]I[Q]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[DFV][Q]FQJR	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[E]E[PI]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[R]V[AF]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[A]S[P]J	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[GE]C[D],[T]FYP	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[C]Y[T]T	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[I]LYQW,[Y]QIN	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[Q]I[O][E]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	T[Q]V[V]I[Q]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[T]Q[V]V[Q]I[Q]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[DFV][Q]FQJR	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[E]E[PI]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[R]V[AF]	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[A]S[P]J	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	[GE]C[D],[T]FYP	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	E,[C]Y[T]T	27					0.005	S
protein,_YDL075W	2	SPCP110, Inner plaque subunit of the Arp2/3 com	R,[I]LYQW,[Y]QIN	27</						

yeast-216_GO-0006325	2	establishment and/or maintenance of chromatin	[VOG]DS[GDT]	26	S[ST]	MDC1 BRCT domain binding	Myb_DNA-binding	1.E-03	-0.8	establishment and/or maintenance of chromatin	0.006	9	
yeast-216_GO-0006323	2	DNA packaging	[VOG]DS[GDT]	26	S[ST]	MDC1 BRCT domain binding	Myb_DNA-binding	1.E-03	-0.8	establishment and/or maintenance of chromatin	0.006	9	
protein_40_YOL139W	2	nuclease containing subunit of Ssu protein	[YCA]O[ST]	26	I	Y	I	1.E-02	-0.5	cullin-RING ubiquitin ligase complex (0.001)	0.005	10	
protein_40_YMR047C	2	NUP116: Subunit of the nuclear pore complex	[RYA][AES]LL	26	DLL	Binding motif for clathrin hex	IBN_N	1.E-06	-0.6	nuclear transport (1e-21)	0.005	10	
protein_40_YOR181W	2	LAS17: Actin assembly factor, activates the A	TG[DNY]	26	STG	EH(3) EF hand domain bindi	SH3_1	1.E-10	-0.5	actin cortical patch (1e-08)	0.005	8	
protein_40_YLR180W	2	SAM1: S-adenosylmethionine synthetase, car	T[KAEJ]	26	T.I	FHA domain bind this ligand	GATase	1.E-02	-0.5		0.005	7	
protein_40_YIL094C	2	LYS12: Homo-isocitrate dehydrogenase, car	E..T[GAR]	26			IBN_N	1.E-02	-0.5		0.005	8	
yeast-256_GO-0016462	2	2':SPT5: Protein involved in pre-rRNA process	DI[VQW]AGKJR	26	[AGIR]	Protease matriptase proteas	DEAD	1.E-08	-0.3	nucleo-le-triphosphatase activity (1e-27)	Y	0.006	9
protein_40_YPR137W	2	RPP6: Protein involved in pre-rRNA process	A[ILMV]L[LUNE]	26	DALDL	14-3-3 binding motif in ExoS	WD40	1.E-03	-0.3	small nucleolar ribonucleoprotein complex (1e-2:	0.005	7	
yeast-295_GO-0016192	2	vesicle-mediated transport	[LCIV].[LMYC]	26			Adaptin_N	1.E-07	-0.2	vesicle-mediated transport (1e-35)	Y	0.006	9
protein_40_YMR229C	2	RPP5: Protein required for the synthesis of K+	VS[TGR]	26	EIVHSR	Binding motif for chlorophyll,	Pkinase	1.E-05	-0.2	cytoplasm organization and biogenesis (1e-19)	0.005	10	
protein_40_YGR090W	2	KAP123: Karophysin beta, mediates nuclear	K..[DME]	26			DEAD	1.E-08	-0.3		Y	0.005	10
protein_40_YER110C	2	2':SPT5: Protein that forms a complex with Spd2	K..[DME]	26	[STIP]	LIG_WW_ALIC_WW_4	I	1.E-02	-0.2	nucleocytoplasmic transport (1e-17)	0.005	10	
yeast-256_GO-0016462	2	Kap123: Karophysin beta, mediates nuclear	E..[KPDY]	26	YE.[IV]	SH2 ligand for Fes (Tyr must	Helicase_C	1.E-13	-0.1	pyrophosphatase activity (1e-13)	Y	0.005	9
protein_40_YLR293C	2	GSP1: GTP binding protein (mammalian Ran	L..[APHV]	26	PLP	motif for interaction with MYH?	IBN_N	1.E-14	-0.1	nucleocytoplasmic transport (1e-19)	Y	0.005	8
protein_40_YOR0490C	2	secretin receptor	[FLIJQ].[FSFJ]	26			EMP24_GP25L	1.E-02	0.1	secretion (1e-51)	0.006	10	
protein_40_YOR0490C	2	ribosome biogenesis	E..[QJTF]	26			SNARE	1.E-02	0.2	vesicle-mediated transport (1e-10)	Y	0.005	10
protein_40_YPR137W	2	SCP24: Component of the evolutionarily cons	D..[VIMV]	26	D..[TV]	Motif in PRS1 and PRS2 rec	DEAD	1.E-06	0.2	microtubule cytoskeleton (0.001)	0.005	10	
protein_40_YPR137W	2	UTP10: Nuclear protein, component of the I	KQ[SOK]	26	GQDQTKQQI	43_KD_PTSYAPTC PA	Y	SMC_N	1.E-02	0.2	rRNA processing (1e-15)	0.005	9
protein_40_YPR137W	2	UTP10: Nuclear protein, component of the I	A[DQCK][KKNR]	26	KR	CLV_PCSK_P1C1E2_1	WD40	1.E-03	0.2	ribosome biogenesis (1e-10)	Y	0.005	10
protein_40_YPR137W	2	UTP10: Nuclear protein, component of the I	G..[HNHD]	26	RGD	LIG_RDGLG_RGD	Y	Y	0.1	small nucleolar ribonucleoprotein complex (1e-2:	0.005	10	
protein_40_YLR222C	2	UTP10: Nuclear protein, component of the I	V[MQH][VQ]	26	GPIQMSPI	JNK1 Kinase substrate motif	WD40	1.E-03	0.2	ribosome biogenesis (1e-10)	Y	0.005	10
protein_40_YLR222C	2	UTP10: Nuclear protein, component of the I	E..[QJTF]	26	[STIP]	LIG_WW_ALIC_WW_4	Y	Y	0.1	vesicle-mediated transport (1e-10)	Y	0.005	10
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	LL..[ITGD][DH]	26	LLG	Beta2-Integrin binding motif	BRCA1	1.E-03	0.3	microtubule cytoskeleton	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	E..[EGJ]	26	Y.E.E	Src phosphorylation site	RRM_1	1.E-03	0.3	rRNA metabolism (1e-45)	0.006	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	K..[EH[EK]]	26	[STJE]	G protein-coupled receptor k	HEAT	1.E-02	0.9	snRNA splicing, via spliceosome (1e-16)	Y	0.005	9
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	L..[STHN]	26	DRY	Binding motif for interaction c	PCI	1.E-06	0.9	proteasome complex (sensu Eukaryota) (1e-18)	0.005	8	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	A..[GKRT]	26			WD40	1.E-02	0.9	snoRNA binding (1e-21)	Y	0.005	9
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	V..[HKVJ]	26			WD40	1.E-04	1.1	nucleocytoplasmic transport (1e-16)	Y	0.005	8
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	R..[GEVY]	26			Y	Y	1.2	nucleolus (1e-23)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	[LPFIE].[GINVA]	26	YE.[IV]	SH2 ligand for Fes (Tyr must	Y	Y	1.3	cytoplasm organization and biogenesis (1e-21)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	L..[EVQ][ATMA]	26	F.D.F	LIG_AP2alpha_1	Ribosomal_60s	1.E-10	1.6	protein kinase activity (1e-15)	Y	0.005	9
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	D..[MPF]	26	Y	Y	Ribosomal_60s	1.E-10	1.6	multicellular organismal development (1e-13)	Y	0.005	10
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	MA[KPF]	26	LMIAEIQIQLYN	ENGRAILED PATTERN	Y	Pkinase	1.E-03	1.3	establishment and/or maintenance of chromatin	0.005	8
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	W[DIL].[GMQG]	26	G..G..K	Sulfonate donor binding site	Ras	1.E-15	1.3	translational elongation (1e-30)	Y	0.005	10
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	G..[ARFQ]	26	WM	Substrate binding motif of ba	Mito_carr	1.E-14	2.1	GTase activity (1e-17)	0.005	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	W[EJM][VQVE]	26	Y	Y	Y	Y	2.1	mitochondrial part (1e-43)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	V..[QJPS]	26	LTILEIFY[AVK_ODC_AZ_PATTER		Y	Pkinase	1.E-16	2.3	nucleic acid binding (1e-23)	0.005	10
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	E..[GKRC]	26	R.L.	Cyclin A motif that binds cdk2	IBN_N	1.E-02	2.4	nuclear envelope (1e-25)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	C..[NKMJ]	26	C..C.	Motif on TIM mitochondrial tr	Pkinase	1.E-03	2.6	protein kinase activity (0.01)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	T..[SNTD]	26			Zn_clus	1.E-08	2.7	ATP binding (1e-29)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	Q..[FIR]	26	[LNJ][RJTY]	PDGFR kinase substrate mo	Y	Y	2.8	nucleolus (1e-12)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	G..[DESM]	26	N..[TS]	N-linked glycosylation site	Y	Y	2.9	protein kinase activity (0.01)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	S..[SDH]	26	S..S	Casien kinase I phosphorvial	Y	Y	3.0	transferease activity, transferring phosphorus-con	Y	0.005	9
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	O..[ALFM]	26	D..[LARIS]		Y	Y	3.2	ribosome biogenesis (1e-24)	0.006	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	E..[K(KP)]	26	S..[TCJD]	Casein Kinase I consensus :	Pkinase	1.E-19	3.7	protein amino acid phosphorylation (1e-24)	0.006	8	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	H..[IAH[EK]KVW]	26	S..[ST]	Casein Kinase I consensus :	Pkinase	1.E-21	5.3	kinase activity (1e-16)	Y	0.006	10
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	Q..[FIR]	26	D..[LNJ]	PDGFR kinase substrate mo	Zn_clus	1.E-08	15.2	transcription (1e-18)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	I[AHQ][LDPJ]	26	[RK R][RKJL]	Cyclin/CDK2 binding motif	Y	Y	Y	integral membrane (1e-50)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	V..[HQC][RDLV]	26			Y	Y	Y	response to stress (1e-91)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	A..[KYLV]	26			Y	Y	Y	cellular localization (1e-64)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	D..[LARIS]	26			Y	Y	Y	chromosome organization and biogenesis (1e-1:	0.006	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	E..[K(KP)]	26			Y	Y	Y	chromosome organization and biogenesis (1e-2:	0.006	8	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	S..[TCJD]	26			Y	Y	Y	chromosome organization and biogenesis (1e-2:	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	H..[IAH[EK]KVW]	26			Y	Y	Y	response to stress (1e-13)	0.006	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	Q..[FIR]	26			Y	Y	Y	multicellular organismal development (1e-21)	0.006	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	I[AHQ][LDPJ]	26			Y	Y	Y	multicellular organismal development (1e-10)	0.006	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	D..[LARIS]	26			Y	Y	Y	regulation of nucleobase, nucleoside, nucleotide	0.006	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	E..[K(KP)]	26			Y	Y	Y	cellular catabolism (1e-21)	0.006	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	S..[TCJD]	26			Y	Y	Y	regulation of transcription, DNA-dependent (1e-3:	0.006	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	H..[IAH[EK]KVW]	26			Y	Y	Y	carboxylic acid metabolism (1e-10)	Y	0.006	8
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	Q..[FIR]	26			Y	Y	Y	carboxylic acid metabolism (1e-10)	Y	0.006	8
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	I[AHQ][LDPJ]	26			Y	Y	Y	vesicle-mediated transport (1e-13)	0.006	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	D..[LARIS]	26			Y	Y	Y	macromolecule catabolism (1e-52)	0.006	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	E..[K(KP)]	26			Y	Y	Y	endomembrane system (1e-31)	0.006	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	S..[TCJD]	26			Y	Y	Y	cellular macromolecule catabolism (1e-33)	0.006	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	H..[IAH[EK]KVW]	26			Y	Y	Y	intracellular protein transport (1e-26)	0.006	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	Q..[FIR]	26			Y	Y	Y	M phase (1e-25)	0.006	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	I[AHQ][LDPJ]	26			Y	Y	Y	nitrogen compound metabolism (1e-27)	0.006	8	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	D..[LARIS]	26			Y	Y	Y	cellular morphogenesis (1e-21)	0.006	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	E..[K(KP)]	26			Y	Y	Y	cellular morphogenesis (1e-21)	0.006	8	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	S..[TCJD]	26			Y	Y	Y	structural constituent of ribosome (1e-24)	0.006	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	H..[IAH[EK]KVW]	26			Y	Y	Y	establishment and/or maintenance of chromatin	0.006	8	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	Q..[FIR]	26			Y	Y	Y	cytoskeleton (1e-54)	0.006	8	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	I[AHQ][LDPJ]	26			Y	Y	Y	cytoskeleton (1e-35)	0.006	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	D..[LARIS]	26			Y	Y	Y	protein modification (1e-08)	0.006	8	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	E..[K(KP)]	26			Y	Y	Y	nucleolus (1e-19)	0.005	7	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	S..[TCJD]	26			Y	Y	Y	protein amino acid phosphorylation (0.01)	Y	0.005	9
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	H..[IAH[EK]KVW]	26			Y	Y	Y	ATPase activity (0.01)	Y	0.005	10
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	Q..[FIR]	26			Y	Y	Y	SWR1 complex (1e-04)	Y	0.005	9
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	I[AHQ][LDPJ]	26			Y	Y	Y	rRNA processing (1e-09)	Y	0.005	10
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	D..[LARIS]	26			Y	Y	Y	nuclear mRNA splicing, via spliceosome (1e-23)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	E..[K(KP)]	26			Y	Y	Y	nucleolus (1e-10)	0.005	10	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	S..[TCJD]	26			Y	Y	Y	establishment of cell polarity (sensu Fungi) (1e-	0.005	9	
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	H..[IAH[EK]KVW]	26			Y	Y	Y	mRNA catabolism (0.001)	Y	0.005	8
protein_40_YLR223C	2	UTP10: Nuclear protein, component of the I	Q..[FIR]	26			Y	Y	Y	protein kinase activity (0.01)	Y	0.005	8
protein_40_YLR223C	2												

protein_40_YLR222C	2	UTP13: Nucleolar protein, component of the : protein_40_YLR197W	2	[KPEJ QKOS]	26	GR,[RNIK QOE]	26	[AG R]	Protease matriptase protease		Y	small nucleolar ribonucleoprotein complex (1e-0)	0.005	10
protein_40_YLR150W	2	ES1: Essential evolutionarily-conserved nucleic acid-binding protein; binds G4 quadruplex and G-quadruplexes	2	[NPFE EJEND]	26	D,[E]AE[ME]	26					cytoplasm organization and biogenesis (1e-08)	0.005	7
protein_40_YLR106C	2	STM1: Protein binds G4 quadruplex and G-quadruplexes	2	[MDNI H]	26	N[NSNA]_T[TSN]I	26	[AG R]	Protease matriptase protease			cytoplasm organization and biogenesis (1e-06)	0.005	9
protein_40_YLR096W	2	KIN2: Serine/threonine protein kinase known to bind G4 quadruplexes	2	[RPLB8 G]	26	S[ICLQ]_R[RR]	26	R.S.S.P	Protease matriptase protease			site of polarized growth (0.01)	0.005	10
protein_40_YLR094C	2	RPLB8: Ribosomal protein L4 of the large (60S) ribosomal subunit	2	[RPLB8 G]	26	[D][DQI][KPCY]	26		14-3-3 binding motifs, Ser/Thr			ribosome biogenesis (1e-06)	0.005	10
protein_40_YLR093C	2	TOR2: Protein-related kinase and rapamycin resistance protein	2	[TOR2 G]	26	C[GID1][FLKL]	26					endocytosis (1e-05)	0.005	8
protein_40_YLR203C	2	TOR2: TOR-related protein kinase and rapamycin resistance protein	2	[TOR2 G]	26	W,A[VCG]	26					actin cytoskeleton organization and biogenesis (1e-05)	0.004	9
protein_40_YLR172W	2	EBP2: Essential protein required for the maturation of the 26S proteasome, involved in the assembly of the 26S proteasome	2	[EBP2 G]	26	R[A[RKE]]	26	GR,A	Protease ITPA proteolytic site			plasma membrane (1e-06)	0.005	7
protein_40_YLR172W	2	EBP2: Essential protein required for the maturation of the 26S proteasome, involved in the assembly of the 26S proteasome	2	[EBP2 G]	26	R[RQI]_S[IVEA]	26	RR.R.S	MAPKAPK1 kinase substrate			cytoplasm organization and biogenesis (1e-09)	0.005	9
protein_40_YKL166C	2	TPI3: Component of the evolutionarily conserved 26S proteasome	2	[IG, EVPI GRN]	26	I.G,[VCAJD]	26					cytoplasm organization and biogenesis (1e-13)	0.005	9
protein_40_YKL104C	2	GFA1: Glutamine-fructose-6-phosphate amidotransferase	2	[GFA1 G]	26	L,[EGT]G	26					amine acid metabolism (0.001)	0.005	9
protein_40_YKL104C	2	GFA1: Glutamine-fructose-6-phosphate amidotransferase	2	[GFA1 G]	26	P,[WTPA]	26					plasma membrane (1e-04)	0.005	8
protein_40_YJR068W	2	TOR1: Protein serine/threonine kinase and rapamycin resistance protein	2	[T0R1 G]	26	VIG,G,I	26					plasma membrane (1e-10)	0.005	10
protein_40_YJR068W	2	TOR1: Protein serine/threonine kinase and rapamycin resistance protein	2	[T0R1 G]	26	K[RKR]	26	CLV,_PCSK_KEX2_1				rRNA processing (1e-14)	0.005	7
protein_40_YLR100C	2	UTP10: Nucleolar protein, component of the 40S ribosomal subunit	2	[UTP10 G]	26	S,[AEJA]_K[KVKS]	26					response to DNA damage stimulus (0.001)	0.005	10
protein_40_YLR098W	2	BCK1: Mitogen-activated protein (MAP) kinase homologous protein	2	[BCK1 G]	26	P,[STIP]KK	26					spindle (0.001)	0.004	9
protein_40_YLR092W	2	SRS2: DNA helicase and DNA-dependent AT binding protein	2	[SRS2 G]	26	R,[RKR]	26	CLV,_PCSK_FUR_1				cytoskeleton organization and biogenesis (0.01)	0.005	9
protein_40_YLI144W	2	TID3: Component of the evolutionarily conserved 26S proteasome	2	[TID3 G]	26	DLL	26					cortical cytoskeleton organization and biogenesis (0.01)	0.003	8
protein_40_YLI144W	2	TID3: Component of the evolutionarily conserved 26S proteasome	2	[TID3 G]	26	D,E[EV]	26					cortical cytoskeleton organization and biogenesis (0.01)	0.005	9
protein_40_YIL095W	2	PRK1: Protein serine/threonine kinase required for the 26S proteasome	2	[PRK1 G]	26	K,[ALD]O	26					nuclear mRNA splicing, via spliceosome (1e-09)	0.005	10
protein_40_YIL095W	2	PRK1: Protein serine/threonine kinase required for the 26S proteasome	2	[PRK1 G]	26	P,[SPD]	26					small nuclear ribonucleoprotein complex (0.01)	0.005	10
protein_40_YIL094C	2	PRK1: Protein serine/threonine kinase required for the 26S proteasome	2	[PRK1 G]	26	T..[IVY APM]	26					mRNA metabolism (0.01)	0.004	8
protein_40_YIL075C	2	PRP2: Subunit of the 26S proteasome, involved in the assembly of the 26S proteasome	2	[PRP2 G]	26	E,[IYG,F]	26					nuclear mRNA splicing, via spliceosome (1e-05)	0.005	10
protein_40_YIL061C	2	SP1: Component of U1 snRNP required for pre-mRNA processing	2	[SP1 G]	26	E,[NDK]	26					nucleolus (1e-05)	0.005	10
protein_40_YIL061C	2	SP1: Component of U1 snRNP required for pre-mRNA processing	2	[SP1 G]	26	R,K[LGV]	26					rRNA processing (1e-15)	0.005	10
protein_40_YIL035C	2	SP2: Component of the evolutionarily conserved 26S proteasome	2	[SP2 G]	26	IETD	26					nucleolus (1e-31)	0.005	9
protein_40_YIL019W	2	SP2: Component of the evolutionarily conserved 26S proteasome	2	[SP2 G]	26	R,[SIVN]EYD	26					histone acetyltransferase complex (1e-22)	0.005	9
protein_40_YHR196W	2	SP3: Nuclear protein, component of the 40S ribosomal subunit	2	[SP3 G]	26	R,[SIVN]EYD	26					cytoplasm organization and biogenesis (1e-20)	0.005	9
protein_40_YHR196W	2	SP3: Nuclear protein, component of the 40S ribosomal subunit	2	[SP3 G]	26	T..[IVY APM]	26					ligase activity, forming aminoacyl-RNA and relat	0.004	7
protein_40_YHR144W	2	SP4: Subunit of SAGA and NuA4 histone acetyltransferases	2	[SP4 G]	26	E,[RPTD]SQI	26					cytoplasm organization and biogenesis (0.001)	0.005	10
protein_40_YHR099W	2	SP4: Subunit of SAGA and NuA4 histone acetyltransferases	2	[SP4 G]	26	T..[IVY APM]	26					nucleolus (1e-07)	0.005	9
protein_40_YHR088W	2	SPF1: Nucleolar protein involved in the assembly of the 26S proteasome	2	[SPF1 G]	26	IY	26					SAGA complex (1e-12)	0.005	10
protein_40_YFR010W	2	SPF2: Subunit of S33 endopeptidase involved in protein processing	2	[SPF2 G]	26	K,[RPTD]SQI	26					cytosolic ribosome (sensu Eukaryota) (1e-08)	0.005	10
protein_40_YFR010W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					proteasome regulatory particle (sensu Eukaryota)	0.005	9
protein_40_YFR010W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					rRNA splicing (1e-12)	0.005	8
protein_40_YFR010W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nuclear mRNA splicing, via spliceosome (1e-11)	0.005	10
protein_40_YFR010W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					endocytosis (0.01)	0.005	9
protein_40_YER125W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					small nuclear ribonucleoprotein complex (1e-13)	0.005	10
protein_40_YER125W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					rRNA export from nucleus (1e-06)	0.005	10
protein_40_YER118C	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nuclear pore (0.001)	0.005	9
protein_40_YER118C	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					ribosome biogenesis (1e-07)	0.005	9
protein_40_YER112W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					actin cytoskeleton (0.01)	0.005	10
protein_40_YER112W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucleoplasm (1e-06)	0.005	10
protein_40_YER112W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					proteasome complex (sensu Eukaryota) (1e-06)	0.005	9
protein_40_YER112W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					endocytosis (1e-04)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					cytoplasm organization and biogenesis (1e-05)	0.005	9
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucleolus (1e-09)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					microtubule nucleation (1e-23)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					spindle pole body (1e-12)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucleolus (1e-09)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					transcription regulator activity (1e-09)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					transcription factor complex (1e-10)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					transcription from RNA polymerase II promoter (1e-05)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					phosphotransferase activity, alcohol group as acyl	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucleolus (1e-09)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					microtubule nucleation (1e-23)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					spindle pole body (1e-12)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucleolus (1e-09)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucleolus (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					rRNA processing (1e-15)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					rRNA processing (1e-15)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	E,[RPTD]SQI	26					nucler (1e-13)	0.005	10
protein_40_YER145W	2	SPU1: Protein component of the large (60S) ribosomal subunit	2	[SPU1 G]	26	T..[IVY APM]	26					nucler (1e-13)	0.005	10
protein_4														

yeast-200	GO-0009057	2	macromolecule catabolism	VE[V EV ALM]	25	Y L V E L V  PLCasma C and N-terminal	Proteasome	1.E-04	-3.2	macromolecule catabolism (t-e48)	0.005	8	
protein_40_YOL191W		2	PSE1: Karypehain/impin that interacts will	VE[G J H ARE]	25	Y L V E L V  PLCasma C and N-terminal	Proteasome	1.E-06	-2.6	proteasome core complex, alpha-subunit comple	0.005	10	
protein_40_YOL139C		2	SAS1: Sarcoplasmic factor activating A	R P T P V Y	25	PP F A L V P P  SH3 binding motif for Abi	S2H3_1	1.E-13	-2	alpha-1-antitrypsin-like (t-e13)	0.005	10	
protein_40_YIL69C		2	CDC31: Cytoskeletal mRNA cap binding protein	ST [KRD IVSR]	25	PP F A L V P P  SH3 binding motif for Abi	Pin kinase	1.E-03	-1.9	protein kinase activity (0.01)	0.005	10	
protein_40_YMR304W		2	UBP15: Ubiquitin-specific protease that may i	R. R K TG	25	R . R K R CLV_PCSK_FUR_1	DEAD	1.E-03	-1.9	cytosolic ribosomes (sensu Eukaryota) (t-e12)	0.005	9	
protein_40_YGL207W		2	SPT16: Subunit of the heterodimeric FACT or	[LS K P Q ]	25	[ST]P LIG_WW_4LG_WW_4	Pin kinase	1.E-02	-1.7	protein kinase activity (1e-06)	0.005	10	
oshei_nucleolus		2	oshei_nucleolus	O. P K G C	25		DEAD	1.E-08	-1.6	nucleolus (t-e10)	0.005	10	
yeast-217	GO-0007046	2	ribosome biogenesis	HR [G A RCN	25		DEAD	1.E-04	-1.4	ribosome biogenesis (t-e10)	0.005	7	
protein_40_YPL203W		2	TPK2: cAMP-dependent protein kinase catal	NT [SOF SRQ	25		Pin kinase	1.E-02	-1.3		0.005	9	
protein_40_YML085C		2	TUB1: Alpha-tubulin; associates with beta-tu	V L D M K	25	K...VPK...V Endothelin receptor motif req	HEAT	1.E-02	-1.2		0.005	9	
protein_40_YMR125W		2	NOP1: Nucleolar protein, component of the s	R S R G K	25	W O D	W640	1.E-03	-1.2	nucleolus (t-e26)	0.005	7	
protein_40_YML085C		2	Large subunit of the nucleolus	R V W H Y	25	W O D	R RM_1	1.E-04	-1.1	nucleic acid binding (t-e11)	0.005	9	
protein_40_YML085C		2	TUB1: Alpha-tubulin; associates with beta-tu	V L E K P W	25	W O D	HEAT	1.E-04	-1.1		0.005	8	
protein_40_YLR002C		2	NOC3: Protein that forms a nuclear complex	D. L RA O	25	W O D	HEAT	1.E-03	-1.1		0.005	10	
yeast-980	GO-00051179	2	localization	GR [R G K A KE	25	[AG R Protease matripeptidase proteasi	DEAD	1.E-04	-1.1	ribosome biogenesis (t-e07)	0.004	8	
protein_40_YER165W		2	PAB1: Poly(A) binding protein, part of the 3'-e	[K N S ,EQ	25	[ST].E Casine kinase II consensus :	IBN_N	1.E-05	-1	cellular localization (t-e11)	0.005	10	
protein_40_YER165W		2	establishment of localization	PP P V K G P N	25	[D E F P P  PP V K G P N  E B H binding motif of Mena	R RM_1	1.E-02	-1	mRNA metabolism (0.01)	0.005	9	
protein_40_YNL031C		2	hydrolytic activity	[K N S ,EQ	25	[ST].E Casine kinase II consensus :	IBN_N	1.E-05	-0.9	cellular localization (t-e11)	0.005	10	
protein_40_YLR175W		2	PP2B: Peptidase superfamily catalytic subu	H. S Q D Y	25	SQ ATM kinase substrate motif	Y	Peptidase_M16	1.E-02	-0.9	hydrolase activity, acting on ester bonds (t-e25)	0.005	10
protein_40_YLR130C		2	URA2: Bifunctional carboxymethylphosphate synt	V F D N J OR H	25	FRG7 Phosphoinositide binding mo	PP2C	1.E-05	-0.9	hydrolase activity, acting on ester bonds (t-e28)	0.006	10	
protein_40_YER165W		2	ohe_bud_neck	T L E Q O	25	GQDQTTQQI 43 POSTSYNAPTIC PA	IBN_N	1.E-12	-0.9		0.005	10	
matsuayama_Spindle		2	hydrolase activity, acting on ester bonds	[V L O N ,E P D ]	25	Y E E Src phosphorylation site	HATPase_c	1.E-02	-0.9	nuclear transport (t-e15)	0.005	9	
protein_40_YLR293C		2	GSP1: GTP binding protein (mammalian Ran	N T S ,E	25	S.D CAMKII phosphorylation site	Zf-box	1.E-03	-0.8	response to stress (t-e14)	0.005	9	
yeast-200	GO-0005260	2	response to stress	N G S ,I SM N J	25	[AG R Protease matripeptidase proteasi	WD40	1.E-02	-0.8	bioplymer catabolism (t-e10)	0.005	9	
yeast-324	GO-0043255	2	beta-1,3-glucanase activity	K S V W Q D	25	[T P K Y K  Protease matripeptidase proteasi	WD40	1.E-02	-0.8	rRNA processing (t-e23)	0.005	8	
protein_40_YPR137W		2	biofilm formation	L A P H J	25	[S T].E Histone chromatin (t-e04)	Y	0.004	-0.8	cytoplasm organization and biogenesis (t-e09)	0.004	10	
protein_40_YLR175W		2	HHT2: One of two identical histone H3 protein	T S A R K	25	PH G-protein-coupled receptor k	Helicase_C	1.E-02	-0.8	protein carrier activity (0.01)	0.005	10	
protein_40_YNL031C		2	CFB5: Peptidase superfamily catalytic subu	P V R A N	25	W O D	HEAT	1.E-02	-0.8	RNA metabolism (t-e09)	0.005	10	
protein_40_YLR175W		2	U2AF: U2AF65 heparin required for phero	N N S H W	25	W O D	R RM_1	1.E-03	-0.8	site of polarized growth (t-e45)	0.005	9	
protein_40_YMR125W		2	response to DNA damage stimulus	R Y R N T	25	KK.RRT L V  DMPK1 kinase substrate mo	SH3_1	1.E-04	-0.8	spindle (t-e10)	0.005	10	
protein_40_YMR125W		2	UBP15: Ubiquitin-specific protease that may i	N S F H K	25	N T S  N-linked glycosylation site	Chromo	1.E-03	-0.8	RNA binding (t-e10)	0.005	7	
protein_40_YPR137W		2	PRP4: Splicing factor that is found in the Ce	T S O I T	25	W O D	R RM_1	1.E-04	-0.7	RNA binding (t-e09)	0.005	8	
protein_40_YLR175W		2	UPB8: Nuclear protein, component of the sr	K S V W Q D	25	K S V W Q D  WD40	W640	1.E-02	-0.7	RNA binding (t-e16)	0.005	9	
protein_40_YDR125C		2	UTP8: Nuclear protein required for export o	F D V A K	25	F K Y D E K S L  Nucleotide binding motif in A	WD40	1.E-02	-0.6	RNA binding (t-e20)	0.005	10	
protein_40_YOL162C		2	U2AF: U2AF65 heparin required for phero	T P K Y K	25	YTK M V  SH2 ligand 19 (Csk) (t-e04)	Histone	1.E-03	-0.6	establishment and/or maintenance of chromatin	0.005	8	
protein_40_YOL162C		2	response to endogenous stimulus	D S C K ,I E N S E	25	[S T].E G-protein-coupled receptor k	PH	1.E-02	-0.4		0.004	9	
protein_40_YOL162C		2	vesicle-mediated transport	A D P P I	25	W O D	Adaplin_1	1.E-06	-0.2	vesicle-mediated transport (t-e11)	0.005	9	
protein_40_YOL162C		2	ohe_bud_neck	V V T G N	25	V V T G N  AA permease	AA permease	1.E-03	-0.2		0.005	10	
protein_40_YOL162C		2	ohe_bud_neck	R A Q S I	25	W O D	Pin kinase	1.E-03	-0.1	response to DNA damage stimulus (t-e09)	0.005	8	
protein_40_YOL162C		2	response to DNA damage stimulus	T E N H D	25	W O D	AA permease	1.E-02	-0.1	cellular morphogenesis (t-e04)	0.005	7	
protein_40_YOL162C		2	UBP15: Ubiquitin-specific protease that may i	N G R Y J S E V R	25	W O D	AA permease	1.E-02	-0.1	nuclear mRNA splicing, via spliceosome (t-e14)	0.005	7	
protein_40_YOL162C		2	PRP4: Splicing factor that is found in the Ce	V K A D K ,F Y K	25	W O D	AA permease	1.E-02	-0.1	rRNA processing (t-e14)	0.005	8	
protein_40_YOL162C		2	UPB8: Nuclear protein, component of the sr	T L D I N W V	25	W O D	AA permease	1.E-02	-0.1	RNA processing (t-e16)	0.005	9	
protein_40_YOL162C		2	UTP8: Nuclear protein required for export o	P N ,G S E K G A	25	W O D	AA permease	1.E-02	-0.1	RNA processing (t-e21)	0.005	9	
protein_40_YOL162C		2	response to endogenous stimulus	D A L D K	25	W O D	AA permease	1.E-02	-0.1	RNA processing (t-e15)	0.005	10	
protein_40_YOL162C		2	vesicle-mediated transport	T D Q L D ,F E T	25	W O D	AA permease	1.E-02	-0.1	RNA processing (t-e22)	0.005	7	
protein_40_YOL162C		2	ohe_bud_neck	I L L W A K	25	W O D	AA permease	1.E-02	-0.1	barrier septum (t-e55)	0.005	10	
protein_40_YOL162C		2	membrane part	N S T P J T E K	25	W O D	AA permease	1.E-02	-0.1	protein binding (t-e71)	0.005	10	
protein_40_YOL162C		2	mitotic cell cycle	T S J P I	25	W O D	AA permease	1.E-02	-0.1	mitotic cell cycle (t-e14)	0.005	10	
protein_40_YOL162C		2	PRP4: Splicing factor that is found in the Ce	R J G K Y	25	W O D	AA permease	1.E-02	-0.1	rRNA processing (t-e17)	0.005	10	
protein_40_YOL162C		2	UPB8: Nuclear protein required for export o	T S J P I T R Q	25	W O D	AA permease	1.E-02	-0.1	RNA processing (t-e86)	0.005	9	
protein_40_YOL162C		2	UTP8: Nuclear protein required for export o	D L W C I K G P L	25	W O D	AA permease	1.E-02	-0.1	small nuclear ribonucleoprotein complex (t-e3)	0.005	9	
protein_40_YOL162C		2	response to endogenous stimulus	T Q S L F D K M K	25	W O D	AA permease	1.E-02	-0.1	small nuclear ribonucleoprotein complex (t-e11)	0.005	10	
protein_40_YOL162C		2	vesicle-mediated transport	A R N V J T R Q	25	W O D	AA permease	1.E-02	-0.1	proteasome complex (sensu Eukaryota) (t-e11)	0.005	10	
protein_40_YOL162C		2	ohe_bud_neck	D L W C I K G P L	25	W O D	AA permease	1.E-02	-0.1	nucleolus (t-e15)	0.005	10	
protein_40_YOL162C		2	response to endogenous stimulus	T L D I N W V	25	W O D	AA permease	1.E-02	-0.1	nuclolus (t-e16)	0.005	7	
protein_40_YOL162C		2	vesicle-mediated transport	P O E J E R F S Y	25	W O D	AA permease	1.E-02	-0.1	endoplasmic reticulum (t-e04)	0.005	7	
protein_40_YOL162C		2	ohe_bud_neck	T S J P I	25	W O D	AA permease	1.E-02	-0.1	cytoplasm organization and biogenesis (t-e23)	0.005	10	
protein_40_YOL162C		2	response to endogenous stimulus	N T J P I	25	W O D	AA permease	1.E-02	-0.1	intracellular transport (t-e39)	0.005	7	
protein_40_YOL162C		2	vesicle-mediated transport	R J G K Y	25	W O D	AA permease	1.E-02	-0.1	RNA processing (t-e17)	0.005	10	
protein_40_YOL162C		2	membrane part	E E D	25	W O D	AA permease	1.E-02	-0.1	response to endogenous stimulus (t-e35)	0.005	10	
protein_40_YOL162C		2	mitotic cell cycle	R J G K Y	25	W O D	AA permease	1.E-02	-0.1	chromate remodeling (t-e08)	0.005	10	
protein_40_YOL162C		2	PRP4: Splicing factor that is found in the Ce	T L D I N W V	25	W O D	AA permease	1.E-02	-0.1	cytoplasm organization and biogenesis (t-e08)	0.005	10	
protein_40_YOL162C		2	UPB8: Nuclear protein required for export o	P O E J E R F S Y	25	W O D	AA permease	1.E-02	-0.1	snoRNA binding (t-e25)	0.005	9	
protein_40_YOL162C		2	UTP8: Nuclear protein required for export o	T L D I N W V	25	W O D	AA permease	1.E-02	-0.1	U4/U6 x snRNP complex (t-e12)	0.005	9	
protein_40_YOL162C		2	response to endogenous stimulus	P O E J E R F S Y	25	W O D	AA permease	1.E-02	-0.1	protein modification (t-e01)	0.005	8	
protein_40_YOL162C		2	vesicle-mediated transport	N T J P I	25	W O D	AA permease	1.E-02	-0.1	snRNP nucleolar ribonucleoprotein complex (t-e2)	0.005	10	
protein_40_YOL162C		2	ohe_bud_neck	N T J P I	25	W O D	AA permease	1.E-02	-0.1	phosphotransferase activity, alcohol group as ac	0.005	8	
protein_40_YOL162C		2	response to endogenous stimulus	R J G K Y	25	W O D	AA permease	1.E-02	-0.1	protein binding (t-e19)	0.005	10	
protein_40_YOL162C		2	vesicle-mediated transport	E E D	25	W O D	AA permease	1.E-02	-0.1	regulation of nitrogen utilization (t-e05)	0.006	8	
protein_40_YOL162C		2	ohe_bud_neck	R J G K Y	25	W O D	AA permease	1.E-02	-0.1	nucleolus (t-e35)	0.005	9	
protein_40_YOL162C		2	response to endogenous stimulus	E S V P J W P	25	W O D	AA permease	1.E-02	-0.1	regulation of metabolism (t-e14)	0.006	9	
protein_40_YOL162C		2	vesicle-mediated transport	K K K H ,E L S L	25	W O D	AA permease	1.E-02	-0.1	endomembrane system (t-e11)	0.005	10	
protein_40_YOL162C		2	membrane part	[E S V P J W P ]	25	W O D	AA permease	1.E-02	-0.1	endomembrane system (t-e18)	0.005	8	
protein_40_YOL162C		2	membrane part	K K K H ,E L S L	25	W O D	AA permease	1.E-02	-0.1	response to stress (t-e10)	0.005	9	
protein_40_YOL162C		2	membrane part	[E S V P J W P ]	25	W O D	AA permease	1.E-02	-0.1	protein modification (t-e29)	0.005	10	
protein_40_YOL162C		2	membrane part	K K K H ,E L S L	25	W O D	AA permease	1.E-02	-0.1	protein modification (t-e21)	0.005	8	
protein_40_YOL162C		2	membrane part	[E S V P J W P ]	25	W O D	AA permease	1.E-02	-0.1	protein modification (t-e21)	0.005	9	
protein_40_YOL162C		2	membrane part	K K K H ,E L S L	25	W O D	AA permease	1.E-02	-0.1	protein modification (t-e21)	0.005	10	
protein_40_YOL162C		2	membrane part	[E S V P J W P ]	25	W O D	AA permease	1.E-02	-0.1	regulation of cellular metabolism (t-e25)	0.005	10	
protein_40_YOL162C		2	membrane part	K K K H ,E L S L	25	W O D	AA permease	1.E-02	-0.1	multicellular organismal development (t-e30)	0.005	9	
protein_40_YOL162C		2	membrane part	[E S V P J W P ]	25	W O D	AA permease	1.E-02	-0.1				

protein_40_YPL204W	2	HR25. Protein kinase involved in regulating protein_40_YPL204W	[AS GRE]	25		Y	0.005	8	
protein_40_YPL204W	2	HR25. Protein kinase involved in regulating protein_40_YPL204W	[IVLQD DERIEJ]	25		Y	0.003	8	
protein_40_YPL204W	2	HR25. Protein kinase involved in regulating protein_40_YPL204W	[SKDQJ QNEF]	25	SQ	ATM kinase substrate motif	Y	0.005	8
FRK1	1	Putative protein kinase, similar to Kin4	K..[TEFK]	25	K..[ST]	PKA kinase substrate motif	Y	0.005	1
protein_40_YPL042C	2	SSN3. Cyclin-dependent protein kinase, cons.	[TIGPE DTSA]	25	E[YDF]YM	PTP1B phosphatase substra	nucleoplasm part (1e-04)	0.005	8
protein_40_YOL324W	2	MYO2. One of two Myo2 vimentin-like proteins.	[PEGYI LYWV]	25			RNA polymerase II transcription mediator activit	0.004	8
protein_40_YOL324W	2	MYO2. One of two Myo2 vimentin-like proteins.	[SGRQI LWV]	25				0.005	8
protein_40_YOL324W	2	MYO2. One of two Myo2 vimentin-like proteins.	[LPD LMLP]	25	LPD	Motif in Cbp for interaction w		0.005	1
protein_40_YOL324W	2	EF1. Elongation factor 2 (EF2), alpha.	[VAP ILJA_E S]	25		Ankyrin G binding motif in vol		0.005	1
protein_40_YOL324W	2	EF1. Elongation factor 2 (EF2), alpha.	[IKRJA_EDEV]	25				0.005	1
protein_40_YOL324W	2	EF1. Elongation factor 2 (EF2), alpha.	[GKTII YEENV]	25		[STIFCGT].[ED] PDK1 phosphorylation motif		0.005	1
protein_40_YOL324W	2	CD33. Cytoskeletal mRNA cap binding prot.	[VNRLD KDAH]	25				0.005	8
protein_40_YOL324W	2	ADH1. Alcohol dehydrogenase, fermentative	[EJKIS KJFYA]	25	IYAP	c-Abi kinase phosphorylation	microtubule cytoskeleton (0.001)	0.005	1
protein_40_YOL086C	2	ADH1. Alcohol dehydrogenase, fermentative	[A SPF IQ]	25	[STQ]	ATM kinase phosphorylation		0.005	8
protein_40_YOL086C	2	ADH1. Alcohol dehydrogenase, fermentative	[IEQDT NED]	25	ITED	Protease Caspase 3-stringer	Y	0.005	8
protein_40_YOL086C	2	EV.[AIP KPD]	25	AEVD	Protease Caspase 10	Y	0.005	1	
protein_40_YOL086C	2	KLI.[Q EDH]	25	LLKL	AP-2 binding motif in CXCR2	Y	0.005	1	
protein_40_YOL086C	2	Q..[N GLI]	25				cytoplasmic mRNA processing body (1e-07)	0.005	8
protein_40_YOL086C	2	R..[R S]	25				cytosolic ribosome (sensu Eukaryota) (1e-19)	0.005	1
protein_40_YOL086C	2	LE.[EPI FC]	25		PAK phosphorylation site		0.005	1	
protein_40_YOL086C	2	L..[O VQ]	25				IDE DE FLI F	0.005	1
protein_40_YOL086C	2	LT OYFQ	25	LLTP	GoLoco motif, G a Glna bint		0.005	8	
protein_40_YOL086C	2	[GQ EFP ].LK	25		WD40 domain of Cdc4 bindir	Y	0.005	1	
protein_40_YOL086C	2	[IARH ENR ]	25				transcription factor complex (1e-15)	0.005	1
protein_40_YOL086C	2	ND N YH DGP	25					0.005	8
protein_40_YOL086C	2	A..[A EDQ]	25	CLILVIA_A LVF CASEIN ALPHA BETA PAT				0.005	8
protein_40_YOL086C	2	Q..[V GEA]	25					0.005	8
protein_40_YOL086C	2	[NSMVI LPRH]	25	EE ENDY IMF	Insulin receptor kinase subst	small nucleolar ribonucleoprotein complex (1e-1:	0.005	1	
protein_40_YOL086C	2	E EK KAN	25			rRNA processing (1e-34)	0.005	8	
protein_40_YOL086C	2	[LA P F EG ]	25					0.005	1
protein_40_YOL086C	2	PN IRK EON	25					0.005	1
protein_40_YOL086C	2	TL..[KMP ILNT ]	25					0.005	1
protein_40_YOL086C	2	P..[AV MV ]	25					0.005	1
protein_40_YOL086C	2	[IHKV K]	25	GOENGHIV KF MARCKS_1 PATTERN				0.005	8
protein_40_YOL086C	2	R..[R AYK ]	25	R RKR	CLV_PCSK_FUR_1	cytosolic ribosome (sensu Eukaryota) (1e-25)	0.005	8	
protein_40_YOL086C	2	[P ST ]	25	FED V IA DE	CAEOLIN PATTERN	cytosolic ribosome (sensu Eukaryota) (1e-29)	0.005	8	
protein_40_YOL086C	2	S...S	25	WD40 binding motif. Ser resi				0.005	1
protein_40_YOL086C	2	AT1G17. Scaffold protein responsible for pre-assembly of the actin filament.	[ARY K P RR ]	25	[K R R]	CLV_PCSK_KEX2_1	cytoplasm organization and biogenesis (1e-06)	0.005	1
protein_40_YOL086C	2	CPK5. Ribosomal protein L10 (10% of total).	[PS NAK VLA ]	25	P ST	DN A dependent Protein kin:		0.005	8
protein_40_YOL086C	2	CPK6. Ribosomal protein L10 (6% of total).	[TY AEF . ELVT ]	25	FED V IA DE			0.005	8
protein_40_YOL086C	2	CPK7. Mitogen-activated protein kinase (MAP kinase).	[E D AT TR ]	25	S...S			0.005	8
protein_40_YOL086C	2	CPK8. Serine/threonine kinase.	[SUDAK.. K P RE ]	25	WD40 binding motif. Ser resi		0.005	1	
protein_40_YOL086C	2	CPK9. Serine/threonine kinase.	[R P K G V K ]	25	TY..[V ]	SH2 ligand for SH2D4A OR :	chromatin remodeling complex (1e-07)	0.005	1
protein_40_YOL086C	2	CPK10. Serine/threonine kinase.	[KVA N.. NKDS	25				0.005	8
protein_40_YOL086C	2	CPK11. Serine/threonine kinase.	[VMS MR SN ]	25				0.005	8
protein_40_YOL086C	2	CPK12. Serine/threonine kinase.	[E AT A N ]	25	KEN	LIG_APCC_KENbox_2	cytoplasm organization and biogenesis (1e-06)	0.005	1
protein_40_YOL086C	2	CPK13. Serine/threonine kinase.	[Y HNA S	25	R..YS	14-3-3 binding motif (Ser mu	ribosome biogenesis (1e-06)	0.005	8
protein_40_YOL086C	2	CPK14. Serine/threonine kinase.	[K.. ARG A	25			rRNA processing (1e-07)	0.005	8
protein_40_YOL086C	2	CPK15. Serine/threonine kinase.	[N.. N VFE	25				0.005	1
protein_40_YOL086C	2	CPK16. Serine/threonine kinase.	[G A S QH ]	25	[I E D DIST IE	Motif in sodium channel that	DNA metabolism (0.01)	0.005	1
protein_40_YOL086C	2	CPK17. Serine/threonine kinase.	[SN PCK ]	25	NPC	N-glycosylation site- aberran		0.005	8
protein_40_YOL086C	2	CPK18. Serine/threonine kinase.	[Y.. V HKT ]	25		SH2 ligand for SH2D4A OR :	cytosolic ribosome (sensu Eukaryota) (1e-25)	0.005	8
protein_40_YOL086C	2	CPK19. Serine/threonine kinase.	[G U V H SD	25			cytosolic ribosome (sensu Eukaryota) (1e-29)	0.005	8
protein_40_YOL086C	2	CPK20. Serine/threonine kinase.	[D.. ER T ]	25				0.005	1
protein_40_YOL086C	2	CPK21. Serine/threonine kinase.	[TK SL T U LM ]	25	R..[R GT ]	CLV_PCSK_FUR_1	cytoplasm organization and biogenesis (1e-06)	0.005	8
protein_40_YOL086C	2	CPK22. Serine/threonine kinase.	[R.. R GT ]	25			ribosome biogenesis (1e-06)	0.005	8
protein_40_YOL086C	2	CPK23. Serine/threonine kinase.	[T ADT K R P ]	25			rRNA processing (1e-07)	0.005	8
protein_40_YOL086C	2	CPK24. Serine/threonine kinase.	[SGD Y VLE W ]	25	Y V LT FIC	LIQ_SH2_STAT5		0.005	1
protein_40_YOL086C	2	CPK25. Serine/threonine kinase.	[E D Q L C EW S	25	SQ	ATM kinase substrate motif		0.005	8
protein_40_YOL086C	2	CPK26. Serine/threonine kinase.	[LE I S Q OKM K	25	LLKL	AP-2 binding motif in CXCR2		0.005	1
protein_40_YOL086C	2	CPK27. Serine/threonine kinase.	[K S V L LHT ]	25	T..[R Q L ]			0.005	1
protein_40_YOL086C	2	CPK28. Serine/threonine kinase.	[W F CF ]	25				0.005	8
protein_40_YOL086C	2	CPK29. Serine/threonine kinase.	[IL.. D AG I ARE	25	F..[R K ]R	PPI binding sites	cohesin complex (1e-04)	0.004	1
protein_40_YOL086C	2	CPK30. Serine/threonine kinase.	[G O PH E IW D W ]	25	GQO	N-methylation motif in E. coli	cytoplasm organization and biogenesis (1e-25)	0.005	8
protein_40_YOL086C	2	CPK31. Serine/threonine kinase.	[G P PH E IW D W ]	25	GP	Protease TTP cleavage site		0.005	8
protein_40_YOL086C	2	CPK32. Serine/threonine kinase.	[L.. R KN P ]	25	IW FY ]K R P W	LIG_WRPW_2	mRNA metabolism (0.001)	0.005	1
protein_40_YOL086C	2	CPK33. Serine/threonine kinase.	[A.. R PSQ ]	25	P P A .R	SH3 binding for binding CIN8	mRNA processing (0.001)	0.005	8
protein_40_YOL086C	2	CPK34. Serine/threonine kinase.	[F.. K P M T ]	25			snRNP U1 (1e-08)	0.005	8
protein_40_YOL086C	2	CPK35. Serine/threonine kinase.	[F.. Q P F Q D QT V	25	F..[R K ]R	PPI binding sites	plasma membrane (0.01)	0.005	1
protein_40_YOL086C	2	CPK36. Serine/threonine kinase.	[F Q W Q D QT V	25	F Q W Q D QT V	EVH binding motif of Men	cytosol (0.01)	0.005	8
protein_40_YOL086C	2	CPK37. Serine/threonine kinase.	[M AN V TR Q F ]	25	IYE	cFPS/FES kinase phosphory	nuclear mRNA splicing, via spliceosome (1e-07)	0.005	8
protein_40_YOL086C	2	CPK38. Serine/threonine kinase.	[E Q L J FK M E	25				0.005	8
protein_40_YOL086C	2	CPK39. Serine/threonine kinase.	[R.. J F P ]	25			nucleolus (1e-14)	0.005	8
protein_40_YOL086C	2	CPK40. Serine/threonine kinase.	[R.. J F P ]	25			transcription factor complex (1e-13)	0.005	8
protein_40_YOL086C	2	CPK41. Serine/threonine kinase.	[E.. K ERS	25			RSC complex (1e-07)	0.004	1
protein_40_YOL086C	2	CPK42. Serine/threonine kinase.	[T.. K F E ]	25				0.005	8
protein_40_YOL086C	2	CPK43. Serine/threonine kinase.	[D.. R Y M ]	25				0.005	1
protein_40_YOL086C	2	CPK44. Serine/threonine kinase.	[P.. Y G G ]	25				0.005	8
protein_40_YOL086C	2	CPK45. Serine/threonine kinase.	[K.. G P G ]	25				0.005	1
protein_40_YOL086C	2	CPK46. Serine/threonine kinase.	[K.. Q Y R ]	25	K R R	Nuclear localization motif		0.005	8
protein_40_YOL086C	2	CPK47. Serine/threonine kinase.	[Q Q T P Q G D ]	25				0.005	1
protein_40_YOL086C	2	CPK48. Serine/threonine kinase.	[I.. V L Y H ]	25	L.R..[ST]	RSK phosphorylation site	nucleolus (1e-14)	0.005	8
protein_40_YOL086C	2	CPK49. Serine/threonine kinase.	[G Y V Y L V N ]	25	[I R K E Q TAG ]	IQRHEQTAG N-terminal methylation site in	transcription factor complex (1e-13)	0.005	8
protein_40_YOL086C	2	CPK50. Serine/threonine kinase.	[G I L S C ]	25				0.005	1
protein_40_YOL086C	2	CPK51. Serine/threonine kinase.	[K.. G P G ]	25				0.005	8
protein_40_YOL086C	2	CPK52. Serine/threonine kinase.	[K.. Q Y R ]	25				0.005	1
protein_40_YOL086C	2	CPK53. Serine/threonine kinase.	[V.. D T W L S G ]	25	K R R	CLV_PCSK_KEX2_1		0.005	8
protein_40_YOL086C	2	CPK54. Serine/threonine kinase.	[M.. N D V R ]	25	HAVDI	M-N Cadherin ligand		0.005	8
protein_40_YOL086C	2	CPK55. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK56. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK57. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK58. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK59. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK60. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK61. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK62. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK63. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK64. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK65. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK66. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK67. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK68. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK69. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK70. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK71. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK72. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK73. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK74. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK75. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK76. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK77. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK78. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK79. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK80. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK81. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK82. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK83. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK84. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK85. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK86. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK87. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK88. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	8
protein_40_YOL086C	2	CPK89. Serine/threonine kinase.	[F V A N W D F ]	25				0.005	1
protein_40_YOL086C	2	CPK90. Serine/threonine kinase.	[F V A N W D F ]	25					

oshea_bud	2	oshea_bud	QI.[IMD][DTL]	25		bud (1e-13)	Y	0.005	10
oshea_ambiguous	2	oshea_ambiguous	NS.[KSGDNIR]	25	STG	bud (1e-09)	Y	0.005	10
oshea_ambiguous	2	oshea_ambiguous	TGCTMHV	25	EH(3) EF hand domain bindi	vacuole (1e-50)	Y	0.006	8
matsuyama_vacuole	2	matsuyama_vacuole	I,[IVAV]	25		spindle (1e-51)	Y	0.006	9
matsuyama_Spindle or SPI	2	matsuyama_Spindle or SPI	K[VHT].[LISLG]	25		spindle pole (1e-15)	Y	0.007	8
matsuyama_Spindle or SPI	2	matsuyama_Spindle or SPI	LS.[KHN][ECK]	25				0.006	10
matsuyama_nucleolus	2	matsuyama_nucleolus	P,[GTNJS]	25	LVRPGS	nuclear envelope (1e-08)	Y	0.006	8
matsuyama_nuclear_envelope	2	matsuyama_nuclear_envelope_or_dots	[FOLJ][THPIP]	25	[STIP]	cell cortex (1e-05)	Y	0.006	10
matsuyama_Cytoplasmic dc	2	matsuyama_Cytoplasmic_dc	[DPW].[VN]	25	YVNV	cell division (1e-04)	Y	0.006	10
matsuyama_Cytoplasmic dc	2	matsuyama_Cytoplasmic_dc	L,[GWIKR]	25	LFG	regulation of cellular physiological process (1e-0		0.005	10
host_life_belle_q110	10	host_life_belle_q110	R,[RSV]	25	F.R.-SF			0.005	10
genetic_YPL240C	2	HS2P: Subunit of the heterotrimeric cochear	K[VHT].[LISLG]	25	PKCeta kinase phosphoryla			0.005	10
genetic_YNL153C	2	GIM3: Subunit of the heterotrimeric cochear	LS.[KHN][ECK]	25	PKA kinase substrate motif			0.005	10
genetic_YLR282C	2	YPT6: GTPase, Ras-like GTP binding protein	P,[GTNJS]	25	MDC1 BRCT domain binding			0.005	10
genetic_YLR200W	2	YKE1: Subunit of the heterotrimeric Gm70	[FISIP][FNKJ]	25	Binding motif for clathrin hea			0.005	10
genetic_YLR039C	2	RIC1: Protein involved in retrograde transport	G,[YLGJ]	25	[STIP]	[PKYTL][AMQ]	Y	0.005	9
genetic_YLR039C	2	RIC1: Protein involved in retrograde transport	[ALAL][RLKIM]	25	LIG_WW_4LIG_WW_4	endoplasmic reticulum (1e-08)	Y	0.005	10
genetic_YGL058W	2	RAD6: Ubiquitin-conjugating enzyme (E2), im	[LAY][RFWC]	25	S[ST]	DNA metabolism (0.001)	Y	0.005	9
genetic_YGL020C	2	GET1: Subunit of the GET complex; required i	D,[ISPJ]	25	DLL	chromosome organization and biogenesis (sensi	Y	0.005	9
genetic_YER083C	2	GET2: Subunit of the GET complex; required i	P[NRNL]	25	AKRRRLSSR PAK1 kinase substrate motif	DNA metabolism (1e-07)	Y	0.005	10
genetic_YER083C	2	GET2: Subunit of the GET complex; required i	R[PEV][VING]	25	[STIP]	cortical cytoskeleton (0.001)	Y	0.005	9
genetic_YER083C	2	GET3: Subunit of the GET complex that stimulates exp	A,[VWV]	25	[PKY][V]	endoplasmic reticulum (1e-08)	Y	0.005	10
genetic_YDL202C	2	RPN1: Transcription factor that stimulates exp	Q,[LDT]	25	PPI binding sites	DNA metabolism (0.001)	Y	0.005	9
genetic_YDL202C	2	LTE1: Putative GDP/GTP exchange factor req	L,[T]	25	RAF1 kinase substrate motif	chromosome organization and biogenesis (sensi	Y	0.005	9
yeast-1939_GO-0003824	2	catalytic activity	[SOT][NA].TT	24		chromosome organization and biogenesis (sensi	Y	0.005	9
yeast-267_GO-0042625	2	cellular macromolecule catabolism	EY.[LIS][EFA]	24	[DEJ]	DNA metabolism (1e-07)	Y	0.005	8
protein_40_YPL031C	2	PH05: Cyclic-dependent kinase, with ten cy	N.[NN][NMR]	24	EGFR kinase substrate motif	transcription regulator activity (1e-07)		0.005	8
protein_40_YMR229C	2	RPP5: Protein required for synthesis of ts	[SACT].[QNR]	24	Pkinase	biopolymer catabolism (1e-08)		0.004	9
protein_40_YOR272W	2	YTM1: Constituent of 66S pre-ribosomal parti	[AKE][RA(GKA]	24	Pkinase	kinase regulator activity (1e-05)	Y	0.005	10
protein_40_YGL105W	2	ARC1: Protein that binds RNA and methiony	SS[GPC][GWD]	24	S[ST]	protein kinase activity (1e-05)	Y	0.005	9
yeast-335_GO-0016772	2	transferase activity, transferring phosphorus-con	S.[SH]	24	MDC1 BRCT domain bindin	ribosomal large subunit assembly and maintenan	Y	0.005	9
protein_40_YMR021W	2	TRP1: GDP-dependent protein kinase	N.[D][STG]	24		transferase activity, transferring phosphorus-con	Y	0.005	8
protein_40_YOR191W	2	U2TP1: U2TP1: nucleolar factor, activates the A	A,[AGC]	24	RPVSSAASVY 14-3 domain binding motif	telomere organization and biogenesis (1e-07)	Y	0.005	8
yeast-249_GO-0016072	2	RNA deubiquitination	D.[TQF]	24	[IV]	actin cortical patch (1e-11)	Y	0.005	10
yeast-215_GO-0007010	2	cytokinesis and biogenesis	D.[TQF]	24	fGFR and Csk kinase shap	rRNA metabolism (1e-23)	Y	0.006	9
protein_40_YPL004C	2	LSP1: Primary component of eosomes, whi	D.[TQF]	24	D..IV.E	cytoskeleton organization and biogenesis (1e-11)	Y	0.005	9
protein_40_YLR222C	2	U2TP1: Nuclear protein, component of the t	E.[ETD][KOH]	24	P[STPKKKKK]	cytoskeleton organization and biogenesis (1e-11)	Y	0.005	8
protein_40_YAL024C	2	U2TP1: Putative GDP/GTP exchange factor re	A.[KYCA]	24	S[DE][DE]	BARD1 BRCT domain bindin	Y	0.005	8
protein_40_YGL105W	2	ARC1: Protein that binds RNA and methiony	E.[ERCIS]	24	Y.E.E	Src phosphorylation site	Y	0.005	7
protein_40_YMR093W	2	UTP15: Nuclear protein, component of the t	L.[EDNS]	24	PKinase	protein kinase activity (1e-10)	Y	0.005	8
protein_40_YKR048C	2	protein binding	T.[NAVJK]	24	D.G.T..K.I	lysophosphatidyl inositol	Y	0.005	9
yeast-243_GO-0006066	2	NAP1: Protein that interacts with mitotic cycl	V.[PA]	24	[VAPI][VLA].E	Ankry G binding motif in vol	Y	0.005	9
yeast-207_CO-0059747	2	transporter activity	P.[TAA]	24	IEAD	Protease Caspase 10	Y	0.005	8
protein_40_YMR133W	2	basic DNA binding	[VTPV][CLCV]	24		Protease Caspase 10	Y	0.005	9
protein_40_YMR133W	2	basic DNA binding, attitudes	F.[KTADE]	24		protection against DNA damage stimuli (1e-38)	Y	0.005	9
protein_40_YMR229C	2	RPP5: Protein required for synthesis of ts	A.[DRCIN]	24	F-box	protein catalysis (1e-04)	Y	0.005	9
protein_40_YMR047C	2	U2TP16: Subunit of the nuclear pore comple	V.[LUKL]	24	LLG	BRCT	Y	0.005	10
protein_40_YML007W	2	U2TP1: Basic leucine zipper (ZIP) transcri	E..[ENYQ]	24	Iron binding motif in ferritin L-	response to stress (1e-18)	Y	0.005	8
protein_40_YAR019C	2	CDC13: Protein kinase of the Scl7 Exi Net	[N].[E]	24	SH3_1	nuucleotyplasmic transport (1e-18)	Y	0.004	7
protein_40_YLR186W	2	EMG1: Protein required for the maturation of	E..[V]	24	WD40	nuucleotyplasmic transport (1e-18)	Y	0.004	7
yeast-511_GO-0051649	2	establishment of cellular localization	[TSN][AD]	24	SH3_1	nuucleoplasma part (1e-19)	Y	0.004	7
yeast-512_GO-0046907	2	intracellular transport	E..[V]	24	WD40	nuucleoplasma part (1e-19)	Y	0.004	7
yeast-303_GO-0006605	2	protein targeting	[FLNE][DTW]	24	SH3_1	protein kinase activity (1e-07)	Y	0.004	7
yeast-543_GO-0051641	2	cellular localization	F.[DQD]	24	WD40	protein catalysis (1e-04)	Y	0.005	9
protein_40_YOL138C	2	NUO1: Nucleolar protein, forms a complex w	[FQD][NSA].VS	24	SH3_1	protein kinase activity (1e-18)	Y	0.005	10
protein_40_YDL148C	2	Oshka_mcl	[V].[L]	24	WD40	nuucleoplasma part (1e-19)	Y	0.005	9
13_Oshea_mc	2	YEP1: Response to stress	[V].[L]	24	SH3_1	protein kinase activity (1e-18)	Y	0.005	9
yeast-424_GO-0006950	2	LSP1: Primary component of eosomes, whi	[T].[L]	24	WD40	nuucleoplasma part (1e-19)	Y	0.005	9
protein_40_YFR004C	2	U2TP1: Putative protein, component of the t	[V].[SER]	24	SH3_1	protein kinase activity (1e-18)	Y	0.005	9
protein_40_YFR052W	2	response to stress	[V].[K]	24	WD40	nuucleoplasma part (1e-19)	Y	0.005	9
protein_40_YOR181W	2	EL1: Acin assembly factor, activates the A	[V].[K]	24	SH3_1	protein kinase activity (1e-18)	Y	0.005	10
protein_40_YJL130C	2	U2TP1: Bifunctional carboxymethyltransferase	[V].[L]	24	WD40	protein kinase activity (1e-01)	Y	0.004	8
matsuyama_nuclear_envelope	2	matsuyama_nuclear_envelope_or_dots	[D..P]	24	SH3_1	nuclear envelope (1e-45)	Y	0.006	9
protein_40_YMR304W	2	U2TP1: Ubiquitin-specific protease that may i	[PA][IPC][LTH]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.004	8
protein_40_YHR030C	2	SL2T: Serine/threonine MAP kinase involved	[R][P]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	establishment of cellular localization	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	WD40	small nucleoplasme-nucleoprotein complex (1e-01)	Y	0.005	10
protein_40_YFR034C	2	U2TP1: Putative protein, component of the t	[V].[L]	24	SH3_1	small nucleoplas			



protein_40_YDR324W	2	UTPA: Nucleolar protein, component of the sr	F[KIEWKA	24	PFI[RLAII]K[HISTONE_H3_2_PATTERN	Y	nucleolus (1e-18)	Y	0.005 9
protein_40_YDR369W	2	YPR14C: A-3'-p-ribose, minor nucleolar protein	P.[N]WVJR	24	P[JININDR..K]SH3 binding motif for HBP S'	Y	phosphotransferase activit, alcohol group as ac	Y	0.005 10
protein_40_YDR205W	2	RPS11: Protein component of the small ribo.	[DFIF].[NEFK]	24	[K[R]P]FETAA	Y	ribonucleoprotein complex (1e-06)	Y	0.005 8
protein_40_YDL213C	2	NOP8: Putative RNA-binding protein implicated	G.[A]EICH	24	GRA	Y	ribosome biogenesis (1e-06)	Y	0.004 9
protein_40_YDL047W	2	SIT4: Type 2A-related serine-threonine phospho.	[HGPRI][TGEJ]	24	Protease Ipa proteolytic site	Y	spliceosome (0.011)	Y	0.005 10
protein_40_YCR034W	2	PRP11: Subunit of the SRS3 splicing factor or	L[FIVM]Y	24	PTL	Y	endoplasmic reticulum (1e-08)	Y	0.005 10
protein_40_YBR217W	2	FEN1: Fatty acid elongase, involved in sphin.	E.[I]GAY	24	Motif in Pfs for prosome c	Y	proteasome regulatory particle (sensu Eukaryota	Y	0.005 9
protein_40_YBR200W	2	BEM1: Protein containing SH3-domains, inv.	E.[G]DQ	24	[RK]I[V].F	Y	excocytosis (1e-08)	Y	0.005 8
protein_40_YBR159W	2	IFAB3: Microsomal beta-keto-reductase; cont.	E.[A]SGM	24	PP1 protein phosphatase sul	Y	endoplasmic reticulum (0.001)	Y	0.004 8
protein_40_YBR106W	2	PHOB: Probable membrane protein, invol.	H.[KAKPIG]	24	cSrc kinase phosphorylation	Y	mRNA metabolism (1e-07)	Y	0.005 10
protein_40_YVR059C	2	SPR1: Splicing factor, component of the U4/U6	G.[D]E[Q]	24	[IVL]Y..[PF]	Y	small nuclear ribonucleoprotein complex (1e-1'	Y	0.005 10
protein_40_YLR047W	2	U2AF: Subunit of pre-mRNA splicing factor	T.[EWDJ][GTWN]	24	ABL phosphorylation site	Y	protein folding (0.01)	Y	0.005 9
protein_40_YAR004C	2	RF14: Subunit of heteromeric Replicase I	Y..[FPQW]	24		Y	nucleic acids (1e-58)	Y	0.005 10
protein_40_YAL024C	2	LTE1: Putative GDP-GTP exchange factor	A.[K]LGD	24		Y	nuclear membrane part (1e-26)	Y	0.005 8
protein_40_YAL005C	2	SSA1: ATPase involved in protein folding and	E.[QEKI].[KPKQ]	24		Y	Golgi apparatus (1e-25)	Y	0.005 10
oschea_nucleolus	2	SSA2: ATPase involved in protein folding and	V.[KHEJD]	24		Y	endosome (1e-08)	Y	0.005 8
oschea_nuclear_periphery	2	SSA3: Nucleolar protein	R.[VKFA]	24		Y	exocytosis (1e-07)	Y	0.005 10
oschea_mitocondrion	2	SSA4: Mitochondrial protein	S..[TONT]	24		Y	bud (0.001)	Y	0.005 10
oschea_Golgi_Or_Golgi_to_vacuole	2	SSA5: Golgi_Go_Golgi_to_vacuole	F[VM]ME	24		Y	barrier septum (1e-06)	Y	0.006 9
oschea_ER	2	SSA6: ER	K.[IERC]	24		Y	spindle (1e-12)	Y	0.006 8
oschea_endosome	2	SSA7: Endosome	E[KEMI][LVDH]	24		Y	microtubule cytoskeleton (1e-39)	Y	0.006 9
oschea_cyttoplasm	2	SSA8: Cytoplasm	[YHM][LVCJSH]	24		Y	ATP binding (1e-04)	Y	0.006 8
oschea_bud	2	SSA9: Bud	[LAPI][FNQJ..NL]	24		Y	cell tip (1e-06)	Y	0.006 10
oschea_disease	2	SSA10: Ambiguous	G.[FLPGER..G.IBC..IBS..IUC]	24		Y	cell cortex (1e-10)	Y	0.005 9
seheg_antibiotic	2	SSA11: Ambiguous	V.[VIIHJA]	24		Y	telomere organization and biogenesis (0.001)	Y	0.005 9
matsuyama_periphery	2	SSA12: Matsuyama_periphery	H.[VADVI]	24		Y	nucleoplasm (1e-04)	Y	0.004 8
matsuyama_nuclear_envelope	2	SSA13: Matsuyama_nuclear_envelope_or_dots	[PNND].[NSCP]	24		Y	establishment of cellular localization (1e-07)	Y	0.004 9
matsuyama_Microlute	2	SSA14: Matsuyama_Microlute	I.[QIKYP]	24		Y	histone deacetylation (0.01)	Y	0.004 9
matsuyama_Cytosol	2	SSA15: Matsuyama_Cytosol	K.R.[RVN]	24		Y	chromosome organization and biogenesis (sensi	Y	0.004 10
matsuyama_Cytoplasmic	2	SSA16: Matsuyama_Cytoplasmic	H.[ASDIL]	24		Y	Phase (1e-09)	Y	0.005 9
matsuyama_Cytosolic	2	SSA17: Matsuyama_Cytosolic	N.[KSQJG]	24		Y	endoplasmic reticulum (1e-22)	Y	0.005 9
genetic_PL005C	2	SSA18: Matsuyama_Cytosolic	V.[DTLJ]	24		Y	establishment and/or maintenance of chromatin	Y	0.005 10
genetic_YLR200W	2	SSA19: Matsuyama_Cytosolic	S.[ST]	24		Y	and/or maintenance of chromatin	Y	0.005 10
genetic_YER039C	2	SSA20: Matsuyama_Cytosolic	F.Y[DEJEL]	24		Y	proteasome complex (sensu Eukaryota) (1e-13)	Y	0.004 9
genetic_YER004C	2	SSA21: Matsuyama_Cytosolic	D.[WJDL]	24		Y	ribosome biogenesis (1e-32)	Y	0.005 9
genetic_YER083C	2	SSA22: Matsuyama_Cytosolic	I.[DOKI]	24		Y	barrier septum (1e-14)	Y	0.006 8
genetic_YER030W	2	SSA23: Matsuyama_Cytosolic	T.[TLFT]	24		Y	protein kinase activity (1e-11)	Y	0.006 7
ucsf_icl_k_means_G6	2	SSA24: Subcellular localization, 6 clusters	I[AACW][GJNV]	23		Y	endoplasmic reticulum (1e-22)	Y	0.005 9
oshea_Total	2	SSA25: Subcellular localization, 6 clusters	[NDGPN][AMR]	23		Y	establishment and/or maintenance of chromatin	Y	0.005 10
yeast-216_GO-0006325	2	SSA26: Subcellular localization, 6 clusters	[NDGPN][AMR]	23		Y	and/or maintenance of chromatin	Y	0.005 10
yeast-216_GO-0006323	2	SSA27: Subcellular localization, 6 clusters	R..[SVKL]	23		Y	proteasome complex (sensu Eukaryota) (1e-13)	Y	0.004 9
protein_40_YGL105W	2	SSA28: Subcellular localization, 6 clusters	S..[SISV]	23		Y	ribosome biogenesis (1e-19)	Y	0.005 10
protein_40_YOR181W	2	SSA29: Subcellular localization, 6 clusters	S.T[QDPI][YVNW]	23		Y	proteasome complex (sensu Eukaryota) (1e-13)	Y	0.004 9
protein_40_YGL245W	2	SSA30: Subcellular localization, 6 clusters	[GSNSJ][APJA]	23		Y	ribosome biogenesis (1e-32)	Y	0.005 9
protein_40_YER224C	2	SSA31: Subcellular localization, 6 clusters	P.G[PKMG]	23		Y	barrier septum (1e-14)	Y	0.006 8
protein_40_YER224C	2	SSA32: Subcellular localization, 6 clusters	G.[E]DKE	23		Y	protein kinase activity (1e-05)	Y	0.005 10
protein_40_YER224C	2	SSA33: Subcellular localization, 6 clusters	W..[D]WJL	23		Y	nucleic chromatin (0.001)	Y	0.005 10
protein_40_YER224C	2	SSA34: Subcellular localization, 6 clusters	[D]WJL[QDQ]	23		Y	cytosol organization and biogenesis (1e-08)	Y	0.005 9
protein_40_YER224C	2	SSA35: Subcellular localization, 6 clusters	O[RYIEV]	23		Y	nucleoplasm (1e-04)	Y	0.004 10
protein_40_YER224C	2	SSA36: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	establishment of cellular localization (1e-07)	Y	0.005 9
protein_40_YER224C	2	SSA37: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	histone deacetylation (0.01)	Y	0.004 10
protein_40_YER224C	2	SSA38: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	chromosome organization and biogenesis (sensi	Y	0.004 10
protein_40_YER224C	2	SSA39: Subcellular localization, 6 clusters	L.V[EDG][FNG]	23		Y	Phase (1e-09)	Y	0.005 10
protein_40_YER224C	2	SSA40: Subcellular localization, 6 clusters	R.Y[QNT]	23		Y	vesicle-mediated transport (1e-09)	Y	0.005 9
protein_40_YER224C	2	SSA41: Subcellular localization, 6 clusters	E.N[ING]	23		Y	vesicle-mediated transport (1e-09)	Y	0.004 10
protein_40_YER224C	2	SSA42: Subcellular localization, 6 clusters	C.Q[RCIO]	23		Y	nucleic acid (1e-24)	Y	0.004 10
protein_40_YER224C	2	SSA43: Subcellular localization, 6 clusters	R..[SHYL]	23		Y	modification-dependent macromolecule catabolit:	Y	0.004 9
protein_40_YER224C	2	SSA44: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	protein kinase activity (1e-19)	Y	0.004 9
protein_40_YER224C	2	SSA45: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	modification-dependent macromolecule catabolit:	Y	0.004 9
protein_40_YER224C	2	SSA46: Subcellular localization, 6 clusters	L.V[EDG][FNG]	23		Y	protein kinase activity (1e-19)	Y	0.004 9
protein_40_YER224C	2	SSA47: Subcellular localization, 6 clusters	R.Y[QNT]	23		Y	actin filament-based process (0.01)	Y	0.004 7
protein_40_YER224C	2	SSA48: Subcellular localization, 6 clusters	R.Y[QNT]	23		Y	macromolecule catabolism (1e-47)	Y	0.005 7
protein_40_YER224C	2	SSA49: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	pyrophosphatase activity (1e-88)	Y	0.005 9
protein_40_YER224C	2	SSA50: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	cullin-RING ubiquitin ligase complex (0.001)	Y	0.005 10
protein_40_YER224C	2	SSA51: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	intracellular protein transport (1e-40)	Y	0.005 9
protein_40_YER224C	2	SSA52: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	nuclear transport (1e-06)	Y	0.005 8
protein_40_YER224C	2	SSA53: Subcellular localization, 6 clusters	L.V[EDG][FNG]	23		Y	vesicle-mediated transport (1e-09)	Y	0.005 9
protein_40_YER224C	2	SSA54: Subcellular localization, 6 clusters	R.Y[QNT]	23		Y	nucleic acid (1e-24)	Y	0.004 10
protein_40_YER224C	2	SSA55: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA processing (1e-21)	Y	0.005 9
protein_40_YER224C	2	SSA56: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	nucleic acid (1e-67)	Y	0.005 8
protein_40_YER224C	2	SSA57: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA processing (1e-10)	Y	0.005 8
protein_40_YER224C	2	SSA58: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	protein kinase activity (1e-23)	Y	0.004 9
protein_40_YER224C	2	SSA59: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	protein kinase activity (1e-23)	Y	0.004 10
protein_40_YER224C	2	SSA60: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.004 10
protein_40_YER224C	2	SSA61: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA62: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA63: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA64: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA65: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA66: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA67: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA68: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA69: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA70: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA71: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA72: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA73: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA74: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA75: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA76: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA77: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA78: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA79: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA80: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA81: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA82: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA83: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA84: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA85: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA86: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA87: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA88: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA89: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA90: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA91: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA92: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA93: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA94: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA95: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA96: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA97: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA98: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA99: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA100: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA101: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA102: Subcellular localization, 6 clusters	H.F[LEY]	23		Y	RNA elongation from RNA polymerase II promot:	Y	0.005 8
protein_40_YER224C	2	SSA103: Subcellular localization, 6 clusters	I[TEFJ][DIEM5]	23					

yeast-792_GO_0006412	2	protein biosynthesis	AA[KRP][KYL]	23		Y		translation (1e-53)	0.005	
yeast-792_GO_0006412	2	protein biosynthesis	G[KHYD]	23	G[KR][IKR]	Amidation after cleavage after		transferring phosphorus-con	0.005	
yeast-792_GO_0006412	2	protein biosynthesis	Q[QVQNA]	23				nucleic acid binding (1e-08)	0.005	
yeast-685_GO_0016740	2	transferase activity	Y..[YVMNC]	23				nucleic acid binding (1e-07)	0.005	
yeast-649_GO_0003376	2	nucleic acid binding	[LPEI]Q[KRTJLV	23				regulation of cellular metabolism (0.01)	0.005	
yeast-649_GO_0003376	2	nucleic acid binding	[SAJSH]A[QEL]	23	[PSAT]Q[QE]E	LIC_TTRAF2_1		regulation of cellular metabolism (0.01)	0.005	
yeast-630_CO_0051244	2	regulation of cellular process	[NWVWIE]TTRTLT	23	PLTLP	RAF1 kinase substrate motif		cellular localization (1e-14)	0.005	
yeast-630_CO_0051244	2	regulation of physiological process	[NWVWIE]TTRTLT	23	PLTLP	RAF1 kinase substrate motif		RNA metabolism (1e-12)	0.005	
yeast-544_GO_0016070	2	cellular localization	[ITQIS..]TTRTLT	23	PLTLP	RAF1 kinase substrate motif		RNA binding (1e-39)	0.005	
yeast-544_GO_0016070	2	cellular localization	[IGILNREJDL	23	RK_SF	PKCepsilon kinase phosphor		RNA binding (1e-39)	0.005	
yeast-424_GO_0006950	2	RNA metabolism	[KNAT]A[GPA]	23	LFDLM	Binding motif in Cln3 for clat		multicellular organismal development (1e-26)	0.005	
yeast-399_GO_0003723	2	RNA binding	[KVMI]RIDEA	23	IEAD	Protease Caspase 10		multicellular organismal development (1e-74)	0.005	
yeast-388_GO_0007275	2	response to stress	[VID]LSPNNA	23	E.Y.[QSG]	Protease TEVProtease TEV		cellular catabolism (1e-28)	0.005	
yeast-358_GO_0004248	2	development	Y[G]F[G]	23				cellular catabolism (1e-34)	0.005	
yeast-358_GO_0004248	2	cellular catabolism	[ALG]P[VKR]	23				endoplasmic reticulum (1e-19)	0.005	
yeast-358_GO_0004248	2	cellular catabolism	G[M]N[W]	23				nucleoplasmin (1e-38)	0.005	
yeast-358_GO_0004248	2	cellular catabolism	R[RKRW]	23	R.R..[ST]	PKB phosphorylation motif		vesicle-mediated transport (1e-47)	0.005	
yeast-358_GO_0004248	2	cellular catabolism	YV[LMV]K	23	Y..[LMVH]	TRG_ENDOCYTIC_2		protein localization (1e-30)	0.005	
yeast-322_CO_0005654	2	embryonic reticulum	[PIAGH]E[NH]	23	PPLP	LIG_WW_2LIG_WW_2		hydrolase activity, acting on ester bonds (1e-66)	0.005	
yeast-295_CO_0016192	2	vehicle-mediated transport	[SNAIS]F[GFM]	23	H.VNK	Motif for targeting CD44 to bi	Y	reproduction (1e-39)	0.005	
yeast-292_GO_0008104	2	protein localization	[LWPN]P[NPKD]	23	HLVNK			intracellular protein transport (1e-35)	0.005	
yeast-281_GO_0016788	2	hydrolyase activity, acting on ester bonds	H[VNSK]	23				intracellular protein transport (1e-26)	0.005	
yeast-267_GO_0000003	2	reproduction	S[GWK]L[OCJE]	23	DLL			intracellular protein transport (1e-31)	0.005	
yeast-259_CO_0015031	2	protein transport	E[EESGD]	23					0.005	
yeast-259_CO_0015031	2	protein transport	[GISM]F[FGNV]	23	E[ST]D	Ankyrin G binding motif in K8	Y	response to chemical stimulus (1e-31)	0.005	
yeast-259_CO_0015031	2	protein transport	[SWSQ]_FG[MC]	23	F.F.	WASP Homology 1 binding n	Y	thiuronucleotide-triphosphatase activity (1e-74)	0.005	
yeast-215_GO_0007010	2	cyclotol organization and biogenesis	S..F.	23	LIG_BRCT_BRCA1_1			lipid metabolism (1e-87)	0.005	
yeast-138_GO_0044260	2	cellular macromolecule metabolism	[SNIGS]F[GCMG]	23				lipid metabolism (1e-75)	0.005	
yeast-1216_GO_0009508	2	biogenesis	N[LNLTD]	23				secretory pathway (1e-34)	0.005	
yeast-1136_GO_0044249	2	cellular biosynthesis	[FTVG]L[LCWJP]	23				cytoskeleton organization and biogenesis (1e-12)	0.005	
protein_40_YLR137W	2	RPRP: Protein involved in pre-mRNA processing	N..[T]MWJC	23				protein modification (1e-14)	0.005	
protein_40_YLR137W	2	RPCAP: RNA intermediate subunit, common to all	D..[EDTD]	23					0.005	
protein_40_YLR137W	2	protein: YPR137W	[LAVI]T[S]HY	23				small nuclear ribonucleoprotein complex (1e-1)	0.005	
protein_40_YLR137W	2	autosome kinase involved in regulating its own	E[EDTD]P[TKI]	23				microtubule cytoskeleton (0.01)	0.005	
protein_40_YLR137W	2	autosome kinase involved in regulating its own	S[SVWV]P	23	G[YKQ]F	LIC_SH2_STAT6		mitotic cell cycle (0.01)	0.005	
protein_40_YLR137W	2	lipid metabolism	S[VLMQ]	23	R.L.			transcription regulator activity (1e-06)	0.005	
protein_40_YLR137W	2	lipid metabolism	V[VHLA]	23	I[ST]D			transcription (1e-20)	0.004	
protein_40_YLR137W	2	generation of precursor metabolites and energy	E..[EOMIE]	23	F..F.				0.004	
protein_40_YLR137W	2	secretion	QSYTNM[JLNT]	23	RE..E	Iron binding motif in ferritin L-			0.004	
protein_252_GO_0006886	2	intracellular protein transport	NN[LTD]	23					0.004	
protein_248_GO_0031966	2	mitochondrial membrane	N[LWPN]P	23					0.004	
protein_248_GO_0031966	2	response to chemical stimulus	L[LHF]D	23					0.004	
protein_236_CO_0017111	2	adenosine-triphosphatase activity	K[DQK]Q[QI]	23	IQ...RG...R	Binding motif in IQGAP for bi	Y		0.004	
protein_233_CO_0006629	2	lipid metabolism	[OIMAK]	23					0.004	
protein_233_CO_0006629	2	lipid metabolism	S[VLMQ]	23					0.004	
protein_230_GO_0006091	2	generation of precursor metabolites and energy	E..[EOMIE]	23					0.004	
protein_219_GO_0046903	2	secretion	QSYTNM[JLNT]	23					0.004	
protein_215_GO_0007010	2	cyclotol organization and biogenesis	NN[LTD]	23					0.004	
yeast-138_GO_0044260	2	cellular macromolecule metabolism	N..[T]MWJC	23					0.004	
yeast-1216_GO_0009508	2	biogenesis	D..[EDTD]	23					0.004	
protein_40_YOR294W	2	RPRP: Protein required in pre-mRNA processing	[LAVI]T[S]HY	23					0.004	
protein_40_YOR294W	2	RPCAP: RNA intermediate subunit, common to all	E[EDTD]P[TKI]	23					0.004	
protein_40_YOR294W	2	protein: YOR137W	S[SVWV]P	23	G[YKQ]F	LIC_SH2_STAT6			0.004	
protein_40_YOR294W	2	autosome kinase involved in regulating its own	S[VLMQ]	23	R.L.				0.004	
protein_40_YOR294W	2	autosome kinase involved in regulating its own	V[VHLA]	23	I[ST]D				0.004	
protein_40_YOR294W	2	lipid metabolism	E..[EOMIE]	23	F..F.				0.004	
protein_40_YOR294W	2	generation of precursor metabolites and energy	QSYTNM[JLNT]	23	RE..E	Iron binding motif in ferritin L-			0.004	
protein_40_YOR113W	2	secretion	NN[LTD]	23					0.004	
protein_40_YOR113W	2	cellular macromolecule metabolism	N..[T]MWJC	23					0.004	
protein_40_YOR113W	2	biogenesis	D..[EDTD]	23					0.004	
protein_40_YOR113W	2	RPRP: Protein required for signal transduction	[LAVI]T[S]HY	23					0.004	
protein_40_YOR113W	2	RPCAP: RNA intermediate subunit, common to all	E[EDTD]P[TKI]	23					0.004	
protein_40_YOR113W	2	protein: YOR137W	S[SVWV]P	23	G[YKQ]F	LIC_SH2_STAT6			0.004	
protein_40_YOR113W	2	autosome kinase required for signal trans	S[VLMQ]	23	R.L.				0.004	
protein_40_YOR113W	2	autosome kinase required for signal trans	V[VHLA]	23	I[ST]D				0.004	
protein_40_YOR113W	2	lipid metabolism	E..[EOMIE]	23	F..F.				0.004	
protein_40_YOR113W	2	generation of precursor metabolites and energy	QSYTNM[JLNT]	23	RE..E	Iron binding motif in ferritin L-			0.004	
protein_40_YOR139W	2	secretion	NN[LTD]	23					0.004	
protein_40_YOR139W	2	cellular macromolecule metabolism	N..[T]MWJC	23					0.004	
protein_40_YOR139W	2	biogenesis	D..[EDTD]	23					0.004	
protein_40_YOR139W	2	RPRP: Protein required for signal trans	[LAVI]T[S]HY	23					0.004	
protein_40_YOR139W	2	RPCAP: RNA intermediate subunit, common to all	E[EDTD]P[TKI]	23					0.004	
protein_40_YOR139W	2	protein: YOR137W	S[SVWV]P	23	G[YKQ]F	LIC_SH2_STAT6			0.004	
protein_40_YOR139W	2	autosome kinase required for signal trans	S[VLMQ]	23	R.L.				0.004	
protein_40_YOR139W	2	autosome kinase required for signal trans	V[VHLA]	23	I[ST]D				0.004	
protein_40_YOR139W	2	lipid metabolism	E..[EOMIE]	23	F..F.				0.004	
protein_40_YOR139W	2	generation of precursor metabolites and energy	QSYTNM[JLNT]	23	RE..E	Iron binding motif in ferritin L-			0.004	
protein_40_YOR242W	2	secretion	NN[LTD]	23					0.004	
protein_40_YOR242W	2	cellular macromolecule metabolism	N..[T]MWJC	23					0.004	
protein_40_YOR242W	2	biogenesis	D..[EDTD]	23					0.004	
protein_40_YOR249W	2	secretion	[LAVI]T[S]HY	23					0.004	
protein_40_YOR249W	2	cellular macromolecule metabolism	E[EDTD]P[TKI]	23					0.004	
protein_40_YOR249W	2	protein: YOR137W	S[SVWV]P	23	G[YKQ]F	LIC_SH2_STAT6			0.004	
protein_40_YOR249W	2	autosome kinase required for signal trans	S[VLMQ]	23	R.L.				0.004	
protein_40_YOR249W	2	autosome kinase required for signal trans	V[VHLA]	23	I[ST]D				0.004	
protein_40_YOR249W	2	lipid metabolism	E..[EOMIE]	23	F..F.				0.004	
protein_40_YOR249W	2	generation of precursor metabolites and energy	QSYTNM[JLNT]	23	RE..E	Iron binding motif in ferritin L-			0.004	
protein_40_YOR168W	2	secretion	NN[LTD]	23					0.004	
protein_40_YOR168W	2	cellular macromolecule metabolism	N..[T]MWJC	23					0.004	
protein_40_YOR168W	2	biogenesis	D..[EDTD]	23					0.004	
protein_40_YOR168W	2	RPRP: Component of the snRNP complex	[LAVI]T[S]HY	23					0.004	
protein_40_YOR168W	2	RPCAP: RNA intermediate subunit, common to all	E[EDTD]P[TKI]	23					0.004	
protein_40_YOR168W	2	protein: YOR137W	S[SVWV]P	23	G[YKQ]F	LIC_SH2_STAT6			0.004	
protein_40_YOR168W	2	autosome kinase required for signal trans	S[VLMQ]	23	R.L.				0.004	
protein_40_YOR168W	2	autosome kinase required for signal trans	V[VHLA]	23	I[ST]D				0.004	
protein_40_YOR168W	2	lipid metabolism	E..[EOMIE]	23	F..F.				0.004	
protein_40_YOR168W	2	generation of precursor metabolites and energy	QSYTNM[JLNT]	23	RE..E	Iron binding motif in ferritin L-			0.004	
protein_40_YLR165C	2	secretion	NN[LTD]	23					0.004	
protein_40_YHR140W	2	cellular macromolecule metabolism	N..[T]MWJC	23					0.004	
protein_40_YHR140W	2	biogenesis	D..[EDTD]	23					0.004	
protein_40_YHR140W	2	RPRP: Component of the U4-U6 snRNP complex	[LAVI]T[S]HY	23					0.004	
protein_40_YHR140W	2	RPCAP: RNA intermediate subunit, common to all	E[EDTD]P[TKI]	23					0.004	
protein_40_YHR140W	2	protein: YOR137W	S[SVWV]P	23	G[YKQ]F	LIC_SH2_STAT6			0.004	
protein_40_YHR140W	2	autosome kinase required for signal trans	S[VLMQ]	23	R.L.				0.004	
protein_40_YHR140W	2	autosome kinase required for signal trans	V[VHLA]	23	I[ST]D				0.004	
protein_40_YHR140W	2	lipid metabolism	E..[EOMIE]	23	F..F.				0.004	
protein_40_YLR075W	2	secretion	NN[LTD]	23					0.004	
protein_40_YLR075W	2	cellular macromolecule metabolism	N..[T]MWJC	23					0.004	
protein_40_YLR075W	2	biogenesis	D..[EDTD]	23					0.004	
protein_40_YLR075W	2	RPRP: Component of the U4-U6 snRNP complex	[LAVI]T[S]HY	23					0.004	
protein_40_YLR075W	2	RPCAP: RNA intermediate subunit, common to all	E[EDTD]P[TKI]	23					0.004	
protein_40_YLR075W	2	protein: YOR137W	S[SVWV]P	23	G[YKQ]F	LIC_SH2_STAT6			0.004	
protein_40_YLR075W	2	autosome kinase required for signal trans	S[VLMQ]	23	R.L.				0.004	
protein_40_YLR075W	2	autosome kinase required for signal trans	V[VHLA]	23	I[ST]D				0.004	
protein_40_YLR075W	2	lipid metabolism	E..[EOMIE]	23	F..F.				0.004	
protein_40_YLR075W	2	generation of precursor metabolites and energy	QSYTNM[JLNT]	23	RE..E	Iron binding motif in ferritin L-			0.004	
protein_40_YGL104C	2	secretion	NN[LTD]	23					0.004	
protein_40_YGL104C	2	cellular macromolecule metabolism	N..[T]MWJC	23					0.004	
protein_40_YGL104C	2	biogenesis	D..[EDTD]	23					0.004	
protein_40_YGL104C	2	RPRP: Component of the U4-U6 snRNP complex	[LAVI]T[S]HY	23					0.004	
protein_40_YGL104C	2	RPCAP: RNA intermediate subunit, common to all	E[EDTD]P[TKI]	23					0.004	
protein_40_YGL104C	2	protein: YOR137W	S[SVWV]P	23	G[YKQ]F	LIC_SH2_STAT6			0.004	
protein_40_YGL104C	2	autosome kinase required for signal trans	S[VLMQ]	23	R.L.				0.004	
protein_40_YGL104C	2	autosome kinase required for signal trans	V[VHLA]	23	I[ST]D				0.004	
protein_40_YGL104C	2	lipid metabolism	E..[EOMIE]	23	F..F.				0.004	
protein_40_YGL104C	2	generation of precursor metabolites and energy	QSYTNM[JLNT]	23	RE..E	Iron binding motif in ferritin L-			0.004	
protein_40_YGL178C	2	secretion	NN[LTD]	23					0.004	
protein_40_YGL178C	2	cellular macromolecule metabolism	N..[T]MWJC	23					0.004	
protein_40_YGL178C	2	biogenesis	D..[EDTD]	23					0.004	
protein_40_YGL178C	2	RPRP: Component of the U4-U6 snRNP complex	[LAVI]T[S]HY	23					0.004	
protein_40_YGL178C	2	RPCAP: RNA intermediate subunit, common to all	E[EDTD]P[TKI]	23					0.004	
protein_40_YGL178C	2	protein: YOR137W	S[SVWV]P	23</td						

protein_40_YDR448W	2 ADA2: Transcriptional coactivator, component t	E[FI]N[QLN]QE	23	VEID	Protease Caspase 6 -stringe	SAGA complex (1e-17)	0.005
protein_40_YDR394W	2 RTPI3: One of six ATPasases of the 19S regul	[DG]V[D]IEVR	23	Y[DE]J[N]IVF	SH2 ligand for SYK-C (Tyr m	proteasome complex (sensu Eukaryota) (0.001)	0.005
protein_40_YDR394W	2 RTPI3: One of six ATPasases of the 19S regul	LI[F]Y ERDIN	23	Y[DE]J[N]IVF	SH2 ligand for SYK-C (Tyr m	microtubule nucleation (1e-24)	0.005
protein_40_YDR394W	2 RVS1: Adenylate cyclase, component of the	[D]G[V]D[G]AW	23	EEEIYEEIE	cFPPS/FES kinase phosphor	nuclear lumen (0.01)	0.004
protein_40_YDR394W	2 S10P: Serine/threonine protein kinase (S10P)	L[NE]P[Q]	23	[PRIS..DADW]		translation (1e-05)	0.004
protein_40_YDR174W	2 HMO1: Chaperone associated with high mobility er	V..[VK]QD	23	I[KR]R	CLV_PCSK_XE2_1	ribonucleoprotein complex (0.001)	0.004
protein_40_YDR025W	2 RPLAB: Protein component of the large (60S)	K[ND]K[J]KVVR	23	S..D	Pyruvate dehydrogenase kin	(RNA processing (1e-07)	0.005
protein_40_YDL213C	2 NOP5: Putative RNA-binding protein implicat	KA[L]R[C]JLNL	23	F.[D]E[IM]		nucleolus (1e-10)	0.005
protein_40_YDL213C	2 NOP5: Putative RNA-binding protein implicat	P[Q]P201: RNA polymerase II largest subunit I	23	F.E	DNA binding motif in MutS	transcription from RNA polymerase II promoter (	0.005
protein_40_YDL055C	2 PSA1: GDP-mannose pyrophosphorylase (m	[EQD][K]QH[J]TT	23	YTT [LM]	Svk N-terminal SH2 domain I	proteasome regulatory particle, base subcomple	0.005
protein_40_YDL055C	2 PSA1: GDP-mannose pyrophosphorylase (m	A[D]..SA[W]	23			nuclear mRNA splicing, via spliceosome (1e-09)	0.005
protein_40_YDL047W	2 S14T: Type 2A related serine-threonine phos	G[T]E[A]R[KS]	23			actin cytoskeleton organization and biogenesis (i	0.004
protein_40_YDL047W	2 ARP2: Essential component of the Arp2/3 co	K[Q]L[E]A	23	[PSI]DENS1..Y[PF] RIBOSOMAL LG_1 PATTER		snoRNA binding (1e-05)	0.004
protein_40_YDL047W	2 ARP2: Essential component of the Arp2/3 co	S[S]T	23	S[S]T	M2C1-BRCT domain bindin	actin cytoskeleton organization and biogenesis (i	0.004
protein_40_YDL047W	2 ARP2: Essential component of the Arp2/3 co	[G]A[H]F LWII	23	E[IV VIW]FY WI	E11 motif binds to egruviro1	microtubule nucleation (1e-24)	0.004
protein_40_YDL015C	2 TSPY1: Tyrosine residue that catalyzes the la	[THQ]NP[ME]M	23	N.P.Y	LIG_PTB..ILG_PTB_1	nucleolus (1e-10)	0.004
protein_40_YDL015C	2 TSPY1: Tyrosine residue that catalyzes the la	[NS]D[E]P	23			translation (1e-05)	0.004
protein_40_YDL014W	2 CSM1: Nuclear protein that forms a comple	V[IO]H D[L]VG	23	Q[MLV]IDG..ID	CLV_TASPASE1	transcription from RNA polymerase II promoter (	0.004
protein_40_YCR086W	2 CSM1: Nuclear protein that forms a comple	S[D]K[J]AEW F	23			proteasome regulatory particle, base subcomple	0.004
protein_40_YCL059C	2 KRR1: Essential nuclear protein required	V[EN]T Q SQA	23	[ST]Q	ATM kinase phosphorylation	nuclear mRNA splicing, via spliceosome (1e-09)	0.005
protein_40_YBR189W	2 RPSS1: Protein component of the small (40S)	R[A]E[D]N LAT	23			actin cytoskeleton organization and biogenesis (i	0.004
protein_40_YBR189W	2 RPSS1: Protein component of the small (40S)	E[D]Q Q[G]KH	23	LFG	Protease Papain substrate, a	snoRNA binding (1e-05)	0.004
protein_40_YBR189W	2 RPSS1: Protein component of the small (40S)	[T]A S F LG	23	S..[ED]	Casein kinase II substrate mi	actin cytoskeleton organization and biogenesis (i	0.004
protein_40_YBR189W	2 RPSS1: Protein component of the small (40S)	K[V]H[A]..KL[F]S	23			mRNA-binding (hnRNP) protein import into nucle	0.005
protein_40_YBR189W	2 RPSS1: Protein component of the small (40S)	[N]E[V]	23			establishment and/or maintenance of chromatin	0.004
protein_40_YBL030C	2 HHT1: One of two identical histone H3 prote	NN..[S]Q[Q]LIS	23			DNA establishment (1e-16)	0.004
protein_40_YBL030C	2 HHT1: One of two identical histone H3 prote	[V]R[P]H TSK	23			chromatin modification (1e-05)	0.004
protein_40_YBL030C	2 HHT2: One of two nearly identical (see also H	D..[Y]VD	23			establishment and/or maintenance of chromatin	0.004
protein_40_YBL030C	2 HHT2: One of two nearly identical (see also H	N..E LPW	23			chromatin assembly or disassembly (1e-05)	0.004
protein_40_YBL020W	2 RFB1: Subunit of heteromeric Replication F	I[G]D HE	23			chromosome organization and biogenesis (sensi	0.004
protein_40_YAR007C	2 RFA1: Subunit of heteromeric Replication F	Q[L]T VIA	23			DNA-dependent DNA replication (1e-05)	0.004
protein_40_YAR007C	2 RFA1: Subunit of heteromeric Replication F	D[Y]D EHW	23			response to DNA damage stimulus (0.001)	0.004
protein_40_YAR007C	2 RFA1: Subunit of heteromeric Replication F	S..[Y NSV]	23	YDE[P]DV	SH2 ligand for Nck1 and Nck	mRNA processing (1e-04)	0.004
protein_40_YAL032C	2 RP48: Protein required for pre-mRNA splic	L...[Q]LE	23			clathrin-coated vesicle (1e-30)	0.004
oschea_Golgi_to_vacuole	2 oschea_Golgi_to_vacuole	T[NIH]H DGP T	23	L... [L]...L	Correceptor nuclear box mol	Golgi apparatus (1e-13)	0.004
oschea_Golgi_to_vacuole	2 oschea_Golgi_to_vacuole	A..P V FT	23	I Y A P	Cdk4 WD40 domain binding	bud (1e-17)	0.004
oschea_Golgi_to_vacuole	2 oschea_Golgi_to_vacuole	R U S H P	23	I R L S TRRR	Nek 2 kinase substrate motif	bud (1e-21)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	R A F V H W L R	23	I Y V AC R V A	RECOMBINASE 1 PATT E	microtubule cytoskeleton (1e-43)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	Q[A]V[M]..Q A CH	23			vesicle-mediated transport (0.001)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	P..E D G	23	[GD]I FWY W G  CAP_GLY_1 PATTERN		chromosome organization and biogenesis (sensi	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	G N F K N	23			chromosome organization and biogenesis (sensi	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	V..[V]K D S	23	[S]T Q	ATM kinase phosphorylation	DNA metabolism (1e-04)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	S..[S]K M S	23	S..S	Casien kinase I phosphoryl	transcriptional regulator activity (1e-10)	0.005
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	Q G N L R	23	G K R J K R	Amidation after cleavage afe	small nucleolar ribonucleoprotein complex (1e-21)	0.005
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	D[A]S P Q	23	[D E]D E P F G	GoLo moff, a G alpha bin	small nucleolar ribonucleoprotein complex (1e-11)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	[G Y K W R L R	23	P PHD SAIS TF LYS HYDROXYYL	PATT E	protein kinase activity (1e-04)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	K M K F N	23	R P H D I K D N	DNA LIGASE A1 PATTERN	nucleolus (1e-10)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J	23	[EDQ H K D N	DNA LIGASE A1 PATTERN	nucleolar snRNP, via spliceosome (1e-20)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I R L S TRRR	Nek 2 kinase substrate motif	snRNP binding (1e-20)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	protein binding (1e-17)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I U C H		ubiquitin-specific protease activity (0.01)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I F B O X		ubiquitin ligase complex (0.001)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	reproduction (1e-75)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	cellular localization (1e-21)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	chromosome organization and biogenesis (sensi	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	protein kinase activity (0.001)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	cytoskeleton organization and biogenesis (1e-10)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	cytoskeleton organization and biogenesis (1e-10)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	small nucleolar ribonucleoprotein complex (1e-11)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	small nucleolar ribonucleoprotein complex (1e-11)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	Golgi apparatus (1e-12)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	cytoskeleton organization and biogenesis (1e-25)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	small nucleolar ribonucleoprotein complex (1e-2)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	cytoskeleton organization and biogenesis (1e-25)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	actin cytoskeleton organization and biogenesis (	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	actin cytoskeleton organization and biogenesis (	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	phosphotransferase activity, alcohol group as ac	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	carboxylic acid metabolism (1e-04)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	protein kinase activity (0.001)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	protein kinase activity (0.001)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	RNA processing (1e-06)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	cytoskeleton organization and biogenesis (1e-13)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	small nucleolar ribonucleoprotein complex (1e-11)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	Golgi apparatus (1e-12)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	cytoskeleton organization and biogenesis (1e-13)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	small nucleolar ribonucleoprotein complex (1e-11)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I L C V C E	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrysugars_Cytoplasmic_dots	I R D J P	23	I P T L C P	F-box	snRNP binding (1e-27)	0.004
oschea_Golgi_to_vacuole	2 matrys						







protein_40_YML007W	2	YAP1: Basic leucine zipper (bZIP) transcriptic	T[EVG]M	20	HEAT	1.E-03	-0.7	nucleoplasm part (1e-09)	Y	0.004	10		
protein_40_YFL037W	2	TUB2: Beta-tubulin; associates with alpha-tub	O.[QIGEP]	20	IBN_N	1.E-03	0.6			0.004	8		
yeast-259_GO-004438	2	EMG1: Protein required for the maturation of	T[AMP][EGC]W	20	F-box	1.E-03	-0.5	cellular catabolism (1e-19)	Y	0.004	10		
protein_40_YMR304W	2	UBP10: Ubiquitin-specific protease that may i	O.G[NHR]	20	WD40	1.E-03	-0.5	rRNA processing (1e-20)	Y	0.004	9		
protein_40_YPR144C	2	NOC4: Nucleolar protein, forms a complex wi	VIKYF E	20	KEN	1.E-02	-0.3	protein kinase activity (0.01)	Y	0.004	7		
protein_40_YPL146C	2	NOP53: Nucleolar protein; involved in biogen	E.[QIA]	20	LIG_APPC_KENbox_2	Pkinase	1.E-05	0	snoRNA binding (1e-31)	Y	0.004	7	
protein_40_YMR117C	2	SPC24: Component of the evolutionarily cont	K.[SGE]E	20	AEVD	Protease Caspase 10	Y	0	cytoplasm organization and biogenesis (1e-08)	Y	0.004	8	
protein_40_YMR125W	2	STO1: Large subunit of the nuclear mRNA ca	K.[DQJ]	20	K-[ST]	PKA kinase substrate motif	Y	0	chromosome segregation (1e-04)	Y	0.004	10	
protein_40_YLR186W	2	EMG1: Protein required for the maturation of	K.M.[EPH]	20	SMC_N	1.E-02	0	nucleic acid binding (1e-06)	Y	0.004	8		
protein_40_YKL101W	2	HSL1: Nim1p-related protein kinase that regu	G.[DRP]G	20	RRM_1	1.E-02	0.2	rRNA processing (1e-17)	Y	0.004	9		
protein_40_YGL029W	2	ARC1: Protein that binds RNA and methionyl/	G.G.[DMC]	20	DnaC	1.E-03	0.6	protein kinase activity (1e-07)	Y	0.004	10		
protein_40_YER112W	2	2: Lsm (Like Sm) protein; part of hetero-	D.[GAAT]	20	D.G.	1.E-06	0.6	small nuclear ribonucleoprotein complex (1e-18)	Y	0.004	7		
protein_40_YDL153C	2	SAS10: Component of the small (ribosomal) :	R.[QPSI]	20	[K[R].J-[ST]]	p70S6k phosphorylation site	Y	0	protein kinase activity (1e-18)	Y	0.004	8	
oshea_Total_-	2	integral to membrane	K.E.[TDM]	20	[EDAY]	Abl kinase substrate motif	Y	0	protein kinase activity (1e-18)	Y	0.004	8	
oshea_Total_-	2	2: oxidoreductase activity	K.V.[VAC]	20	R.GSF	F12Kdelta kinase phosphovri:	Y	0	oxidoreductase activity (1e-09)	Y	0.004	8	
oshea_Total_-	2	2: oseha vacuole	G.FITAY	20	KGSST	elf4f motif phosphorylation m	Y	0	storage vacuole (1e-11)	Y	0.004	9	
oshea_Total_-	2	2: oseha vacuole	G.R.[VON]	20	WD40	1.E-03	1.6	protein kinase activity (0.01)	Y	0.004	10		
protein_40_YKR048C	2	NOC4: Nucleolar protein, forms a complex wi	W[DQI].[GMQD]	20	[EDY]	TC-PTP phosphatase substr	Y	0	small nuclear ribonucleoprotein complex (1e-1-	Y	0.004	10	
protein_40_YPR144C	2	2: cellular localization	[IRKJA].[PKQG]	20	Ras	1.E-12	2	cellular localization (1e-13)	Y	0.005	7		
yeast-548_GO-0051641	2	2: cellular localization	A.[EVNC]	20	Pinase	1.E-18	2.1	protein kinase activity (1e-17)	Y	0.004	7		
protein_40_YDL153C	2	SAS10: Component of the small (ribosomal) :	A.HNHC].[TEG]	20	PT.[DII]	FHA binding motif	Y	0	protein kinase activity (1e-17)	Y	0.007	10	
oshea_Totale_-	2	8: oseha_Total_-	Y[VLTFCIC]	20	LIG_SH2_STAT5	SRP1_TIP1	1.E-37	2.2	SRP1_TIP1	Y	0.007	10	
oshea_Totale_-	2	8: oseha_Total_-	VE..VYFGCIVRC	20	G.G..K	Sulfonate donor binding site	Y	0	SRP1_TIP1	Y	0.007	10	
oshea_Totale_-	2	8: oseha_Total_-	D[EPL].NLNFV	20	P.L	Motif in Fos for protein inst	Y	0	SRP1_TIP1	Y	0.008	10	
oshea_Totale_-	2	8: oseha_Total_-	FIO(KF).HPCKT	20	P.L.	Motif in Fos for protein inst	Y	0	SRP1_TIP1	Y	0.007	10	
oshea_Totale_-	2	8: oseha_Total_-	HL..[DEA]YTRYN	20	[EDY]	TC-PTP phosphatase substr	Y	0	SRP1_TIP1	Y	0.008	10	
protein_40_YPL093W	2	NOG1: Putative GTPase that associates with	[IRKJA].[PKQG]	20	DEAD	1.E-05	2.8	ribosome biogenesis (1e-05)	Y	0.004	7		
protein_40_YNL272C	2	SEC22: Guanyl-nucleotide exchange factor for	G..[H]RVA	20	Pinase	1.E-15	2.9	protein kinase activity (1e-15)	Y	0.004	10		
protein_40_YER186W	2	UBP10: Ubiquitin-specific protease that deub	H..[GILH]	20	HE.GH	Protease AAA proteases - cu	Y	0	protein kinase activity (1e-16)	Y	0.004	9	
protein_40_YDL153C	2	SAS10: Component of the small (ribosomal) :	G..[K]LVK	20	G..G.K	Sulfonate donor binding site	Y	0	protein kinase activity (1e-16)	Y	0.004	9	
oshea_Totale_-	2	8: oseha_Total_-	[ITFY].[PYCQW]	20	P.L.	cFGR and Csk kinase phase	Y	0	protein kinase activity (1e-15)	Y	0.004	9	
protein_40_YML046C	2	2: TEF1: GTP-binding protein of the rns superfi	[KGPIK].[L]	20	P.WYVII [STR SRP1_TIP1] PATTERN	SRP1_TIP1	1.E-45	3.1	protein kinase activity (1e-15)	Y	0.008	10	
oshea_Totale_-	2	8: oseha_Total_-	Y[WL].[RPLR]L	20	DEAD	1.E-05	3.2	macromolecule biosynthetic process (1e-06)	Y	0.004	9		
protein_40_YPL093W	2	NOG1: Putative GTPase that associates with	[ICLVK].[FKA]	20	SRP1_TIP1	1.E-53	3.3	protein binding (1e-12)	Y	0.007	10		
protein_40_YHR030C	2	SEC22: Guanyl-nucleotide exchange factor for	D[TFG]	20	DEAD	1.E-03	3.4	chromosome organization and biogenesis (1e-1t)	Y	0.005	8		
protein_40_YER080C	2	RPF2: Essential protein involved in the proce	H..[GKHK]	20	SRP1_TIP1	1.E-37	3.4	response to stress (1e-15)	Y	0.004	7		
protein_40_YER080C	2	2: macromolecule biosynthesis	Y[QLN].[R]RH	20	SH2 ligand for PLCgamma1	SRP1_TIP1	1.E-37	3.4	response to stress (1e-16)	Y	0.004	9	
protein_40_YER080C	2	2: protein binding	[TC]K[SWP]	20	KSPP	ERK1,ERK2,SAKP,CDK5 :	SRP1_TIP1	1.E-37	3.4	multicellular organismal development (1e-29)	Y	0.004	9
protein_40_YER080C	2	2: cellular catabolism	R[PW].[RLRQ]	20	Cdk5	CDK5	SRP1_TIP1	1.E-37	3.4	cellular catabolism (1e-28)	Y	0.005	7
protein_40_YER080C	2	2: cellular catabolism	GQ[Q]Q	20	GGQ	N-methylation motif in E. coli	SRP1_TIP1	1.E-37	3.4	cellular catabolism (1e-24)	Y	0.005	10
protein_40_YER080C	2	2: cellular catabolism	T[TFV].[J]	20	YINNAV[TYVNI]	Bidentate motif of the env-se	SRP1_TIP1	1.E-37	3.4	macromolecule biosynthetic process (1e-06)	Y	0.005	8
protein_40_YER080C	2	2: macromolecule catabolism	[IQ]SQG [QVM]	20	G..M..H	SH2 ligand for PLCgamma1	SRP1_TIP1	1.E-37	3.4	protein binding (1e-12)	Y	0.005	8
protein_40_YER080C	2	2: reproduction	[KML].[F]RFA	20	L.R..[ST]	RSK phosphorylation site	SRP1_TIP1	1.E-37	3.4	chromosome organization and biogenesis (1e-1t)	Y	0.005	8
protein_40_YER080C	2	2: response to stress	R[PW].[RLRQ]	20	LTP	RAF1 kinase substrate motif	SRP1_TIP1	1.E-37	3.4	response to stress (1e-16)	Y	0.004	7
protein_40_YER080C	2	2: response to stress	G..[Q]RIVM	20	F..[R].[RK]	PPI binding sites	SRP1_TIP1	1.E-37	3.4	response to stress (1e-15)	Y	0.004	9
protein_40_YER080C	2	2: response to stress	[ETD].[QMWK]	20	Y[L][I]	SH2 ligand for PLCgamma1	SRP1_TIP1	1.E-37	3.4	multicellular organismal development (1e-29)	Y	0.004	9
protein_40_YER080C	2	2: response to stress	Y[DCM]	20	Y[DY]	cCbl and Cbl-b TK domain I	SRP1_TIP1	1.E-37	3.4	cellular catabolism (1e-34)	Y	0.005	7
protein_40_YER080C	2	2: response to stress	G..[T]LK].[AEWT]	20	G..[R].[RK]	Grb2 SH2 domain binding mi	SRP1_TIP1	1.E-37	3.4	cellular catabolism (1e-28)	Y	0.005	7
protein_40_YER080C	2	2: response to stress	[KFR].[ASC]GK	20	Y[DY]	cCbl and Cbl-b TK domain I	SRP1_TIP1	1.E-37	3.4	cellular catabolism (1e-24)	Y	0.005	10
protein_40_YER080C	2	2: reproduction	E[AMH].[S]IR	20	F..[R].[RK]	PPI binding sites	SRP1_TIP1	1.E-37	3.4	macromolecule biosynthetic process (1e-06)	Y	0.005	8
protein_40_YER080C	2	2: reproduction	E[AMH].[S]IR	20	Y[L][I]	SH2 ligand for PLCgamma1	SRP1_TIP1	1.E-37	3.4	protein binding (1e-12)	Y	0.005	8
protein_40_YER080C	2	2: reproduction	N..[DMS]	20	T..[L..L]	FHA2 binding motif, Thr mutu	SRP1_TIP1	1.E-37	3.4	chromosome organization and biogenesis (1e-1t)	Y	0.005	8
protein_40_YER080C	2	2: reproduction	N..[DMS]	20	DGS..S	WD40 binding motif, Ser resi	SRP1_TIP1	1.E-37	3.4	response to stress (1e-16)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	[DEIMVYH].[H]	20	Y[IYVNI][FLIV]	Grb2 SH2 domain binding mi	SRP1_TIP1	1.E-37	3.4	response to stress (1e-15)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	[SGC]DIEHC R	20	DYR	cCbl and Cbl-b TK domain I	SRP1_TIP1	1.E-37	3.4	ribosome biogenesis (0.001)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	M[SN]F	20	LLG	Receptor recycling motif	SRP1_TIP1	1.E-37	3.4	spliceosome (1e-15)	Y	0.004	9
protein_40_YER080C	2	2: reproduction	M[SN]F	20	G[S]AJLNK	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	ribosome biogenesis (1e-18)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	S..[M]N	20	LLG	Beta2-Integrin binding motif	SRP1_TIP1	1.E-37	3.4	RNA polymerase II transcription mediator activity	Y	0.004	9
protein_40_YER080C	2	2: reproduction	[L]NKHII[H]T	20	G[S]AJLNK	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	cytoskeleton organization and biogenesis (1e-16)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	G..[Q]GY	20	GIVTFWJE	DIDEI.G..[VII]T DNA polymerase interaction	SRP1_TIP1	1.E-37	3.4	general RNA polymerase II transcription factor a	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nuclear chromatin (1e-05)	Y	0.004	8
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	endoplasmic reticulum (0.01)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	plasma membrane (0.01)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-16)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	plasma membrane (1e-11)	Y	0.004	8
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nuclear mRNA splicing, via spliceosome (1e-25)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_TIP1	1.E-37	3.4	nucleolus (1e-13)	Y	0.004	7
protein_40_YER080C	2	2: reproduction	A.[EVNC]	20	G..[WVJ]	GDP-mannose binding motif	SRP1_T						

protein_40_YDR004W	2	RPS15: Protein component of the small (40S	[EF1D VAC]	20	P.V.L	Shadow-Chrom domain bin	small nuclear ribonucleoprotein complex (1e-1'	0.004	10	
protein_40_YDL219C	2	RP19: Putative RNA-binding protein implied	[PKIVN]	20	[FVIVW]	EH(D) EF hand domain bin1	nucleolus (1e-13)	0.004	8	
protein_40_YDL229C	2	RP20: Protein implied to have RNA-binding	[MECVIVW]	20	[NTJKD]	Motif for binding guanine nuc	spliceosome (1e-12)	0.003	7	
protein_40_YDL185W	2	TFP1: Vacuolar ATPase V1 domain subunit A	[K.DIFIP]	20	[AGJ R]	Protease matriptase proteas	hydrogen ion homeostasis (1e-05)	0.004	7	
protein_40_YDL185W	2	TFP1: Vacuolar ATPase V1 domain subunit A	S [AQG R]	20			hydrogen ion homeostasis (1e-04)	0.004	8	
protein_40_YDL147W	2	RPL38: Protein component of the large (60S	N..[DGV]	20			proteasome complex (sensu Eukaryota) (1e-10)	0.004	8	
protein_40_YDL055C	2	PSA1: GDP-mannose pyrophosphorylase (m	E..[GLYV]	20	KR	CLV_PCSK_PC1ET2_1	cytosolic ribosome (sensu Eukaryota) (1e-13)	0.004	8	
protein_40_YDL047W	2	SPT4: Type 2A-related serine-threonine phos	N..[SARY]	20			ligase activity (0.01)	Y	0.004	8
protein_40_YCR034W	2	FEN1: Fatty acid elongase, involved in sphing	V..[TVW]	20				Y	0.004	8
protein_40_YBR217W	2	ATG12: Ubiquitin-like modifier, conjugated via	G[VANQ]	20					0.004	8
protein_40_YBR217W	2	CMB1: Calmodulin, C-terminal binding protein that	[EEIYIEE]	20			actin filament binding (0.01)	Y	0.004	10
protein_40_YBR109W	2	CPY1: Putative protein implied to have RNA-binding	C..[V]	20	CPV	Heme binding site in mitoch	transporter activity (1e-07)	0.004	7	
protein_40_YBR017C	2	KAP104: Transferrin, cytosolic-binding protein b	[TOKIG LSIF]	20	M...L	PMSA motif for internalizat	tRNA export from nucleus (1e-07)	Y	0.004	9
protein_40_YLR009C	2	HIF1: One of two identical histone H4 protein	M..[KAMJ]	20					0.004	8
protein_40_YBL003C	2	H2A: One of two nearly identical (see also H	Q..[DMJ]	20	P.Q.D	LIG_TRAF2_2		0.004	8	
protein_40_YBL003C	2	H2A: One of two nearly identical (see also H	M..[ELHD]	20				0.004	9	
protein_40_YBL002W	2	H2B: One of two nearly identical (see HTB1	GT..[PWLI KET]	20				0.004	7	
oshea_vacuole	2	oshea_vacuole	K..[L EDF]	20	LLK1	AP-2 binding motif in CXCR2	transcription, DNA-dependent (0.001)	0.004	8	
oshea_spindle_pole	2	oshea_spindle_pole	K..[CDMKJ]	20	P.[ST]PKKK	Cdc2c protein kinase sub	vacuole (1e-05)	0.004	8	
oshea_bud	2	oshea_bud	RYT [TSN]	20	DRY	Binding motif for interaction c	microtubule cytoskeleton (1e-53)	0.004	9	
oshea_bud	2	oshea_bud	M..[MALS]	20	LMA[EO GLYN]	ENGRAILED PATTERN	site of polarized growth (1e-19)	0.004	8	
oshea_bud	2	oshea_bud	R..[SDF]	20	R.R..[ST]	PQ phosphorylation motif	bud (1e-08)	0.004	7	
oshea_bud	2	oshea_bud	ALI[KRI I FY]	20			bud (0.01)	0.004	7	
oshea_bud	2	oshea_bud	RECA_1 PATTERN				establishment and/or maintenance of chromatin	0.004	7	
oshea_Total	10	Protein abundance, quantified	Zn...clus	1.E-03	0.1					
protein_40_YDR324C	6	Sub-cellular localization, 6 clusters	AA_permease	1.E-02	0.1					
yeast-1939_GO-0003824	8	oshea_Total	SRP1..TIP1	1.E-48	-9.2					
protein_40_YCL059C	2	catalytic activity	WD40	1.E-06	-1.4					
protein_40_YCL059C	2	KRR1: Essential nuclear protein required to	Zn...clus	1.E-05	-1.3					
protein_40_YFR027C	2	DEAEAH: DnaE-like RNA helicase of the D	Helicase_C	1.E-02	-1.2					
protein_40_YFR027C	2	U2AF: U2AF-specific protein that dead	DEB1	1.E-03	-1.1					
protein_40_YLN186W	2	establishment of localization	LSQE	1.E-07	-1.0					
protein_40_YOR016C	2	ERPF4: Protein with similarity to Em2pd4 and	PKinase	1.E-17	-0.9					
yeast-261_GO-0016491	2	oxidoreductase activity	IBN_N	1.E-02	-0.8					
protein_40_YAR019C	2	PAB1: Poly(A) binding protein, part of the 3'-	MFS_1	1.E-02	-0.7					
Oshea_mcl	2	CDC15: Protein kinase of the Mitotic Exit Net	Thioredoxin	1.E-04	-0.6					
protein_40_YOR165W	13	Oshes_mcl	F..[T KFM]	19	RRM_1	AP-2 binding motif in CXCR2	oxidoreductase activity (1e-39)	0.004	9	
protein_40_YOR165W	2	establishment of localization	F..[S PAJ]	19	Pkinase	Cdc2c protein kinase sub	oxidoreductase activity (1e-38)	0.004	8	
protein_40_YLR129W	2	DIF2: Nuclear protein, specifically associate	V /[YF]	19	MFS_1	ATM kinase substrate motif	oxidoreductase activity (1e-37)	0.004	7	
protein_40_YLR129W	2	UTP6: Nuclear protein, component of the sr	RHK_SF	19	Mito_car	ATM kinase substrate motif	oxidoreductase activity (1e-36)	0.004	6	
protein_40_YGR128C	2	DBP9: ATP-dependent RNA helicase of the D	WD40	1.E-07	1		establishment of cellular localization (1e-97)	0.004	7	
protein_40_YGR128C	2	U2AF: U2AF-specific protein required for export o	WD40	1.E-02	0.9		small nuclear ribonucleoprotein complex (1e-1:	0.004	7	
protein_40_YGR128C	2	ribonuclease protein required for export o	Brix	1.E-03	0.8		rRNA binding (1e-27)	0.004	7	
protein_40_YGR128C	2	ribonuclease protein complex	WD40	1.E-02	0.7		small nuclear ribonucleoprotein complex (1e-1:	0.004	7	
protein_40_YGR128C	2	metabolic cycle	WD40	1.E-02	0.6		rRNA binding (1e-26)	0.004	7	
protein_40_YGR128C	2	chromosome organization and biogenesis (se	Y /[Q]	19	PC1	ATM kinase substrate motif	ribonucleoprotein complex (1e-13)	0.005	8	
protein_40_YGR128C	2	chromosome organization and biogenesis (se	R /[DGS]	19	PCI	ATM kinase substrate motif	mitotic cell cycle (1e-20)	0.005	9	
AMR HEIJ LVF	19	Ankyrin G binding motif in Kn	SRP1..TIP1	1.E-02	2		proteasome complex (sensu Eukaryota) (1e-08)	Y	0.004	8
[NDQY..F TART	19	Y..F	SH2 ligand group 3 (HCP-nT	Y	SRP1..TIP1	ATM kinase substrate motif	spliceosome (1e-15)	Y	0.004	7
V /[V]	19	Y..F	DSPc	1.E-03	3		cytoskeleton (1e-15)	Y	0.004	8
L K VLS	19	M..E	PKinase	1.E-08	3.3		reproduction (1e-23)	Y	0.004	8
R /[T G ]	19	SQ TQ	ATM phosphorylation of this i				kinase activity (1e-06)	Y	0.004	7
F /[K V Q ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	translation (1e-07)	Y	0.004	7
E /[D K O P S P ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	DNA metabolism (1e-43)	Y	0.004	9
ESD DOK GPSP	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	chromosome organization and biogenesis (sensi	Y	0.004	9
Y /[Q ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	protein localization (1e-24)	Y	0.004	9
R /[D G S ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	rRNA export from nucleus (1e-13)	Y	0.004	8
AMR HEIJ LVF	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	reproduction (1e-73)	Y	0.004	7
[NDQY..F TART	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	response to chemical stimulus (1e-13)	Y	0.004	7
V /[V ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	protein targeting (1e-35)	Y	0.004	10
L K VLS	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	amine metabolism (1e-28)	Y	0.004	7
R /[T G ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	G1/S transition of mitotic cell cycle (0.001)	Y	0.004	8
F /[Q V K ,ETWM	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	spliceosome (1e-12)	Y	0.004	8
E /[D K O P S P ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	ribosome biogenesis (1e-05)	Y	0.004	7
Y /[Q ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	cytoplasm organization and biogenesis (1e-11)	Y	0.004	9
R /[D G S ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	cytoplasm organization and biogenesis (1e-15)	Y	0.004	8
AMR HEIJ LVF	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	protein localization (1e-24)	Y	0.004	9
[NDQY..F TART	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	rRNA export from nucleus (1e-13)	Y	0.004	8
V /[V ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	reproduction (1e-73)	Y	0.004	7
L K VLS	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	response to chemical stimulus (1e-13)	Y	0.004	7
R /[T G ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	protein targeting (1e-35)	Y	0.004	10
F /[Q V K ,ETWM	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	amine metabolism (1e-28)	Y	0.004	7
E /[D K O P S P ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	G1/S transition of mitotic cell cycle (0.001)	Y	0.004	8
Y /[Q ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	spliceosome (1e-12)	Y	0.004	8
R /[D G S ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	ribosome biogenesis (1e-05)	Y	0.004	7
AMR HEIJ LVF	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	cytoplasm organization and biogenesis (1e-11)	Y	0.004	9
[NDQY..F TART	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	protein localization (1e-24)	Y	0.004	9
V /[V ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	rRNA export from nucleus (1e-13)	Y	0.004	8
L K VLS	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	reproduction (1e-73)	Y	0.004	7
R /[T G ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	response to chemical stimulus (1e-13)	Y	0.004	7
F /[Q V K ,ETWM	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	protein targeting (1e-35)	Y	0.004	10
E /[D K O P S P ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	amine metabolism (1e-28)	Y	0.004	7
Y /[Q ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	G1/S transition of mitotic cell cycle (0.001)	Y	0.004	8
R /[D G S ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	spliceosome (1e-12)	Y	0.004	8
AMR HEIJ LVF	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	ribosome biogenesis (1e-05)	Y	0.004	7
[NDQY..F TART	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	cytoplasm organization and biogenesis (1e-11)	Y	0.004	9
V /[V ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	protein localization (1e-24)	Y	0.004	9
L K VLS	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	rRNA export from nucleus (1e-13)	Y	0.004	8
R /[T G ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	reproduction (1e-73)	Y	0.004	7
F /[Q V K ,ETWM	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	response to chemical stimulus (1e-13)	Y	0.004	7
E /[D K O P S P ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	protein targeting (1e-35)	Y	0.004	10
Y /[Q ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	amine metabolism (1e-28)	Y	0.004	7
R /[D G S ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	G1/S transition of mitotic cell cycle (0.001)	Y	0.004	8
AMR HEIJ LVF	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	spliceosome (1e-12)	Y	0.004	8
[NDQY..F TART	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	ribosome biogenesis (1e-05)	Y	0.004	7
V /[V ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	cytoplasm organization and biogenesis (1e-11)	Y	0.004	9
L K VLS	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	protein localization (1e-24)	Y	0.004	9
R /[T G ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	rRNA export from nucleus (1e-13)	Y	0.004	8
F /[Q V K ,ETWM	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	reproduction (1e-73)	Y	0.004	7
E /[D K O P S P ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	response to chemical stimulus (1e-13)	Y	0.004	7
Y /[Q ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40	ATM kinase substrate motif	protein targeting (1e-35)	Y	0.004	10
R /[D G S ]	19	Y /[V V N L V ]	Y /[V V N L V ]	19	WD40					

protein_40_YMR304W	2	UBP15. Ubiquitin-specific protease that may target proteins.	L...[NWKIP]	18	[R...LPLP...P	SH3 binding motif for Shp1p	PKinase	1.E-05	1.5	protein kinase activity (1e-05)	
protein_40_YER125W	2	Usp15. Ubiquitin-specific ligase involved in ubiquitination.	R...[KR]KHP	18	R...PLPLPLP...P	SH3 binding motif for Lyn	PKinase	1.E-05	2	protein kinase activity (1e-04)	
oschea_Total	8	oschea_Total_	T[EKT]...[PVRJC]	18	[FQDQD...P]	[IFY][LIVMKJ]...H CYTOCHROME_B5_1 PATT	SRP1_TIP1	1.E-33	2.1		
oschea_Total	8	oschea_Total_	F[NK]GAKD[DF]	18	[LSK]G[D]G[H]R		SRP1_TIP1	1.E-37	2.3		
oschea_Total	8	oschea_Total_	H[RCID]	18	S.D	CAMKII phosphorylation site	SRP1_TIP1	1.E-41	2.3		
protein_40_YER210W	2	RPB10. RNA polymerase subunit ABCC10-acetyltransferase.	H[GGMCR]	18	[TTS]H.J.D	Zinc binding motif conserves	SRP1_TIP1	1.E-39	2.6		
protein_40_YOR063W	2	RPL3. Protein component of the large (60S) ribosomal subunit.	D[NQR]QV	18	[AG]R	Protease matriptase protease	Helicase_C	1.E-07	5.6		
yeast-544_GO-0016070	2	RNA metabolism	Q[RIV]IV	18							
yeast-371_GO-0009056	2	catalysis	Q[RIV]IV	18							
yeast-358_GO-0044248	2	cellular catalysis	ER...[GYN VM D]	18	[SP]T[SPQ]	GIFLIPGER...G_LIG_IBS_1LIG_IBS_1	Y				
yeast-320_GO-0003635	2	regulation of transcription, DNA-dependent	P...[RAWR]	18	[K R]R	SP ERK1/ERK2 Kinase substr	ERK1	1.E-03	2.3		
yeast-357_Go-0003635	35	yeast_clustered_interaction_both	S...SS	18	[Q]P[IVN]	CLV_PCSK_KEX2_1					
protein_40_YPL203W	2	TPK2. cAMP-dependent protein kinase catalytic subunit.	K[LQG]R...[IQTG]	18	[Q]P[IVN]						
protein_40_YNL110C	2	S625. Cyclic AMP-dependent protein kinase catalytic subunit.	T...[KHY]P	18	[IDE]AT...[IDE]P	Ph4/P1P2 binding motif in epi-					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L[PAA]V	18	[LPKY]	LW motif (non-conventional					
protein_40_YNL110C	2	S625. Cyclic AMP-dependent protein kinase catalytic subunit.	H[YV]IV	18	[EDY]V	TC-PTP phosphatase substr					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R[P]N[EW]	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A...[QNKQ]	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[VSC SI OMF ]	18	R.R.SI	PKA kinase phosphorylation					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[KHY H DKVY ]	18	[EDY]Y	TC-PTP phosphatase substr					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[ER QKS KMAJ ]	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	K...[DYTE]	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	I...[K R]R	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	T[D PHC]	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[KDM J R H J ]	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	I H AV	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	Q Y F P D	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	H H K K M	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G N G Q Y	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L R Y G E	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	I J AR L	18	L.R...[ST]	RSK phosphorylation site					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A Q D Q I	18	R RL STRRR	Nek 2 kinase substrate motif					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	S D Q H I	18	W AQ K W	Motif in Cet1 RNA triphosphat					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	V Y V G M	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	I Y Q AT	18	H A V D I	N-Cadherin ligand					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	D H D P M	18	I V Y L Y L T Y A	SH2P2 N-terminal SH2 domai					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	K S W M D	18	K...[ST]	PKA kinase substrate motif					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	N A P W M	18	[DN]Y...[DE]	cCB1 TBK domain binding mo	Y				
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	F D Q L Y	18	NPF D	Clathrin endocytosis signal fc					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[GM G D V ]	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	K V P Y	18	V P	Interleukin converting enzym					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G K A K	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L A P I	18							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[S K K... SL YA	18	K...[ST]	PKA kinase substrate motif					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G T K S E	18	D G T... K I	Pyrophosphate binding motif					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L... Q	18	[IDE]I D E F L I F	Goloco motif, A g alpha bin					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	C C G E L	18	C...C	Motif on TIM mitochondrial tr.	Y	zfl-C2H2	1.E-04	5.8	membrane fusion (1e-14)
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	E E E D Y	18	Y E E	Src phosphorylation site	Brix	1.E-03	-1	cytoplasm organization and biogenesis (1e-05)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	S K E W A	18	I G GA G A S C I	ADOMET SYNTHETASE 2	PH	1.E-03	-1	cytoplasm organization and biogenesis (1e-05)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	Q G N H R	18	W K Q R K R	Amidation after cleavage afe	WD40	1.E-03	-0.4	ribosome biogenesis (1e-17)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L S E R W	18	W L N S	Lipid binding motif in C	IBN_N	1.E-07	0.1	protein localization (1e-14)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	D I W H Y	18	D J Y E	Lin kinase phosphorylation s	SH1	1.E-04	0.9	protein kinase activity (0.01)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A D O Q K I	18	H A U O	N-Cadherin ligand	DEAD	1.E-07	1	nucleus (1e-59)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G J G L T	18	G G G	Oxygenase can attackm	IBN_N	1.E-02	0.1	bud (0.01)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	I M C L G H	18	S G H S L	14-3-3-sigma binds motif in r	WD40	1.E-07	1.6	snRNA binding (1e-13)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	V R V T	18	R A L A H G V R V	Mitochondrial targeting motif	S4	1.E-03	1.8	iRNA processing (1e-15)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	V L D O S L	18			WD40	1.E-02	2	cytoplasm organization and biogenesis (1e-27)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[E G Y T P V E D ]	18	C P V	Heme binding site in mitoch	SRP1_TIP1	1.E-39	2.3		
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	N L C F P	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	N L C F P	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[P V P T ... R H J ]	17	[K R]R	CLV_PCSK_KEX2_1	Y				
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	F S V D P L Y	17	[S T P]	LIG_WW_4LIG_WW_4	Y				
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[Q G Q L N P T ]	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L Y L K R K L E	17	Y L J	SH2 ligand for PLCgamma1					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R H G E R	17	F K Y D E K S L	Nucleotide binding motif in A					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R F R T W L	17	[A G R]	Protease matriptase protease					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R T R W L	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	C C G I	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[Y V Y S L I N T Y ]	17	[S T Q]	ATM kinase phosphorylation					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L S U F	17	DLL	Binding motif for clathrin hea	Y				
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	V P V A P	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G M Q E	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	H V Y G Y	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	C C G I	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	[Y V Y S L I N T Y ]	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	F V Q S L I N T Y	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R T N C H	17	K R R	ZIP kinase substrate motif					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R T A S G D P T	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	F T N M T	17							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	W J I G L	17	Y M	SH2 ligand for Vav1 (group II					
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	H G S Q J	16							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	I L Q H S T	16							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L Q Y K W K	16							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L U F U F	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A T A R I M	15	R J R R	CLV_PCSK_FUR_1	DEAD	1.E-07	-1.5	cytoplasm organization and biogenesis (1e-10)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	T W S G Y	15	K R K R	CLV_PCSK_PCIE12_1	Helicase_C	1.E-04	-0.7	cytoplasm organization and biogenesis (1e-10)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R F G H N	15	[A G J R]	Protease matriptase protease	DEAD	1.E-03	0.9	cytosol ribosome (sensu Eukaryota) (1e-09)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G G G Y H K R	15	[D S R Q W E Q T R ]	ATM kinase phosphorylation	SRP1_TIP1	1.E-31	1.9	endoplasmic reticulum (1e-09)	
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L U F U F	15			SRP1_TIP1	1.E-36	2.6		
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A T R I M	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	T W S G Y	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R F G H N	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G G G Y H K R	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L U F U F	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A T R I M	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	T W S G Y	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R F G H N	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G G G Y H K R	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L U F U F	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A T R I M	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	T W S G Y	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R F G H N	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G G G Y H K R	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L U F U F	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A T R I M	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	T W S G Y	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R F G H N	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G G G Y H K R	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L U F U F	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A T R I M	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	T W S G Y	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R F G H N	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G G G Y H K R	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L U F U F	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A T R I M	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	T W S G Y	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	R F G H N	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	G G G Y H K R	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	L U F U F	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	A T R I M	15							
protein_40_YNL110C	2	TPK2. Cyclic AMP-dependent protein kinase catalytic subunit.	T W S G Y								

ucsf_loc_k_mean_G6	6	Sub-cellular localization, 6 clusters	P[LIA].[KTCDC]R	13	KR	CLV_PCSK_PCTET2_1	Mito_carr	1.E-19	1.1	transferase activity (1e-08)	0.010	10
vesat_clustered_interaction	33	yeast_clustered_interaction_protein	K[KRKTK]	13	DLL	Binding motif for clathrin hex	Brd	1.E-02	-0.9	nuclei lumen (1e-07)	0.023	10
matsuyma_K_G15	15	matsuyma_K_G15	[LAVIY][LGEVIV]	13	Y.HQ	LIG_SH2_STAT3	pbase	1.E-04	2.4	barrier septum (1e-04)	0.012	9
Huh_Matrix_K_G17	17	Huh_Matrix_K_G17	[YHIIY]FQ	13	D.SII.FF	SRP1_TIP1	SRP1_TIP1	1.E-41	2.5		0.010	10
oshea_Total_	8	oshea_Total_	S[DEW][RIG]A	13	D.SII.FF	SRP1_TIP1	SRP1_TIP1	1.E-45	2.6		0.010	10
Huh_Matrix_K_G17	17	Huh_Matrix_K_G17	V[KDIFAL][GLS]	13	LLG	SRP1_TIP1	SRP1_TIP1	1.E-48	3.1		0.005	8
matsuyma_K_G15	15	matsuyma_K_G15	V[PLC]W[YKF]	13	VP	SRP1_TIP1	SRP1_TIP1	1.E-53	3.2	protein serine/threonine kinase activity (1e-12)	0.013	10
Huh_Matrix_K_G17	17	Huh_Matrix_K_G17	GGL[FTL][CEP]	13	IVY.L	SRP1_TIP1	SRP1_TIP1	1.E-53	3.9	cell wall (0.01)	0.010	10
yeast_clustered_interaction_	33	yeast_clustered_interaction_protein	I[LILF]	13	D.SII.FF	SRP1_TIP1	SRP1_TIP1	1.E-45	3.1	snRNP protein import into nucleus (1e-07)	0.013	8
vesat_clustered_interaction	33	yeast_clustered_interaction_protein	[GSI]GLFNLIQ	13	CKI	SRP1_TIP1	SRP1_TIP1	1.E-48	3.1	integral to membrane (1e-16)	0.023	10
vesat_clustered_interaction	35	yeast_clustered_interaction_both	[GWA]EH	13	Beta2-Integrin binding motif	SRP1_TIP1	SRP1_TIP1	1.E-45	3.1	snRNP protein import into nucleus (1e-08)	0.015	9
protein_40_k_D334W	2	RPT3: One of six ATPases of the 19S regulat	D[EHD]R	13	DEHD	SRP1_TIP1	SRP1_TIP1	1.E-48	3.1	protein import complex (sensu Eukaryota) (0.01)	0.015	9
matsuyma_K_G15	15	matsuyma_K_G15	H[KIKD]	13	Protease Caspase 1 ICE	SRP1_TIP1	SRP1_TIP1	1.E-48	3.1	nuclear pore (1e-09)	0.013	7
yeast_clustered_interaction_	35	yeast_clustered_interaction_both	T[GEP][FPIK]RE	12	[SAG]GGTG[S TUBULIN PATTERN	SRP1_TIP1	SRP1_TIP1	1.E-45	3.1	RNA helicase activity (1e-18)	0.015	9
huh_multiclass_55	55	huh_multiclass_55	I[EDHN]	12	IVL[FIC]	SRP1_TIP1	SRP1_TIP1	1.E-03	-1	site of polarized growth (1e-08)	0.035	10
huh_multiclass_55	55	huh_multiclass_55	[LTK][GAMIVVV	12	P.VL	SRP1_TIP1	SRP1_TIP1	1.E-05	-0.7	endoplasmic reticulum (1e-35)	0.035	10
Huh_Matrix_K_G17	17	Huh_Matrix_K_G17	C.C[GKE]	12	C..C	SRP1_TIP1	SRP1_TIP1	1.E-45	3.1		0.009	9
Huh_Matrix_K_G17	17	Huh_Matrix_K_G17	N..L[RKT]	12	Zn..clus	SRP1_TIP1	SRP1_TIP1	1.E-03	12.1	transcription (1e-09)	0.011	10
yeast_clustered_interaction_	33	yeast_clustered_interaction_protein	[TVAJM][TVPIG]	12		SRP1_TIP1	SRP1_TIP1	1.E-45	3.1		0.021	10
oshea_Total_	8	oshea_Total_	[AVG][TSN]TT	12	KGST	SRP1_TIP1	SRP1_TIP1	1.E-45	3.1		0.005	8
Huh_Matrix_K_G17	17	Huh_Matrix_K_G17	H[RSG].[TSNL]TA	12	eif4 motif phosphorylation m	SRP1_TIP1	SRP1_TIP1	1.E-45	3.1		0.009	9
matsuyma_K_G15	15	matsuyma_K_G15	TG.GD[VIVTFY]	11	TGY	SRP1_TIP1	SRP1_TIP1	1.E-09	-1.5	ATP-dependent RNA helicase activity (1e-09)	0.009	9
Oshea_Total_	13	Oshea_Total_	I[LLEK]	11	ERK6/SAPK3 activation sites	SRP1_TIP1	SRP1_TIP1	1.E-10	-1.1	RNA helicase activity (1e-11)	0.011	8
huh_multiclass_55	55	huh_multiclass_55	T[RTS].[ITGOMI]	11	Y	SRP1_TIP1	SRP1_TIP1	1.E-02	1.1	Myb-DNA binding	0.034	9
Huh_Matrix_K_G17	17	Huh_Matrix_K_G17	I[ITFC].[PWCIW]	11	[FW]W	SRP1_TIP1	SRP1_TIP1	1.E-48	3	nucleoplasm (1e-31)	0.008	9
Huh_Matrix_K_G17	17	Huh_Matrix_K_G17	V[PWWNN]V[D]IS	11	VP	SRP1_TIP1	SRP1_TIP1	1.E-47	3.1		0.009	9
Huh_Matrix_K_G17	17	Huh_Matrix_K_G17	K[LAYR]R[EHP]	11	[AGIR	SRP1_TIP1	SRP1_TIP1	1.E-58	3.7	cell wall (0.01)	0.009	9
yeast_phase_q10	10	cell_cycle_phase microarray	T..[SLF]	11	T..ISA	SRP1_TIP1	SRP1_TIP1	1.E-29			0.045	8
huh_multiclass_55	55	huh_multiclass_55	K..[KGVR]	11	[KR]R	SRP1_TIP1	SRP1_TIP1	1.E-29		nuclear pore (1e-29)	0.034	10
half_life_belle	37	half_life_belle_continuous	D[EROE]VVFN	10	SEDEE	SRP1_TIP1	SRP1_TIP1	1.E-48	3.2		0.025	10
Huh_Matrix_K_G17	17	Huh_Matrix_K_G17	I..L[LFM]	10	CKII kinase phosphorylation	SRP1_TIP1	SRP1_TIP1	1.E-48	3.2		0.008	9
yeast_clustered_interaction	35	yeast_clustered_interaction_both	Q[QIP]Q	10	GQDQTQQI	SRP1_TIP1	SRP1_TIP1	1.E-07		DNA replication initiation (1e-07)	0.018	10
yeast_clustered_interaction	35	yeast_clustered_interaction_both	V[PVD]D[C]	10	44 KD POSTSYNAPTIC PA	SRP1_TIP1	SRP1_TIP1	1.E-07		nucleoplasm part (1e-17)	0.019	9
half_life_belle_q15	15	half_life_belle_quantize15	K[LRL]	10	HAVDI	SRP1_TIP1	SRP1_TIP1	1.E-07			0.014	7
half_life_belle	37	half_life_belle_continuous	L[LKL]	10	N-Cadherin ligand	SRP1_TIP1	SRP1_TIP1	1.E-07			0.024	10
matsuyma_K_G15	15	matsuyma_K_G15	[TRK10][GES]KT	9	LLKL	SRP1_TIP1	SRP1_TIP1	1.E-12	4.8	AP-2 binding motif in CXCR2	0.010	7
yeast_clustered_interaction	33	yeast_clustered_interaction_protein	O..[ODP]Q	9	P.Q.D	SRP1_TIP1	SRP1_TIP1	1.E-12	4.8	ATP-dependent RNA helicase activity (1e-11)	0.018	9
huh_multiclass_55	55	huh_multiclass_55	I[RWIA]	9	LiG_TRAF2_2	SRP1_TIP1	SRP1_TIP1	1.E-12	4.8	general RNA polymerase II transcription factor a	0.029	10
yeast_clustered_interaction_	35	yeast_clustered_interaction_both	L[DMC]A	8	[LIV].[LMILAA	SRP1_TIP1	SRP1_TIP1	1.E-11		plasma membrane (1e-08)	0.017	9
raw_half_life_belle	37	raw_half_life_belle	K.F[KMA]	8	LiG_Sin3_1	SRP1_TIP1	SRP1_TIP1	1.E-11		DNA repair (1e-11)	0.021	8
			K.F[KQ].F	8	GY[KQ].F	SRP1_TIP1	SRP1_TIP1	1.E-11				
					LiG_SH2_STAT6	SRP1_TIP1	SRP1_TIP1	1.E-11				