

ORF Name	Gene Name	Description	Degree	Number of Interfaces	Singlish/Multi	GO Biological Process	GO Molecular Function	GO Cellular Component	Main Data Source (Y2H or TAP)
Q0045	COX1	Subunit I of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; one of three mitochondrially-encoded subunits	7	7	Multi	aerobic respiration	cytochrome c oxidase activity	respiratory chain complex IV (sensu Eukaryota)	Pulldown
Q0105	COB	Cytochrome b	6	6	Multi	aerobic respiration	ubiquinol-cytochrome c reductase activity	respiratory chain complex III (sensu Eukaryota)	Pulldown
Q0250	COX2	Subunit II of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; one of three mitochondrially-encoded subunits	6	6	Multi	aerobic respiration	cytochrome c oxidase activity	respiratory chain complex IV (sensu Eukaryota)	Pulldown
Q0275	COX3	Subunit III of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; one of three mitochondrially-encoded subunits	7	7	Multi	aerobic respiration	cytochrome c oxidase activity	respiratory chain complex IV (sensu Eukaryota)	Pulldown
YAL029C	MYO4	One of two type V myosins; required for mother-specific HO expression, for the bud tip localization of ASH1 and IST2 mRNA; facilitates growth and orientation of ER tubules along with She3p	7	6	Multi	intracellular mRNA localization	microfilament motor activity	mitochondrion	Pulldown
YAL030W	SNC1	Involved in mediating targeting and transport of secretory proteins; forms a complex with Snc2p and Sec9p; homolog of Snc2p, vesicle-associated membrane protein (synaptobrevin) homolog, forms a complex with Snc2p and Sec9p	8	6	Multi	endocytosis	v-SNARE activity	transport vesicle	Pulldown
YAL040C	CLN3	role in cell cycle START; involved in G(sub)1 size control; G(sub)1 cyclin	7	2	Singlish	G1/S transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	nucleus	Y2H
YBL002W	HTB2	One of two nearly identical (see HTB2) histone H2B subtypes required for chromatin assembly and chromosome function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation	8	8	Multi	chromatin assembly or disassembly	DNA binding	nuclear nucleosome	Pulldown

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YBL003C	HTA2	One of two nearly identical (see also HTA1) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p	7	7	Multi	chromatin assembly or disassembly	DNA binding	nuclear nucleosome	Pulldown
YBL007C	SLA1	Cytoskeletal protein binding protein required for assembly of the cortical actin cytoskeleton; contains 3 SH3 domains; interacts with proteins regulating actin dynamics and with proteins required for endocytosis	6	4	Multi	cell wall organization and biogenesis	protein binding, bridging	actin cortical patch	Pulldown
YBL037W	APL3	clathrin Associated Protein complex Large subunit; Large subunit of clathrin associated protein complex	5	3	Multi	vesicle-mediated transport	molecular_ function unknown	AP-2 adaptor complex	Pulldown
YBL041W	PRE7	20S proteasome beta-type subunit	11	7	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, beta-subunit complex (sensu Eukaryota)	Pulldown
YBL045C	COR1	Core subunit of the ubiquinol-cytochrome c reductase complex (bc1 complex), which is a component of the mitochondrial inner membrane electron transport chain	7	6	Multi	aerobic respiration	ubiquinol-cytochrome c reductase activity	respiratory chain complex III (sensu Eukaryota)	Pulldown
YBR009C	HHF1	One of two identical histone H4 proteins (see also HHF2); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity	8	8	Multi	chromatin assembly or disassembly	DNA binding	nuclear nucleosome	Pulldown
YBR010W	HHT1	One of two identical histone H3 proteins (see also HHT2); core histone required for chromatin assembly, involved in heterochromatin-mediated telomeric and HM silencing; regulated by acetylation, methylation, and mitotic phosphorylation	7	7	Multi	chromatin assembly or disassembly	DNA binding	nucleus	Pulldown
YBR109C	CMD1	Calmodulin; Ca++ binding protein that regulates Ca++ independent processes (mitosis, bud growth, actin organization, endocytosis, etc.) and Ca++ dependent processes (stress-activated pathways), targets include Nuf1p, Myo2p and calcineurin	10	4	Multi	cytoskeleton organization and biogenesis	calcium ion binding	cytoplasm	Pulldown

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YBR142W	MAK5	Essential nucleolar protein, putative DEAD-box RNA helicase required for maintenance of M1 dsRNA virus; involved in biogenesis of large (60S) ribosomal subunits	14	9	Multi	rRNA processing	ATP-dependent RNA helicase activity	nucleolus	Pulldown
YBR160W	CDC28	Catalytic subunit of the main cell cycle cyclin-dependent kinase (CDK); alternately associates with G1 cyclins (CLNs) and G2/M cyclins (CLBs) which direct the CDK to specific substrates	28	2	Singlish	protein amino acid phosphorylation	cyclin-dependent protein kinase activity	cytoplasm	Pulldown
YBR189W	RPS9B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity to E. coli S4 and rat S9 ribosomal proteins	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukaryota)	Pulldown
YBR200W	BEM1	Protein containing SH3-domains, involved in establishing cell polarity and morphogenesis; functions as a scaffold protein for complexes that include Cdc24p, Ste5p, Ste20p, and Rsr1p	6	4	Multi	establishment of cell polarity (sensu Fungi)	protein binding	bud neck	Y2H
YBR237W	PRP5	RNA helicase in the DEAD-box family	8	8	Multi	U2-type nuclear mRNA branch site recognition	pre-mRNA splicing factor activity	spliceosome complex	Y2H
YCR035C	RRP43	Protein involved in rRNA processing; component of the exosome 3->5 exonuclease complex with Rrp41p, Rrp42p, Rrp4p and Dis3p; required for efficient maturation of 5.8S, 18S and 25S rRNA	5	5	Multi	35S primary transcript processing	3'-5'-exoribonuclease activity	nuclear exosome (RNase complex)	Pulldown
YCR088W	ABP1	Actin-binding protein of the cortical actin cytoskeleton, important for activation of the Arp2/3 complex that plays a key role actin in cytoskeleton organization	7	6	Multi	establishment of cell polarity (sensu Fungi)	protein binding	cytoplasm	Pulldown
YDL007W	RPT2	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for normal peptide hydrolysis by the core 20S particle	6	6	Multi	ubiquitin-dependent protein catabolism	ATPase activity	proteasome regulatory particle (sensu Eukaryota)	Pulldown

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YDL029W	ARP2	Essential component of the Arp2/3 complex, which is a highly conserved actin nucleation center required for the motility and integrity of actin patches; involved in endocytosis and membrane growth and polarity	5	3	Multi	actin filament organization	structural constituent of cytoskeleton	mitochondrion	Pulldown
YDL111C	RRP42	Protein involved in rRNA processing; component of the exosome 3->5 exonuclease complex with Rrp4p, Rrp41p, Rrp43p and Dis3p	5	5	Multi	35S primary transcript processing	3'-5'-exoribonuclease activity	nuclear exosome (RNase complex)	Pulldown
YDL140C	RPO21	RNA polymerase II largest subunit B220, part of central core; phosphorylation of C-terminal heptapeptide repeat domain regulates association with transcription and splicing factors; similar to bacterial beta-prime	9	9	Multi	transcription from Pol II promoter	DNA-directed RNA polymerase activity	mitochondrion	Pulldown
YDL143W	CCT4	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	7	7	Multi	protein folding	unfolded protein binding	cytoplasm	Pulldown
YDL155W	CLB3	Involved in mitotic induction and perhaps in DNA replication and spindle assembly; G(sub)2-specific B-type cyclin	9	2	Singlish	G2/M transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	cytoplasm	Y2H
YDR188W	CCT6	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, essential protein that is required for the assembly of actin and tubulins in vivo; contains an ATP-binding motif	7	7	Multi	protein folding	unfolded protein binding	cytoplasm	Pulldown
YDR212W	TCP1	tailless complex polypeptide 1; chaperonin subunit alpha	7	7	Multi	protein folding	unfolded protein binding	cytoplasm	Pulldown
YDR224C	HTB1	One of two nearly identical (see HTB2) histone H2B subtypes required for chromatin assembly and chromosome function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation and H3 methylation	7	7	Multi	chromatin assembly or disassembly	DNA binding	nuclear nucleosome	Pulldown
YDR225W	HTA1	One of two nearly identical (see also HTA2) histone H2A subtypes; core histone required for chromatin assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; acetylated by Nat4p	7	7	Multi	chromatin assembly or disassembly	DNA binding	nuclear nucleosome	Pulldown

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YDR243C	PRP28	RNA helicase in the DEAD-box family, involved in RNA isomerization at the 5' splice site	8	8	Multi	cis assembly of U2-type pre-catalytic spliceosome	pre-mRNA splicing factor activity	spliceosome complex	Pulldown
YDR280W	RRP45	Protein involved in rRNA processing; component of the exosome 3->5 exonuclease complex	5	5	Multi	35S primary transcript processing	3'-5'-exoribonuclease activity	nuclear exosome (RNase complex)	Pulldown
YDR328C	SKP1	Evolutionarily conserved kinetochore protein that is part of multiple protein complexes, including the SCF ubiquitin ligase complex, the CBF3 complex that binds centromeric DNA, and the RAVE complex that regulates assembly of the V-ATPase	9	4	Multi	ubiquitin-dependent protein catabolism	protein binding	cytoplasm	Pulldown
YDR388W	RVS167	Actin-associated protein, subunit of a complex (Rvs161p-Rvs167p) involved in regulation of actin cytoskeleton, endocytosis, and viability following starvation or osmotic stress; homolog of mammalian amphiphysin	6	4	Multi	endocytosis	cytoskeletal protein binding	actin cortical patch	Pulldown
YDR394W	RPT3	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; substrate of N-acetyltransferase B	6	6	Multi	ubiquitin-dependent protein catabolism	ATPase activity	proteasome regulatory particle (sensu Eukaryota)	Pulldown
YDR432W	NPL3	RNA-binding protein that carries poly(A)+ mRNA from the nucleus into the cytoplasm; phosphorylation by Sky1p in the cytoplasm may promote release of mRNAs	6	4	Multi	mRNA-nucleus export	mRNA binding	cytoplasm	Pulldown
YDR468C	TLG1	member of the syntaxin family of t-SNAREs; tSNARE that affects a Late Golgi compartment	10	6	Multi	vesicle fusion	v-SNARE activity	Golgi trans face	Pulldown
YDR471W	RPL27B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Ap and has similarity to rat L27 ribosomal protein	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota)	Pulldown
YDR477W	SNF1	AMP-activated serine/threonine protein kinase found in a complex containing Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis	5	2	Singlish	protein amino acid phosphorylation	AMP-activated protein kinase activity	cytoplasm	Pulldown

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YDR529C	QCR7	Subunit 7 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; oriented facing the mitochondrial matrix; N-terminus appears to play a role in complex assembly	5	5	Multi	aerobic respiration	ubiquinol-cytochrome-c reductase activity	respiratory chain complex III (sensu Eukaryota)	Y2H
YEL024W	RIP1	Ubiquinol-cytochrome-c reductase, a Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex; transfers electrons from ubiquinol to cytochrome c1 during respiration	6	6	Multi	aerobic respiration	ubiquinol-cytochrome-c reductase activity	respiratory chain complex III (sensu Eukaryota)	Y2H
YER012W	PRE1	20S proteasome beta-type subunit; localizes to the nucleus throughout the cell cycle	6	5	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	nucleus	Pulldown
YER013W	PRP22	DEAH-box RNA-dependent ATPase/ATP-dependent RNA helicase, associates with lariat intermediates before the second catalytic step of splicing; mediates ATP-dependent mRNA release from the spliceosome and unwinds RNA duplexes	8	8	Multi	U2-type spliceosome disassembly	pre-mRNA splicing factor activity	spliceosome complex	Pulldown
YER094C	PUP3	Beta subunit of the 20S proteasome involved in ubiquitin-dependent catabolism; human homolog is subunit C10	11	7	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, beta-subunit complex (sensu Eukaryota)	Pulldown
YER114C	BOI2	Protein implicated in polar growth, functionally redundant with Boi1p; interacts with bud-emergence protein Bem1p; contains an SH3 (src homology 3) domain and a PH (pleckstrin homology) domain	5	2	Singlish	establishment of cell polarity (sensu Fungi)	phospholipid binding	bud neck	Y2H
YER136W	GDI1	GDP dissociation inhibitor, regulates vesicle traffic in secretory pathways by regulating the dissociation of GDP from the Sec4/Ypt/rab family of GTP binding proteins	9	1	Singlish	vesicle-mediated transport	RAB GDP-dissociation inhibitor activity	membrane fraction	Pulldown
YER172C	BRR2	RNA-dependent ATPase RNA helicase involved in the facilitation and disruption of snRNA interactions, required for disruption of U4/U6 base-pairing in native snRNPs to activate the spliceosome for catalysis	8	8	Multi	U2-type spliceosome conformational change to release U4 and U1	pre-mRNA splicing factor activity	snRNP U5	Pulldown

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YFL002C	SPB4	Putative ATP-dependent RNA helicase, nucleolar protein required for synthesis of 60S ribosomal subunits at a late step in the pathway; sediments with 66S pre-ribosomes in sucrose gradients	5	1	Singlish	35S primary transcript processing	ATP-dependent RNA helicase activity	nucleolus	Pulldown
YFL039C	ACT1	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions	7	2	Singlish	cell wall organization and biogenesis	structural constituent of cytoskeleton	actin cortical patch	Pulldown
YFR050C	PRE4	20S proteasome beta-type subunit	12	6	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, beta-subunit complex (sensu Eukaryota)	Pulldown
YGL011C	SCL1	Alpha subunit of the 20S core complex of the 26S proteasome involved in the degradation of ubiquitinated substrates; essential for growth; detected in the mitochondria	8	6	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	mitochondrion	Pulldown
YGL048C	RPT6	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; bound by ubiquitin-protein ligases Ubr1p and Ufd4p; localized mainly to the nucleus throughout the cell cycle	7	6	Multi	ubiquitin-dependent protein catabolism	ATPase activity	nucleus	Pulldown
YGL106W	MLC1	Essential light chain for myosin Myo2p; may stabilize Myo2p by binding to the neck region; may interact with Myo1p, Iqg1p, and Myo2p to coordinate formation and contraction of the actomyosin ring with targeted membrane deposition	5	2	Singlish	endocytosis	microfilament motor activity	actin cap	Pulldown
YGL120C	PRP43	RNA helicase in the DEAH-box family, involved in release of the lariat-intron from the spliceosome	13	9	Multi	U2-type spliceosome disassembly	pre-mRNA splicing factor activity	mitochondrion	Pulldown
YGL123W	RPS2	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukaryota)	Pulldown

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YGL187C	COX4	Subunit IV of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; N-terminal 25 residues of precursor are cleaved during mitochondrial import	5	5	Multi	aerobic respiration	cytochrome c oxidase activity	respiratory chain complex IV (sensu Eukaryota)	Y2H
YGL191W	COX13	Subunit VIa of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; not essential for cytochrome c oxidase activity but may modulate activity in response to ATP	6	6	Multi	aerobic respiration	enzyme regulator activity	respiratory chain complex IV (sensu Eukaryota)	Pulldown
YGR034W	RPL26B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Ap and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota)	Pulldown
YGR095C	RRP46	Protein involved in rRNA processing; component of the exosome 3->5 exonuclease complex	5	5	Multi	35S primary transcript processing	3'-5'-exoribonuclease activity	nuclear exosome (RNase complex)	Pulldown
YGR108W	CLB1	Involved in mitotic induction; G(sub)2-specific B-type cyclin	9	2	Singlish	G2/M transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	nucleus	Y2H
YGR109C	CLB6	role in DNA replication during S phase; B-type cyclin	9	2	Singlish	G1/S transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	cellular_comp onent unknown	Pulldown
YGR135W	PRE9	20S proteasome beta-type subunit; the only nonessential 20S subunit	13	8	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, alpha-subunit complex (sensu Eukaryota)	Pulldown
YGR158C	MTR3	3'5' exoribonuclease, exosome subunit; nucleolar protein involved in export of mRNA and ribosomal subunits; homologous to the E. coli exonuclease RNase PH	5	1	Singlish	35S primary transcript processing	3'-5'-exoribonuclease activity	nuclear exosome (RNase complex)	Y2H

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YGR195W	SKI6	3'-to-5' phosphorolytic exoribonuclease that is a subunit of the exosome; required for 3' processing of the 5.8S rRNA; involved in 3' to 5' mRNA degradation and translation inhibition of non-poly(A) mRNAs	5	5	Multi	35S primary transcript processing	3'-5'-exoribonuclease activity	nuclear exosome (RNase complex)	Pulldown
YGR253C	PUP2	Alpha subunit of the 20S proteasome involved in ubiquitin-dependent catabolism; human homolog is subunit zeta	9	5	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, alpha-subunit complex (sensu Eukaryota)	Pulldown
YGR261C	APL6	beta3-like subunit of the yeast AP-3 complex which functions in transport of alkaline phosphatase to the vacuole via the alternate pathway, suppressor of loss of casein kinase 1 function; putative beta adaptin component of the membrane-associate clathrin assembly complex	5	4	Multi	Golgi to vacuole transport	molecular_function unknown	AP-3 adaptor complex	Pulldown
YGR270W	YTA7	Protein of unknown function, member of CDC48/PAS1/SEC18 family of ATPases, potentially phosphorylated by Cdc28p	6	1	Singlish	protein catabolism	ATPase activity	nucleus	Pulldown
YHL001W	RPL14B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl14Ap and has similarity to rat L14 ribosomal protein	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota)	Y2H
YHL031C	GOS1	v-SNARE protein involved in Golgi transport, homolog of the mammalian protein GOS-28/GS28	6	5	Multi	vesicle fusion	v-SNARE activity	integral to membrane	Pulldown
YHR010W	RPL27A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Bp and has similarity to rat L27 ribosomal protein	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota)	Pulldown
YHR023W	MYO1	Type II myosin heavy chain, required for wild-type cytokinesis and cell separation; localizes to the actomyosin ring; binds to myosin light chains Mlc1p and Mlc2p through its IQ1 and IQ2 motifs respectively	7	6	Multi	cytokinesis	microfilament motor activity	contractile ring (sensu Saccharomyces)	Pulldown

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YHR030C	SLT2	Serine/threonine MAP kinase involved in regulating the maintenance of cell wall integrity and progression through the cell cycle; regulated by the PKC1-mediated signaling pathway	8	2	Singlish	cell wall organization and biogenesis	MAP kinase activity	cytoplasm	Pulldown
YHR135C	YCK1	Palmitoylated, plasma membrane-bound casein kinase I isoform; shares redundant functions with Yck2p in morphogenesis, proper septin assembly, endocytic trafficking; provides an essential function overlapping with that of Yck2p	9	4	Multi	protein amino acid phosphorylation	casein kinase I activity	endoplasmic reticulum	Pulldown
YHR169W	DBP8	Putative ATP-dependent RNA helicase of the DEAD-box family involved in biogenesis of the 40S ribosomal subunit	5	1	Singlish	35S primary transcript processing	ATP-dependent RNA helicase activity	nucleolus	Pulldown
YIL004C	BET1	Type II membrane protein required for vesicular transport between the endoplasmic reticulum and Golgi complex; v-SNARE with similarity to synaptobrevins	8	7	Multi	ER to Golgi transport	v-SNARE activity	endoplasmic reticulum membrane	Y2H
YIL021W	RPB3	RNA polymerase II third largest subunit B44, part of central core; similar to prokaryotic alpha subunit	6	6	Multi	transcription from Pol II promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase II, core complex	Pulldown
YIL035C	CKA1	Alpha subunit of protein kinase casein kinase-2 (CK2), a spontaneously active, ubiquitous, pleiotropic enzyme that phosphorylates seryl/threonyl residues specified by multiple negatively charged side chains (consensus S/T-x-x-E/D/S(P)/T(P))	5	4	Multi	protein amino acid phosphorylation	protein kinase CK2 activity	protein kinase CK2 complex	Pulldown
YIL061C	SNP1	U1snRNP 70K protein homolog	6	3	Multi	nuclear mRNA splicing, via spliceosome	mRNA binding	commitment complex	Y2H
YIL142W	CCT2	Subunit beta of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	7	7	Multi	protein folding	unfolded protein binding	cytoplasm	Pulldown
YIR001C	SGN1	Cytoplasmic RNA-binding protein, contains an RNA recognition motif (RRM); may have a role in mRNA translation, as suggested by genetic interactions with genes encoding proteins involved in translational initiation	5	1	Singlish	mRNA metabolism	poly(A) binding	cytoplasm	Pulldown

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YJL001W	PRE3	20S proteasome beta-type subunit, responsible for cleavage after acidic residues in peptides	9	7	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, beta-subunit complex (sensu Eukaryota)	Pulldown
YJL008C	CCT8	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	7	7	Multi	protein folding	unfolded protein binding	cytoplasm	Pulldown
YJL014W	CCT3	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	7	7	Multi	protein folding	unfolded protein binding	cytoplasm	Pulldown
YJL033W	HCA4	Putative nucleolar DEAD box RNA helicase; high-copy number suppression of a U14 snoRNA processing mutant suggests an involvement in 18S rRNA synthesis	5	1	Singlish	35S primary transcript processing	ATP-dependent RNA helicase activity	nucleolus	Pulldown
YJL111W	CCT7	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	7	7	Multi	protein folding	unfolded protein binding	cytoplasm	Y2H
YJL166W	QCR8	Subunit 8 of ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; oriented facing the intermembrane space; expression is regulated by Abf1p and Cpf1p	6	6	Multi	aerobic respiration	ubiquinol-cytochrome-c reductase activity	respiratory chain complex III (sensu Eukaryota)	Y2H
YJL190C	RPS22A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Bp and has similarity to E. coli S8 and rat S15a ribosomal proteins	8	8	Multi	protein biosyntheses	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukaryota)	Y2H
YJR064W	CCT5	Subunit of the cytosolic chaperonin Cct ring complex, related to Tcp1p, required for the assembly of actin and tubulins in vivo	7	7	Multi	protein folding	unfolded protein binding	cytoplasm	Pulldown
YKL006W	RPL14A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl14Bp and has similarity to rat L14 ribosomal protein; rpl14a csh5 double null mutant exhibits synthetic slow growth	5	5	Multi	protein biosyntheses	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota)	Pulldown
YKL078W	DHR2	Predominantly nucleolar DEAH-box RNA helicase, required for 18S rRNA synthesis	8	8	Multi	ribosome biogenesis	RNA helicase activity	nucleolus	Pulldown

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YKL129C	MYO3	One of two type I myosins; localizes to actin cortical patches; deletion of MYO3 has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization	9	6	Multi	cell wall organization and biogenesis	microfilament motor activity	actin cortical patch	Pulldown
YKL144C	RPC25	RNA polymerase III subunit C25	5	4	Multi	transcription from Pol III promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	Pulldown
YKL145W	RPT1	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for optimal CDC20 transcription; interacts with Rpn12p and the E3 ubiquitin-protein ligase Ubr1p	6	6	Multi	ubiquitin-dependent protein catabolism	ATPase activity	proteasome regulatory particle (sensu Eukaryota)	Pulldown
YKL196C	YKT6	v-SNARE (synaptobrevin) essential for endoplasmic reticulum-Golgi transport; has similarity to Sec22p, Snc1p, and Snc2p	7	2	Singlish	vesicle fusion	v-SNARE activity	mitochondrion	Pulldown
YKR014C	YPT52	rab5-like GTPase involved in vacuolar protein sorting and endocytosis; probable purine nucleotide-binding protein	5	2	Singlish	protein-vacuolar targeting	GTPase activity	late endosome	Pulldown
YKR086W	PRP16	RNA helicase in the DEAH-box family involved in the second catalytic step of splicing, exhibits ATP-dependent RNA unwinding activity	8	8	Multi	formation of catalytic U2-type spliceosome for second transesterification step	pre-mRNA splicing factor activity	spliceosome complex	Y2H
YLL008W	DRS1	Nucleolar DEAD-box protein required for ribosome assembly and function, including synthesis of 60S ribosomal subunits; constituent of 66S pre-ribosomal particles	7	2	Singlish	35S primary transcript processing	ATP-dependent RNA helicase activity	nucleolus	Pulldown
YLR026C	SED5	cis-Golgi t-SNARE syntaxin required for vesicular transport between the ER and the Golgi complex, binds at least 9 SNARE proteins	12	6	Multi	ER to Golgi transport	t-SNARE activity	Golgi cis-face	Pulldown
YLR029C	RPL15A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl15Bp and has similarity to rat L15 ribosomal protein; binds to 5.8 S rRNA	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota)	Pulldown

ORF Name	Gene Name	Description	Degree	Number of Interfaces	Singlish/Multi	GO Biological Process	GO Molecular Function	GO Cellular Component	Main Data Source (Y2H or TAP)
YLR038C	COX12	Subunit VIb of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; required for assembly of fully active cytochrome c oxidase but not required for activity after assembly	5	5	Multi	cytochrome c oxidase complex assembly	cytochrome c oxidase activity	respiratory chain complex IV (sensu Eukaryota)	Y2H
YLR078C	BOS1	v-SNARE (vesicle specific SNAP receptor), localized to the endoplasmic reticulum membrane and necessary for vesicular transport from the ER to the Golgi	5	5	Multi	ER to Golgi transport	v-SNARE activity	endoplasmic reticulum membrane	Y2H
YLR182W	SWI6	Transcription cofactor, forms complexes with DNA-binding proteins Swi4p and Mbp1p to regulate transcription at the G1/S transition; involved in meiotic gene expression; localization regulated by phosphorylation; potential Cdc28p substrate	5	3	Multi	meiosis	protein binding	cytoplasm	Pulldown
YLR210W	CLB4	Involved in mitotic induction; G(sub)2-specific B-type cyclin	9	2	Singlish	G2/M transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	nucleus	Y2H
YLR229C	CDC42	Small rho-like GTPase, essential for establishment and maintenance of cell polarity; mutants have defects in the organization of actin and septins	7	2	Singlish	establishment of cell polarity (sensu Fungi)	GTPase activity	plasma membrane	Y2H
YLR268W	SEC22	R-SNARE protein; assembles into SNARE complex with Bet1p, Bos1p and Sed5p; cycles between the ER and Golgi complex; involved in anterograde and retrograde transport between the ER and Golgi; synaptobrevin homolog	7	7	Multi	ER to Golgi transport	v-SNARE activity	endoplasmic reticulum	Pulldown
YLR276C	DBP9	ATP-dependent RNA helicase of the DEAD-box family involved in biogenesis of the 60S ribosomal subunit	5	1	Singlish	35S primary transcript processing	ATP-dependent RNA helicase activity	nucleolus	Pulldown
YLR293C	GSP1	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, RNA processing and transport; regulated by Prp20p, Rna1p, Yrb1p, Yrb2p, Yrp4p, Yrb30p, Cse1p and Kap95p; yeast Gsp2p homolog	13	2	Singlish	rRNA processing	GTPase activity	cytoplasm	Pulldown

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YLR344W	RPL26A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl26Bp and has similarity to E. coli L24 and rat L26 ribosomal proteins; binds to 5.8S rRNA	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota)	Y2H
YLR362W	STE11	Signal transducing MEK kinase involved in pheromone response and pseudohyphal/invasive growth pathways, where it phosphorylates Ste7p, and the high osmolarity response pathway, via phosphorylation of Pbs2p; regulated by Ste20p and Ste50p	6	4	Multi	protein amino acid phosphorylation	MAP kinase kinase activity	cytoplasm	Y2H
YLR367W	RPS22B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Ap and has similarity to E. coli S8 and rat S15a ribosomal proteins	8	8	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukaryota)	Pulldown
YML092C	PRE8	20S proteasome beta-type subunit	12	7	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, alpha-subunit complex (sensu Eukaryota)	Pulldown
YMR109W	MYO5	One of two type I myosins; contains proline-rich tail homology 2 (TH2) and SH3 domains; MYO5 deletion has little effect on growth, but myo3 myo5 double deletion causes severe defects in growth and actin cytoskeleton organization	14	6	Multi	cell wall organization and biogenesis	microfilament motor activity	actin cortical patch	Pulldown
YMR121C	RPL15B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl15Ap and has similarity to rat L15 ribosomal protein; binds to 5.8 S rRNA	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota)	Pulldown
YMR183C	SSO2	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; syntaxin homolog that is functionally redundant with Sso1p	5	5	Multi	vesicle fusion	t-SNARE activity	cytoplasm	Pulldown
YMR186W	HSC82	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10-fold higher basal levels that HSP82 and induced 2-3 fold by heat shock	5	2	Singlish	response to stress	unfolded protein binding	cytoplasm	Pulldown

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YMR197C	VTI1	Involved in cis-Golgi membrane traffic; Vti1p is a v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p	11	5	Multi	vesicle fusion	v-SNARE activity	integral to Golgi membrane	Pulldown
YMR199W	CLN1	role in cell cycle START; G(sub)1 cyclin	8	2	Singlish	regulation of cyclin dependent protein kinase activity	cyclin-dependent protein kinase regulator activity	cytoplasm	Pulldown
YMR290C	HAS1	ATP-dependent RNA helicase; localizes to both the nuclear periphery and nucleolus; highly enriched in nuclear pore complex fractions; constituent of 66S pre-ribosomal particles	8	1	Singlish	rRNA processing	molecular function unknown	nucleolus	Pulldown
YMR308C	PSE1	Karyopherin/importin that interacts with the nuclear pore complex; acts as the nuclear import receptor for specific proteins, including Pdr1p, Yap1p, Ste12p, and Aft1p	5	5	Multi	mRNA-nucleus export	protein carrier activity	cytoplasm	Pulldown
YMR314W	PRE5	20S proteasome alpha-type subunit	8	5	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, alpha-subunit complex (sensu Eukaryota)	Pulldown
YNL016W	PUB1	Poly(A)+ RNA-binding protein, abundant mRNP-component protein hypothesized to bind a pool of non-translatable mRNAs; not reported to associate with polyribosomes	5	3	Multi	mRNA catabolism, nonsense-mediated decay	nucleic acid binding	cytoplasm	Pulldown
YNL030W	HHF2	One of two identical histone H4 proteins (see also HHF1); core histone required for chromatin assembly and chromosome function; contributes to telomeric silencing; N-terminal domain involved in maintaining genomic integrity	7	7	Multi	chromatin assembly or disassembly	DNA binding	nuclear nucleosome	Pulldown
YNL031C	HHT2	One of two identical histone H3 proteins (see also HHT1); core histone required for chromatin assembly, involved in heterochromatin-mediated telomeric and HM silencing; regulated by acetylation, methylation, and mitotic phosphorylation	7	7	Multi	chromatin assembly or disassembly	DNA binding	nuclear nucleosome	Pulldown

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YNL052W	COX5A	Subunit Va of cytochrome c oxidase, which is the terminal member of the mitochondrial inner membrane electron transport chain; predominantly expressed during aerobic growth while its isoform Vb (Cox5Bp) is expressed during anaerobic growth	7	7	Multi	aerobic respiration	cytochrome c oxidase activity	respiratory chain complex IV (sensu Eukaryota)	Pulldown
YNL098C	RAS2	GTP-binding protein that regulates the nitrogen starvation response, sporulation, and filamentous growth; farnesylation and palmitoylation required for activity and localization to plasma membrane; homolog of mammalian Ras proto-oncogenes	5	2	Singlish	sporulation (sensu Fungi)	GTPase activity	plasma membrane	Pulldown
YNL113W	RPC19	RNA polymerase subunit, common to RNA polymerases I and III	8	8	Multi	transcription from Pol I promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	Pulldown
YNL178W	RPS3	Protein component of the small (40S) ribosomal subunit, has apurinic/aprimidinic (AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat S3 ribosomal proteins	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic small ribosomal subunit (sensu Eukaryota)	Y2H
YNL298W	CLA4	Involved in localizing cell growth with respect to the septin ring; protein kinase, homologous to Ste20p, interacts with CDC42	6	2	Singlish	protein amino acid phosphorylation	protein serine/threonine kinase activity	actin cap	Y2H
YNR011C	PRP2	RNA-dependent ATPase in the DEAH-box family, required for activation of the spliceosome before the first transesterification step in RNA splicing	8	8	Multi	U2-type catalytic spliceosome formation for first transesterification step	pre-mRNA splicing factor activity	nucleus	Pulldown
YOL005C	RPB11	RNA polymerase II subunit B12.5; part of central core; similar to Rpc19p and bacterial alpha subunit	5	5	Multi	transcription from Pol II promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase II, core complex	Pulldown
YOL018C	TLG2	member of the syntaxin family of t-SNAREs; tSNARE that affects a Late Golgi compartment	10	6	Multi	vesicle fusion	v-SNARE activity	Golgi trans face	Pulldown

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YOL038W	PRE6	20S proteasome alpha-type subunit	13	6	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, alpha-subunit complex (sensu Eukaryota)	Pulldown
YOR036W	PEP12	Target membrane receptor (t-SNARE) for vesicular intermediates traveling between the Golgi apparatus and the vacuole; controls entry of biosynthetic, endocytic, and retrograde traffic into the prevacuolar compartment; syntaxin	7	6	Multi	Golgi to vacuole transport	t-SNARE activity	Golgi apparatus	Y2H
YOR061W	CKA2	may have a role in regulation and/or execution of the eukaryotic cell cycle; alpha' subunit of casein kinase II	5	4	Multi	protein amino acid phosphorylation	protein kinase CK2 activity	protein kinase CK2 complex	Pulldown
YOR063W	RPL3	Protein component of the large (60S) ribosomal subunit, has similarity to E. coli L3 and rat L3 ribosomal proteins; involved in the replication and maintenance of killer double stranded RNA virus	6	6	Multi	protein biosynthesis	structural constituent of ribosome	cytosolic large ribosomal subunit (sensu Eukaryota)	Pulldown
YOR065W	CYT1	Cytochrome c1, component of the mitochondrial respiratory chain; expression is regulated by the heme-activated, glucose-repressed Hap2p/3p/4p/5p CCAAT-binding complex	9	7	Multi	mitochondrial electron transport, ubiquinol to cytochrome c	electron transporter, transferring electrons within CoQH2-cytochrome c reductase complex activity	mitochondrial inner membrane	Y2H
YOR089C	VPS21	Rab5-like GTPase involved in vacuolar protein sorting and endocytosis post vesicle internalization; geranylgeranylated; geranylgeranylation required for membrane association	5	2	Singlish	protein-vacuolar targeting	GTPase activity	mitochondrion	Pulldown
YOR116C	RPO31	RNA polymerase III subunit C160, part of core enzyme; similar to bacterial beta-prime subunit	12	10	Multi	transcription from Pol III promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	Pulldown

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YOR117W	RPT5	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; recruited to the GAL1-10 promoter region upon induction of transcription	6	6	Multi	ubiquitin-dependent protein catabolism	ATPase activity	proteasome regulatory particle (sensu Eukaryota)	Pulldown
YOR151C	RPB2	RNA polymerase II second largest subunit B150, part of central core; similar to bacterial beta subunit	10	9	Multi	transcription from Pol II promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase II, core complex	Pulldown
YOR157C	PUP1	Endopeptidase with trypsin-like activity that cleaves after basic residues; beta-type subunit of 20S proteasome synthesized as a proprotein before being proteolytically processed for assembly into 20S particle; human homolog is subunit Z	9	5	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, beta-subunit complex (sensu Eukaryota)	Y2H
YOR207C	RET1	Second-largest subunit of RNA polymerase III, which is responsible for the transcription of tRNA and 5S RNA genes, and other low molecular weight RNAs	11	8	Multi	transcription from Pol III promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	Pulldown
YOR210W	RPB10	RNA polymerase subunit ABC10-beta, common to RNA polymerases I, II, and III	7	7	Multi	transcription from Pol II promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	Pulldown
YOR224C	RPB8	RNA polymerase subunit ABC14.5, common to RNA polymerases I, II, and III	10	10	Multi	transcription from Pol II promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	Pulldown
YOR259C	RPT4	One of six ATPases of the 19S regulatory particle of the 26S proteasome involved in the degradation of ubiquitinated substrates; required for spindle pole body duplication; localized mainly to the nucleus throughout the cell cycle	6	6	Multi	ubiquitin-dependent protein catabolism	ATPase activity	nucleus	Pulldown
YOR326W	MYO2	One of two type V myosins, involved in polarized distribution of mitochondria; required for mitochondrion and vacuole inheritance and nuclear spindle orientation; moves multiple cargo	7	6	Multi	endocytosis	microfilament motor activity	actin cap	Pulldown
YOR327C	SNC2	mediate the targeting and transport of secretory proteins; vesicle-associated membrane protein (synaptobrevin) homolog	7	7	Multi	endocytosis	v-SNARE activity	transport vesicle	Y2H

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YOR341W	RPA190	RNA polymerase I subunit; largest subunit of RNA polymerase I	10	8	Multi	transcription from Pol I promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase I complex	Pulldown
YOR362C	PRE10	20S proteasome alpha-type subunit	11	6	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, alpha-subunit complex (sensu Eukaryota)	Pulldown
YOR370C	MRS6	Rab escort protein, forms a complex with the Ras-like small GTPase Ypt1p that is required for the prenylation of Ypt1p by protein geranylgeranyltransferase type II (Bet2p-Bet4p)	5	2	Singlish	intracellular protein transport	Rab escort protein activity	cytoplasm	Pulldown
YPL031C	PHO85	Cyclin-dependent kinase, with ten cyclin partners; involved in environmental stress response; in phosphate-rich conditions, Pho85p-Pho80p complex phosphorylates Pho4p which in turn represses PHO5	8	2	Singlish	protein amino acid phosphorylation	cyclin-dependent protein kinase activity	nucleus	Y2H
YPL081W	RPS9A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Ap and has similarity to E. coli S4 and rat S9 ribosomal proteins	5	5	Multi	protein biosynthesis	structural constituent of ribosome	cytoplasm	Pulldown
YPL204W	HRR25	Protein kinase involved in regulating diverse events including vesicular trafficking, gene expression, DNA repair, and chromosome segregation; binds the CTD of RNA pol II; homolog of mammalian casein kinase 1delta (CK1delta)	6	4	Multi	DNA repair	protein kinase activity	nucleus	Pulldown
YPL232W	SSO1	Plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane; forms a complex, with t-SNARE Sec9p, that binds v-SNARE Snc2p; also required for sporulation; syntaxin homolog that is functionally redundant with Sso2p	7	6	Multi	vesicle fusion	t-SNARE activity	integral to plasma membrane	Pulldown
YPL240C	HSP82	Cytoplasmic chaperone (Hsp90 family) required for pheromone signaling and negative regulation of Hsf1p; docks with the mitochondrial import receptor Tom70p for preprotein delivery; interacts with co-chaperones Cns1p, Cpr6p, Cpr7p, and Sti1p	7	2	Singlish	response to stress	ATPase activity, coupled	cytoplasm	Pulldown

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YPL256C	CLN2	role in cell cycle START; G(sub)1 cyclin	8	2	Singlish	regulation of cyclin dependent protein kinase activity	cyclin-dependent protein kinase regulator activity	cytoplasm	Pulldown
YPR010C	RPA135	RNA polymerase I subunit A135	10	8	Multi	transcription from Pol I promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase I complex	Pulldown
YPR103W	PRE2	20S proteasome beta-type subunit, responsible for the chymotryptic activity of the proteasome	12	7	Multi	ubiquitin-dependent protein catabolism	endopeptidase activity	proteasome core complex, beta-subunit complex (sensu Eukaryota)	Pulldown
YPR110C	RPC40	RNA polymerase subunit, common to RNA polymerase I and III	7	7	Multi	transcription from Pol I promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	Pulldown
YPR119W	CLB2	Involved in mitotic induction; G(sub)2-specific B-type cyclin	10	2	Singlish	G2/M transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	cytoplasm	Y2H
YPR120C	CLB5	B-type cyclin with a role in DNA replication during S phase; has an additional functional role in formation of mitotic spindles along with Clb3p and Clb4p	10	2	Singlish	G1/S transition of mitotic cell cycle	cyclin-dependent protein kinase regulator activity	nucleus	Y2H
YPR165W	RHO1	GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p)	7	3	Multi	cell wall organization and biogenesis	GTPase activity	mitochondrion	Pulldown
YPR187W	RPO26	RNA polymerase subunit ABC23, common to RNA polymerases I, II, and III; part of central core; similar to bacterial omega subunit	8	8	Multi	transcription from Pol II promoter	DNA-directed RNA polymerase activity	DNA-directed RNA polymerase III complex	Pulldown
YPR191W	QCR2	Subunit 2 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial inner membrane electron transport chain; transcription is regulated by Hap1p, Hap2p/Hap3p, and heme	5	5	Multi	aerobic respiration	ubiquinol-cytochrome-c reductase activity	mitochondrion	Pulldown