

Metabolism	35	tRNA modification other tRNA-transcription activities mRNA synthesis mRNA processing (splicing) mRNA processing (5'-end, 3'-end processing and mRNA degradation) other mRNA-transcription activities RNA transport other transcription activities	mitochondrial transport vesicular transport (Golgi network, etc.) peroxisomal transport vacuolar transport extracellular transport cellular import other intracellular-transport activities
Energy	40	Protein synthesis	48
glycolysis gluconeogenesis pentose-phosphate pathway tricarboxylic-acid pathway respiration fermentation metabolism of energy reserves (glycogen and trehalose) other energy-generation activities		ribosomal proteins translation (initiation, elongation and termination) translational control tRNA synthetases other protein-synthesis activities	organization and biogenesis of cell wall and plasma membrane organization and biogenesis of cytoskeleton organization and biogenesis of endoplasmic reticulum and Golgi organization and biogenesis of chromosome structure mitochondrial organization and biogenesis peroxisomal organization and biogenesis endosomal organization and biogenesis vacuolar and lysosomal organization and biogenesis other cellular organization and biogenesis activities
Cell growth, cell division and DNA synthesis	41	Protein destination	49
cell growth budding, cell polarity and filament formation pheromone response and mating-type determination sporulation and germination meiosis DNA synthesis and replication recombination and DNA repair cell-cycle control and mitosis cytokinesis other cell-growth, cell-division and DNA- synthesis activities		protein folding and stabilization protein targeting, sorting and translocation protein modification (glycosylation, acylation, myristylation, palmitylation, farnesylation and processing) assembly of protein complexes proteolysis other protein-destination activities	
Transcription	45	Transport facilitation	51
rRNA synthesis rRNA processing other rRNA-transcription activities tRNA synthesis tRNA processing		ion channels ion transporters sugar and carbohydrate transporters amino-acid transporters lipid transporters purine and pyrimidine transporters allantoin and allantoate transporters transport ATPases ABC transporters drug transporters other transport-facilitators	
Intracellular transport	53	Signal transduction	58
nuclear transport		pheromone response generation morphogenesis osmosensing nutritional response other signal-transduction activities	
Unclassified proteins	60	Cell rescue	59
		stress response generation DNA repair (direct repair, base excision repair and nucleotide excision repair) detoxification cell death and ageing degradation of exogenous polynucleotides other cell-rescue activities	

Metabolism

amino-acid metabolism

amino-acid biosynthesis

[ORF]	[Gene]	[Encoded or related protein]
YHR037w	<i>PUT2</i>	1-pyrroline-5-carboxylate dehydrogenase
YDR035w	<i>ARO3</i>	2-dehydro-3-deoxyphosphohexonate aldolase, phenylalanine-inhibited
YBR249c	<i>ARO4</i>	2-dehydro-3-deoxyphosphohexonate aldolase, tyrosine-inhibited
YNL104c	<i>LEU4</i>	2-isopropylmalate synthase
YGL009c	<i>LEU1</i>	3-isopropylmalate dehydratase
YPR167c	<i>MET16</i>	3'-phosphoadenyl sulphate reductase
YGR019w	<i>UGA1</i>	4-aminobutyrate aminotransferase (GABA transaminase)
YER091c	<i>MET6</i>	5-methyltetrahydropteroylglutamate-homocysteine methyltransferase
YMR108w	<i>ILV2</i>	acetolactate synthase
YCL009c	<i>ILV6</i>	acetolactate synthase, regulatory subunit
YER069w	<i>ARG5,6</i>	acetylglutamate kinase and acetylglutamyl-phosphate reductase
YJL071w	<i>ARG2</i>	acetylglutamate synthase
YOL140w	<i>ARG4</i>	acetylornithine aminotransferase
YDR234w	<i>LYS4</i>	aconitate hydratase
YER086w	<i>ILV1</i>	anabolic serine and threonine dehydratase
YDR354w	<i>TRP4</i>	anthranilate phosphoribosyltransferase
YER090w	<i>TRP2</i>	anthranilate synthase component I
YKL21c	<i>TRP3</i>	anthranilate synthase component II
YJR109c	<i>CPA2</i>	arginine-specific carbamoylphosphate synthase, large subunit
YOR303w	<i>CPA1</i>	arginine-specific carbamoylphosphate synthase, small subunit
YOL058w	<i>ARG1</i>	argininosuccinate synthetase
YHR018c	<i>ARG4</i>	arginosuccinate lyase
YDR127w	<i>ARO1</i>	arom pentafunctional enzyme
YPR145w	<i>ASN1</i>	asparagine synthetase
YGR124w	<i>ASN2</i>	asparagine synthetase
YLR027c	<i>AAT2</i>	aspartate aminotransferase, cytosolic
YKL106w	<i>AA1</i>	aspartate transaminase, mitochondrial
YDR158w	<i>AA1</i>	aspartate-semialdehyde dehydrogenase
YFR030w	<i>MET10</i>	assimilatory sulphite reductase flavin-binding subunit
YER055c	<i>HIS1</i>	ATP phosphoribosyltransferase
YCL018w	<i>LEU2</i>	β -isopropyl-malate dehydrogenase
YJR148w	<i>TWT2</i>	branched-chain amino acid aminotransferase, cytosolic
YHR208w	<i>TWT1</i>	branched-chain amino acid aminotransferase, mitochondrial
YGR204w	<i>ADE3</i>	C1-tetrahydrofolate synthase, cytoplasmic

<i>YPR084W</i>	<i>MIS1</i>	C1-pyrrole-5-carboxylate synthase, mitochondrial
<i>YPR060c</i>	<i>ARO7</i>	chorismate mutase
<i>YLG148w</i>	<i>ARO2</i>	chorismate synthase
<i>YGR155w</i>	<i>CYS4</i>	cystathione β -synthase
<i>YAL012w</i>	<i>CYS3</i>	cystathione γ -lyase
<i>YER023w</i>	<i>PRO3</i>	8 α -pyrroline-5-carboxylate reductase
<i>YHR068w</i>	<i>DYS1</i>	deoxyhypusine synthase
<i>YOR236w</i>	<i>DFR1</i>	dihydrofolate reductase
<i>YFL018c</i>	<i>LPD1</i>	dihydroloipoamide dehydrogenase
<i>YJR016c</i>	<i>ILV3</i>	dihydroxy-acid dehydratase
<i>YLR172c</i>	<i>DPH5</i>	diphthamide methyltransferase
<i>YKL191w</i>	<i>DPH2</i>	diphtheria toxin resistance protein
<i>YOR323c</i>	<i>PRO2</i>	γ -glutamyl phosphate reductase
<i>YDR300c</i>	<i>PRO1</i>	glutamate 5-kinase
<i>YDL171c</i>	<i>GLT1</i>	glutamate synthase (NADPH) (GOGAT)
<i>YPR035w</i>	<i>GLN1</i>	glutamate-ammonia ligase
<i>YBR248c</i>	<i>HIS7</i>	glutamine amidotransferase/cyclase
<i>YFR025c</i>	<i>HIS2</i>	histidinol phosphatase
<i>LIL116w</i>	<i>HIS5</i>	histidinol-phosphate aminotransferase
<i>YMR038c</i>	<i>LYS7</i>	homocitrate dehydrogenase
<i>YDL182w</i>	<i>LYS20</i>	homocitrate synthase
<i>YJR139c</i>	<i>HOM6</i>	homoserine dehydrogenase
<i>YHR025w</i>	<i>THR1</i>	homoserine kinase
<i>YNL277w</i>	<i>MET2</i>	homoserine O-acetyltransferase
<i>YOR202w</i>	<i>HIS3</i>	imidazoleglycerol-phosphate dehydratase
<i>YLR355c</i>	<i>ILV5</i>	ketol-acid reducto-isomerase
<i>YBL115c</i>	<i>LYS2</i>	L-aminoacidate-semialdehyde dehydrogenase, large subunit
<i>YGL154c</i>	<i>LYS5</i>	L-aminoacidate-semialdehyde dehydrogenase, small subunit
<i>YER052c</i>	<i>HOM3</i>	L-aspartate 4-P-transferase
<i>YLR303w</i>	<i>MET27</i>	O-acetylhomoserine sulphhydrylase
<i>YLR438w</i>	<i>CAR2</i>	ornithine aminotransferase
<i>YJL088w</i>	<i>ARG3</i>	ornithine carbamoyltransferase
<i>YCL030c</i>	<i>HIS4</i>	phosphoribosyl-AMP cyclodrolase/phosphoribosyl-ATP pyrophosphatase/histidinol dehydrogenase
<i>YDR007w</i>	<i>TRP1</i>	phosphoribosylanthranilate isomerase
<i>YGR208w</i>	<i>SER2</i>	phosphoserine phosphatase
<i>YOR184w</i>	<i>SER1</i>	phosphoserine transaminase
<i>YNL316c</i>	<i>PHA2</i>	prephenate dehydratase
<i>YBR166c</i>	<i>TYR1</i>	prephenate dehydrogenase (NADP $^+$)
<i>YLR142w</i>	<i>PUR1</i>	proline oxidase
<i>YOL064c</i>	<i>MET22</i>	protein ser/thr phosphatase
<i>YCR054c</i>	<i>CTR86</i>	putative threonine biosynthesis pathway protein
<i>YEL046c</i>	<i>GLY1</i>	required for glycine prototrophy in SHMT1 and SHMT2 double mutant
<i>YIR034c</i>	<i>LYS1</i>	saccharopine dehydrogenase
<i>YNR050c</i>	<i>LYS9</i>	saccharopine dehydrogenase (NADP $^+$, L-glutamate forming)

		similarity to acetolactate synthase III small subunit
YLR089c		similarity to alanine transaminases
YGL184c		similarity to cystathione β -lyase
YHR112c		similarity to cystathione γ -synthases
YIL074c		similarity to <i>E. coli</i> phosphoglycerate dehydrogenase
YGR012w		similarity to <i>E. nidulans</i> cysteine synthase
YMR250w		similarity to glutamate decarboxylases
YMR062c		similarity to glutamate N-acetyltransferase
YDL131w		similarity to homocitrate synthases and isopropylmalate synthases
YIL094c		similarity to isopropyl malate and tartrate dehydrogenases
YEL038w	UTR4	similarity to <i>K. oxytoca</i> endonuclease-phosphatase E-1
YML082w		similarity to <i>N. crassa</i>
		O-succinylhomoserine (thiol)-lyase
YJR130c		similarity to O-succinylhomoserine (thiol)-lyase
YKL215c		similarity to <i>P. aeruginosa</i> hyuA and hyuB
YOR280c		similarity to <i>S. pombe</i> dihydrofolate reductase
YFL030w		similarity to several transaminases
YOR108w		strong similarity to 2-isopropylmalate synthase
YAL004w		strong similarity to <i>A. klebsiana</i> glutamate dehydrogenase
YDR111c		strong similarity to alanine transaminase
YFR055w		strong similarity to β -cystathionases
YHR033w		strong similarity to glutamate 5-kinase
YHR070w		strong similarity to <i>N. crassa</i> met-10+ protein
YLL058w		strong similarity to <i>N. crassa</i>
		O-succinylhomoserine (thiol)-lyase
YER081w		strong similarity to phosphoglycerate dehydrogenases
YJR010w	MET3	sulphate adenylyltransferase
YCR053w	THR4	threonine synthase (o-p-homoserine p-lyase)
YPR074c	TKL1	transketolase 1
YBR117c	TKL2	transketolase 2
YGL026c	TRP5	tryptophan synthase
YML096w		weak similarity to asparagine synthases
regulation of amino-acid metabolism		
YDR173c	ARG82	arginine metabolism transcription factor
YKL112w	ABF1	ARS-binding factor
YER055c	HIS1	ATP phosphoribosyltransferase
YBR253w	SRB6	DNA-directed RNA polymerase II
		suppressor protein
YNL236w	SIN4	global regulator protein

YFL010w-a	AUA1	involved in ammonia regulation of amino-acid transport	other amino-acid metabolism activities	nucleotide metabolism
YIL046w	MET30	involved in regulation of sulphur assimilation genes	YKL157w <i>APE2</i> aminopeptidase yscII YGL017w <i>ATE1</i> arginyl tRNA transferase YPR069c <i>SPE3</i> putrescine aminopropyltransferase (spermidine synthase)	YLR028c <i>ADE16</i> 5-aminoimidazole-4-carboxamide ribotide transformylase
YJR060w	CBF1	kinetochore protein	YFR018c similarity to human glutaminyl-peptide cyclotransferase	YGR061c <i>ADE6</i> 5'-phosphoribosylformyl glycaminidine synthetase
YDR159w	SAC3	leucine permease transcriptional regulator		YML022w <i>APT1</i> adenine phosphoribosyltransferase
YDR207c	UME6	negative transcriptional regulator		YDR441c <i>APT2</i> adenine phosphoribosyltransferase
YKL015w	PUT3	positive activator of the proline utilisation pathway		YNL220w <i>ADE12</i> adenylosuccinate synthetase
YCR028c	FEN2	similarity to allantioate permease transporter		YIR027c <i>DAL1</i> allantoinase
YMR116c		strong similarity to <i>N. crassa</i> CPC2 protein		YIR029w <i>DAL2</i> allantoinase
YKR099w	BAS1	transcription factor		YMR300c <i>ADE4</i> amidophosphoribosyltransferase
YLR098c	CHA4	transcription factor		YML035c <i>AMD1</i> AMP deaminase
YLR451w	LEU3	transcription factor		YGR204w <i>ADE3</i> C1-tetrahydrofolate synthase, cytoplasmic
YMR042w	ARG80	transcription factor involved in arginine metabolism		YBR084w <i>MIS1</i> C1-tetrahydrofolate synthase, mitochondrial
YML099c	ARG81	transcription factor involved in arginine metabolism		YOR236w <i>DFR1</i> dihydrofolate reductase
YMR043w	MCM1	transcription factor of the MADS box family		YMR217w <i>GUA1</i> GMP synthase (glutamine-hydrolyzing) IMP dehydrogenase
YIR023w	DAL81	transcriptional activator for allantoin and GABA catabolic genes		YHR216w <i>PUR5</i> malate synthase 2
YEL009c	GCN4	transcriptional activator of amino acid biosynthetic genes		YIR031c <i>DAL7</i> methylenetetrahydrofolate dehydrogenase (NAD ⁺)
YDR034c	LYS14	transcriptional activator of lysine pathway genes		YAR015w <i>ADE1</i> phosphoribosylamidoimidazole-succinocarboxamide synthase
YIR017c	MET28	transcriptional activator of sulphur amino acid metabolism		YGL234w <i>ADE5,7</i> phosphoribosylamine-glycine ligase and phosphoribosylformylglycaminidine cyclo-ligase
YNL103w	MET4	transcriptional activator of sulphur metabolism		YOR128c <i>ADE2</i> phosphoribosylaminoimidazole carboxylase
amino-acid transport				
YBR068c	BAP2	amino-acid permease		YDR408c <i>ADE8</i> phosphoribosylglycaminide formyltransferase (GART)
YEL063c	CAN1	amino-acid permease		YKL181w <i>PRPS1</i> ribose-phosphate pyrophosphokinase
YBR069c	VAP1	amino-acid permease		YER099c <i>PRS2</i> ribose-phosphate pyrophosphokinase
YCL025c	AGP1	asparagine and glutamine permease		YHL011c <i>PRS3</i> ribose-phosphate pyrophosphokinase
YPL265w	DIP5	dicarboxylic amino-acid permease		YBL068w <i>PRS4</i> ribose-phosphate pyrophosphokinase
YKR039w	GAP1	general amino-acid permease		YLR058c <i>SHM2</i> serine hydroxymethyltransferase, cytoplasmic
YDR508c	GNP1	high-affinity glutamine permease		YBR263w <i>SHM1</i> serine hydroxymethyltransferase, mitochondrial
YGR055w	MUP1	high-affinity methionine permease		YNL141w similarity to adenosine deaminase
YNL270c	ALP1	high-affinity permease for basic amino acids		YBR284w similarity to AMP deaminase
YOL020w	SCM2	high-affinity tryptophan transport protein		YJL070c similarity to AMP deaminases
YGR191w	HIP1	histidine permease		YLR017w similarity to human 5'-methylthioadenosine phosphorylase
YLR375w	STP3	involved in pre-tRNA splicing and in uptake of branched-chain amino acids		YOL061w similarity to ribose-phosphate pyrophosphokinases
YDL048c	STP4	involved in pre-tRNA splicing and in uptake of branched-chain amino acids		YOR280c similarity to <i>S. pombe</i> dihydrofolate reductase
YNL268w	LYP1	lysine-specific high affinity permease		YDR020c similarity to uridine kinases and phosphoribulokinases
YOR130c	ARG11	member of the mitochondrial carrier family (MCF)		YLR359w strong similarity to adenylosuccinate lyase
YHL036w	MUP3	methionine permease		YMR120c strong similarity to chicken purH bifunctional enzyme
YOR348c	PUT4	proline and γ -aminobutyrate permease		YJR105w strong similarity to human adenosine kinase
YFL055w		similarity to Gap1p and other amino-acid permeases		YAR075w strong similarity to IMP dehydrogenases
YDR160w		similarity to lysine transport protein LYP1		YML056c strong similarity to IMP dehydrogenases
YLL061w		strong similarity to amino-acid transport protein Gap1p		YAR073w <i>FUN63</i> strong similarity to IMP dehydrogenases
YPL274w		strong similarity to amino-acid transport proteins		YLR432w strong similarity to IMP dehydrogenases, Pur5p and YML056c
YDR046c (PAP1)		strong similarity to amino-acid transport proteins		YLR209c strong similarity to purine-nucleoside phosphorylases
YBR132c		strong similarity to amino-acid permeases		YBR208c <i>DUR1,2</i> dUTP pyrophosphatase, mitochondrial ureidoglycolate hydrolase
amino-acid degradation				
YPL111w	CAR1	arginase		YLR39c <i>URA7</i> CTP synthase 1
YDR321w	ASP1	asparaginase		YJR103w <i>URA8</i> CTP synthase 2
YOR375c	GDH1	glutamate dehydrogenase (NADP ⁺)		YHR144c <i>DCD1</i> deoxycytidylate deaminase
YMR189w	GSD2	glycine decarboxylase subunit		YLR240w <i>URA4</i> dihydroorotate
YDR109c	GCV2	glycine decarboxylase T subunit		YKL216w <i>URA1</i> dihydroorotate dehydrogenase
YDR272w	GLC2	glyoxalase II		YJR057w <i>CDC8</i> dTMP kinase
YOR040w	GLC4	glyoxalase II		YBR252w <i>DUT1</i> dUTP pyrophosphatase, mitochondrial multifunctional pyrimidine biosynthesis protein
YLR155c	ASP3A	L-asparaginase II		YJL130c <i>URA2</i> protein
YLR157c	ASP3B	L-asparaginase II		YML106w <i>URA5</i> orotate phosphoribosyltransferase 1
YLR158c	ASP3C	L-asparaginase II		YMR271c <i>URA10</i> orotate phosphoribosyltransferase 2
YLR160c	ASP3D	L-asparaginase II		YEL021w <i>URA3</i> orotidine-5'-phosphate decarboxylase
YCL064c	CHAI	L-serine/L-threonine deaminase		YFL058w <i>THI5</i> pyrimidine biosynthesis protein
YAL062w	GDH3	NADP-glutamate dehydrogenase		YKL181w <i>PPRS1</i> ribose-phosphate pyrophosphokinase
YDL215c	GDH2	NAD-specific glutamate dehydrogenase (NAD)		YER099c <i>PRS2</i> ribose-phosphate pyrophosphokinase
YKL184w	ORD1	ornithine decarboxylase		YHL011c <i>PRS3</i> ribose-phosphate pyrophosphokinase
YLR142w	PUT11	proline oxidase		YBL068w <i>PRS4</i> ribose-phosphate pyrophosphokinase
YLR180w	SAM1	S-adenosylmethionine synthetase 1		YOL061w similarity to ribose-phosphate pyrophosphokinases
YDR502c	SAM2	S-adenosylmethionine synthetase 2		YOR280c similarity to <i>S. pombe</i> dihydrofolate reductase
YIL167w	SDL1	serine dehydratase		YLR245c strong similarity to <i>B. subtilis</i> cytidine deaminase
YDR294c		similarity to glutamate decarboxylases		YNL332w strong similarity to <i>Thi5p</i> , YJR156c, YDL244w and <i>A. parasiticus</i> , <i>S. pombe</i> Nmt1p
YJR078w		similarity to indoleamine 2,3-dioxogenase		YDL244w strong similarity to <i>Thi5p</i> , YJR156c, YNL332w and <i>A. parasiticus</i> , <i>S. pombe</i> nmt1 protein
YIL042c		similarity to rat branched-chain α -ketoadic dehydrogenase kinase		
YGL202w		similarity to rat kynurenine/ α -aminoacidate aminotransferase		
YHR137w		similarity to rat kynurenine/ α -aminoacidate aminotransferase		
YFL030w		similarity to several transaminases		
YDR111c		strong similarity to alanine transaminase		
YBR006w		strong similarity to <i>E. coli</i> succinate semialdehyde dehydrogenase		
YAL044c	GCV3	strong similarity to human glycine cleavage system protein H		
YIL168w	SDL1	strong similarity to L-serine dehydratase Cha1p		
YLR231c		strong similarity to rat kynureninase		
YKL218c		strong similarity to threonine dehydratase		
YBR208c	DUR1,2	urea amidolyase		
nitrogen and sulphur transport				
YGR121c	MEP1	ammonia permease of high capacity and moderate affinity		
YNL142w	MEP2	high-affinity low-capacity ammonia permease		
YBR294w	SUL1	high-affinity sulphate transport protein		
YPR003c	MEP3	similarity to sulphate transporter proteins		
YLR092w	SEL2	strong similarity to ammonium transport proteins		
YHL016c	DUR3	strong similarity to Sul1p		
nitrogen and sulphur utilization				
YGR019w	UGA1	4-aminobutyrate aminotransferase (GABA transaminase)		
YPL111w	CAR1	arginase		
YKL112w	ABF1	ARS-binding factor		
YNL216w	RAP1	DNA-binding protein with repressor and activator activity		
YFL010w-a	AUA1	involved in ammonia regulation of amino acid transport		
YIR030c	DCG1	involved in nitrogen-catabolite metabolism		
YBR213w	MET8	involved in the expression of PAPS reductase and sulphite reductase		
YDR207c	UME6	negative transcriptional regulator		
YNL229c	URE2	nitrogen catabolite repression regulator		
YEL062w	NPR2	nitrogen permease regulator		
YNL183c	NPR1	ser/thr protein kinase		
YRC028c	FEN2	similarity to allantioate permease transporter		
YLR013w		similarity to nitrogen regulatory proteins		
YGL254w	FZF1	sulphite resistance protein		
YFL021w	GAT1	transcription factor for nitrogen regulation		
YER040w	GLN3	transcription factor for positive nitrogen regulation		
YMR042w	ARG80	transcription factor involved in arginine metabolism		
YML099c	ARG81	transcription factor involved in arginine metabolism		
YMR043w	MCM1	transcription factor of the MADS box family		
YIR023w	DAL81	transcriptional activator for allantoin and GABA catabolic genes		
YDL170w	UGA3	transcriptional activator for GABA catabolic genes		
YNL103w	MET4	transcriptional activator of sulphur metabolism		
YKR034w	DAL80	transcriptional repressor for allantoin and GABA catabolic genes		
pyrimidine-ribonucleotide metabolism				
YBL039c	URA7	CTP synthase 1		
YJR103w	URA8	CTP synthase 2		
YHR144c	DCD1	deoxycytidylate deaminase		
YLR240w	URA4	dihydroorotate		
YKL216w	URA1	dihydroorotate dehydrogenase		
YJR057w	CDC8	dTMP kinase		
YBR252w	DUT1	dUTP pyrophosphatase, mitochondrial multifunctional pyrimidine biosynthesis protein		
YJL130c	URA2	protein		
YML106w	URA5	orotate phosphoribosyltransferase 1		
YMR271c	URA10	orotate phosphoribosyltransferase 2		
YEL021w	URA3	orotidine-5'-phosphate decarboxylase		
YFL058w	THI5	pyrimidine biosynthesis protein		
YKL181w	PPRS1	ribose-phosphate pyrophosphokinase		
YER099c	PRS2	ribose-phosphate pyrophosphokinase		
YHL011c	PRS3	ribose-phosphate pyrophosphokinase		
YBL068w	PRS4	ribose-phosphate pyrophosphokinase		
YOL061w		similarity to ribose-phosphate pyrophosphokinases		
YOR280c		similarity to <i>S. pombe</i> dihydrofolate reductase		
YLR245c		strong similarity to <i>B. subtilis</i> cytidine deaminase		
YNL332w		strong similarity to <i>Thi5p</i> , YJR156c, YDL244w and <i>A. parasiticus</i> , <i>S. pombe</i> Nmt1p		
YDL244w		strong similarity to <i>Thi5p</i> , YJR156c, YNL332w and <i>A. parasiticus</i> , <i>S. pombe</i> nmt1 protein		
deoxyribonucleotide metabolism				
YDR513w	TRR1	glutaredoxin		
YER070w	RNR1	uracil phosphoribosyltransferase		
		uridine kinase		
		uridine-monophosphate kinase		

YJL026w	RNR2	ribonucleoside-diphosphate reductase, small subunit	YHR043c	DOG2	2-deoxyglucose-6-phosphate phosphatase	YPR001w	CIT3	citrate (si)-synthase, mitochondrial			
YGR180c	RNR4	ribonucleotide reductase small subunit	YMR282c	AEP2	2'-O-ribosyl phosphate transferase	YCR005c	CIT2	citrate (si)-synthase, peroxisomal			
YIL066c	RNR3	ribonucleotide reductase, repair inducible large subunit	YBR092c	PHO3	constitutive acid phosphatase	YML086c	ALO	D-arabinino-1,4-lactone oxidase			
YBR014c		similarity to glutaredoxin	YHR201c	PPX1	exopolyphosphatase	YNL071w	LAT1	dihydrolipoamide S-acetyltransferase			
YPL059w		similarity to glutaredoxins	YBR011c	IPP1	inorganic pyrophosphatase, cytoplasmic	YDL174c	DLD1	D-lactate ferricytochrome c oxidoreductase (D-LCR)			
YOR269w	PAC1	similarity to human LIS-1 protein	YMR267w	PPA2	inorganic pyrophosphatase, mitochondrial	YER062c	HOR2	DL-glycerol phosphatase			
YDL010w		similarity to hypothetical protein YBR014c and glutaredoxins	YBR093c	PHO5	repressible acid phosphatase	YIL053w	RHR2	DL-glycerol phosphatase			
YCL035c		strong similarity to glutaredoxin	YAR071w	PHO11	secreted acid phosphatase	YPL227c	ALG5	dolichol-P-glucose synthetase			
YDR353w		strong similarity to thioredoxin reductase (NADPH)	YHR215w	PHO12	secreted acid phosphatase	YPR183w	DPM1	dolichyl-phosphate β -D-mannosyltransferase			
YHR106w		strong similarity to thioredoxin reductases	YDL024c	PPD3	strong similarity to acid phosphatase	YIR143c	PMT4	dolichyl-phosphate-mannose-protein O-mannosyl transferase			
YOR074c	CDC21	thymidylate synthase	YNL330c	RPD3	transcription modifier protein	YOR095c	RK11	D-ribose-5-phosphate ketol-isomerase			
metabolism of cyclic and unusual nucleotides											
YJL005w	CYR1	adenylate cyclase	YOL001w	PHO80	cyclin	YJL121c	POS18	D-ribulose-5-phosphate 3-epimerase			
YCL050c	APA1	ATP adenyllyltransferase I	YGR233c	PHO81	cyclin-dependent kinase inhibitor	YGR282c	BGL2	endo-1,3-glucanase of the cell wall			
YDR530c	APA2	ATP adenyllyltransferase II	YPL031c	PHO85	cyclin-dependent protein kinase	YLR286c	CTS1	endochitinase			
YOL081w	IRA2	GTPase-activating protein for RAS proteins	YML121w	GTR1	GTP-binding protein	YGR254w	ENO1	enolase I (2-phosphoglycerate dehydratase)			
YOR360c	PDE2	high affinity 3',5'-cyclic-nucleotide phosphodiesterase	YDL106c	GRF10	homeodomain protein	YHR174w	ENO2	enolase II (2-phosphoglycerate dehydratase)			
YPL212c	PUS1	pseudouridine synthase 1	YBR106w	PHO88	involved in phosphate transport	YOR393w	ERR1	enolase-related protein			
YGL063w	PUS2	pseudouridine synthase 2	YFR034c	PHO4	transcription factor	YPL281c	ERR2	enolase-related protein			
regulation of nucleotide metabolism											
YOL081w	IRA2	GTPase-activating protein for RAS proteins	YLR348c		dicarboxylate carrier protein	YOR190w	SPR1	exo-1,3-glucanase			
YOR101w	RAS1	GTP-binding protein	YML123c	PHO84	high-affinity inorganic phosphate/H ⁺ symporter	YDR261c	EXG2	exo-1,3-glucanase minor isoform			
YNL098c	RAS2	GTP-binding protein	YJL117w	PHO86	inorganic phosphate transporter	YLR300w	EXG1	exo-1,3-glucanase (I/II), major isoform			
YDL106c	GRF10	homeodomain protein	YBR106w	PHO88	involved in phosphate transport	YIR019c	STA1	extracellular 1,4-glucan glucosidase			
YGL248w	PDE1	low-affinity 3',5'-cyclic-nucleotide phosphodiesterase	YCR037c	PHO87	member of the phosphate permease family	YLR377c	FBP1	fructose-1,6-bisphosphatase			
YNL076w	MKS1	negative regulator of RAS-cAMP pathway	YJR077c	MIR1	phosphate transport protein, mitochondrial (MCF)	YJL155c	FBP26	fructose-2,6-bisphosphatase			
YJL096w		putative regulator of purine and/or pyrimidine biosynthesis	YNR013c		similarity to membrane protein Pho87p and hypothetical protein YJL198w	YKL060c	FBA1	functional homologue of Kre9p			
YOL110w	SHR5	RAS suppressor	YCR098c	GIT1	similarity to phosphate transporter proteins	YDL049c	KNH1	galactokinase			
YKR099w	BAS1	transcription factor	YER053c		strong similarity to mitochondrial phosphate transporter protein	YBR020w	GAL1	galactokinase			
YLR014c	PPR1	transcription factor regulating pyrimidine pathway	YJL198w		strong similarity to phosphate-repressible phosphate permease	YDR009w	GAL3	galactose-induced protein of aldo/keto reductase family			
YIR023w	DAL81	transcriptional activator for allantoin and GABA catabolic genes	YBR296c		strong similarity to phosphate-repressible phosphate permease	YOR120w	GCY1	glucan synthase subunit			
YNL314w	DAL82	transcriptional activator for allantoin catabolic genes	polynucleotide degradation								
YMR287c	MSU1	3'-5' exonuclease for RNA 3' ss-tail, mitochondrial	YDL236w	PHO13	4-nitrophenylphosphatase	YPR159w	KRE6	glucan synthase subunit			
YPL029w	SUV3	ATP-dependent RNA helicase, mitochondrial	YOR008c	SLG1	weak similarity to <i>L. mexicana</i> lmsap2 gene	YGR143w	SKN1	glucan synthase subunit			
YOR033c	DHS1	exonuclease, interacting with Msh2p	carbohydrate metabolism								
YKL149c	DBR1	lariat-debranching enzyme	YLR342w	FKS1	1,3-D-glucan synthase, catalytic subunit	YKL104c	GFA1	glucosamine-fructose-6-phosphate transaminase			
YGL173c	KEM1	multifunctional nuclease	YGR032w	GSC2	1,3-D-glucan synthase, subunit	YNL241c	ZWF1	glucose-6-phosphate dehydrogenase			
YLR363c	NMD4	Nam7p/Ulp1p-interacting protein	YEL011w	GLC3	1,4-glucan branching enzyme (glycogen branching enzyme)	YBR196c	PGI1	glucose-6-phosphate isomerase			
YJR132w	NMD5	Nam7p/Ulp1p-interacting protein	YHR044c	DOG1	2-deoxyglucose-6-phosphate phosphatase	YBR229c	ROT2	glucosidase II, catalytic subunit			
YMR080c	NAM7	nonsense-mediated mRNA decay protein	YHR043c	DOG2	2-deoxyglucose-6-phosphate phosphatase	YOR002w	ALG6	glucosyltransferase			
YGR072w	UPF3	nonsense-mediated mRNA decay protein	YIL125w	KGD1	2-oxoglutarate dehydrogenase complex E1 component	YOR067c	ALG8	glucosyltransferase			
YHR077c	NMD2	nonsense-mediated mRNA decay protein 2	YDR148c	KGD2	2-oxoglutarate dehydrogenase complex E2 component	YJL052w	TDH1	glyceraldehyde-3-phosphate dehydrogenase 1			
YJL208c	NUC1	nuclease, mitochondrial	YGR240c	PFK1	6-phosphofructokinase, α subunit	YJR009c	TDH2	glyceraldehyde-3-phosphate dehydrogenase 2			
YMR234w	RNH1	ribonuclease H	YMR205c	PFK2	6-phosphofructokinase, β subunit	YGR192c	TDH3	glyceraldehyde-3-phosphate dehydrogenase 3			
YPL123c		similarity to ribonucleases	YOL136c	PFK27	6-phosphofructose-2-kinase, isoenzyme 1	YHL032c	GUT1	glycerol kinase			
YGR195w		weak similarity to <i>P. aeruginosa</i> RNase PH	YOL136c	PFK27	6-phosphofructose-2-kinase, isoenzyme 2	YDL022w	GPD1	glycerol-3-phosphate dehydrogenase (NAD ⁺)			
nucleotide transport			YJR183w	GND1	6-phosphofructokinase dehydrogenase	YOL059w	GPD3	cytoplasmic			
YMR056c	AAC1	ADP/ATP carrier protein (MCF)	YBR074w	TPS2	α , α -trehalose	YIL155c	GUT2	glycerol-3-phosphate dehydrogenase (NAD ⁺)			
YBL030c	AAC2	ADP/ATP carrier protein (MCF)	YMR261c	TPS3	α , α -trehalose-phosphate synthase, 105K subunit	YPR160w	GPH1	glycogen phosphorylase			
YBR085c	AAC3	ADP/ATP carrier protein (MCF)	YOL107c	TPK26	α , α -trehalose-phosphate synthase, 115K subunit	YFL014w	HSP12	heat-shock protein			
YER056c	FCY2	purine-cytosine permease	YOL136c	TPK27	α , α -trehalose-phosphate synthase, 115K subunit	YFR053c	HXK1	hexokinase I			
YER060w	FCY21	purine-cytosine permease	YDR074w	TPS2	α , α -trehalose-phosphate synthase, 105K subunit	YGL253w	HXK2	hexokinase II			
YOR222w		similarity to ADP/ATP carrier proteins	YMR261c	TPS3	α , α -trehalose-phosphate synthase, 123K subunit	YDL013w	HEX3	hexose metabolism-related protein			
YPR011c		similarity to ADP/ATP carrier proteins and Graves disease carrier protein	YML100w	TSL1	α , α -trehalose-phosphate synthase, 123K subunit	YDL182w	LYS20	homocitrate synthase			
YOR071c		similarity to allantoin or uracil transport proteins	YBR126c	TPS1	α , α -trehalose-phosphate synthase, 56K subunit	YOR126c	EST2	isoamyl acetate hydrolytic enzyme			
YOR192c		similarity to allantoin or uracil transport proteins	YJR131w	MNS1	α , α -trehalose-phosphate synthase, 56K subunit	YNL037c	IDH1	isocitrate dehydrogenase (NAD ⁺) subunit 1			
YLR237w		similarity to allantoin transport protein	YDR483w	KRE2	α , α -trehalose-phosphate synthase, 56K subunit	YOR136w	IDH2	isocitrate dehydrogenase (NAD ⁺) subunit 2			
YGR096w		similarity to bovine Graves disease carrier protein	YER001w	MNN1	α , α -trehalose-phosphate synthase, 56K subunit	YDL066w	IDP1	isocitrate dehydrogenase (NADP ⁺), mitochondrial			
YHR002w		similarity to bovine mitochondrial carrier protein/Graves's disease carrier protein	YGL038c	OCH1	α , α -trehalose-phosphate synthase, 56K subunit	YLR174w	IDP2	isocitrate dehydrogenase, cytosolic			
YGL186c		similarity to hypothetical protein YER060w and weak similarity to Fcy2p	YAL054c	ACS1	acetyl-CoA synthetase	YER065c	ICL1	isocitrate dehydrogenase, cytosolic			
YBL042c		strong similarity to allantoin and uracil transport proteins	YLR153c	ACS2	acetyl-CoA synthetase	YOR336w	KRE5	killer toxin-resistance protein			
YER060w-a	FCY22	strong similarity to Fcy2p	YPR026w	ATH1	acetyl trehalase, vacuolar	YML054c	CYB2	lactate dehydrogenase cytochrome b2			
YBR021w	FUR4	uracil permease	YBR299w	MAL32	α -glucosidase	YDL168w	SFA1	long-chain alcohol dehydrogenase			
other nucleotide-metabolism activities			YGR292w	MAL12	α -glucosidase of the MAL1 locus	YOL126c	MHD2	malate dehydrogenase, cytoplasmic			
YDR226w	ADK1	adenylate kinase, cytosolic	YOL086c	ADH1	alcohol acetyltransferase	YKL085w	MHD1	malate dehydrogenase, mitochondrial			
YER170w	ADK2	adenylate kinase, mitochondrial	YOL377w	ATF1	alcohol dehydrogenase I	YDL078c	MDH3	malate dehydrogenase, peroxisomal			
YDR454c	GUK1	guanylate kinase	YOL086c	ADH1	alcohol dehydrogenase II	YNL117w	MLS1	malate synthase 1			
YKL067w	YNK1	nucleoside diphosphate kinase	YMR030c	ADH2	alcohol dehydrogenase III	YOR061w	KTR2	mannosyltransferase			
YDL125c	HNT1	similarity to protein kinase C inhibitor-I	YMR083w	ADH3	alcohol dehydrogenase IV	YDL095w	PMT1	mannosyltransferase			
YDR305c	HNT2	strong similarity to <i>S. pombe</i> diadenosine 5',5''-P ₄ -tetraphosphate asymmetric hydrolyase	YGL027c	CWH41	alcohol dehydrogenase V	YAL023c	PMT2	mannosyltransferase			
phosphate metabolism			YGL256w	ADH4	alcohol dehydrogenase VI	YOR321w	PMT3	mannosyltransferase			
phosphate utilization			YGR177c	ATF2	alcohol O-acetyltransferase	YBL082c	RHK1	mannosyltransferase			
YHR044c	DOG1	2-deoxyglucose-6-phosphate phosphatase	YOL040w	GLK1	alcohol dehydrogenase VII	YIL139c	YUR1	mannosyltransferase			
			YGL156w	AMS1	α -mannosidase	YIL153c	INO1	myo-inositol-1-phosphate synthase			
			YGL027c	CWH41	β -1,6-glucan assembly protein	YPL178w	SPT1	N-acetylglucosaminyltransferase			
			YHR101c	BIG1	big cells phenotype	YOR100c	NTH1	neutral trehalase (α , α -trehalase)			
			YBR110w	ALG1	β -mannosyltransferase	YPR006c	ICL2	non-functional isocitrate lyase			
			YBR084w	MIS1	C1-tetrahydrofolate synthase, mitochondrial	YJL002c	OST1	oligosaccharyltransferase α subunit			
			YNL322c	KRE1	cell-wall protein	YMR149w	SWP1	oligosaccharyltransferase δ subunit			
			YJL174w	KRE9	cell-wall synthesis protein	YOR103c	OST2	oligosaccharyltransferase ϵ subunit			
			YJL099w	CHS6	chitin biosynthesis protein	YOR085w	OST3	oligosaccharyltransferase γ subunit			
			YNL127w	CHS1	chitin synthase I	YDL232w	OST4	oligosaccharyltransferase subunit			
			YBR038w	CHS2	chitin synthase II	YGL022w	STT3	oligosaccharyltransferase subunit			
			YBR023c	CHS3	chitin synthase III	YEL058w	PCM1	phosphoacetylglucosamine mutase			
			YNR001c	CIT1	citrate (si)-synthase, mitochondrial	YKR097w	PCK1	phosphoenolpyruvate carboxykinase			
						YMR105c	PGM2	phosphoglucomutase, major isoform			
						YKL152c	PGM1	phosphoglucomutase, minor isoform			
						YKL152c	PGM1	phosphoglyceraldehyde dehydrogenase			
						YCR012w	PGK1	phosphoglycerate kinase			
								phosphoglycerate mutase			

YOL056w	<i>GPM3</i>	phosphoglycerate mutase	YJL218w	strong similarity to <i>E. coli</i> galactoside O-acetyltransferase	YCR081w	<i>SRB8</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit
YFL045c	<i>SEC53</i>	phosphomannomutase	YDR248c	strong similarity to <i>E. coli</i> thermostable gluconokinase	YNL025c	<i>SSN8</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue
YCR034w	<i>GNS1</i>	probable 1,3-glucan synthase subunit	YIL172c	strong similarity to Fsp2p	YLR071c	<i>RGR1</i>	DNA-directed RNA polymerase II holoenzyme subunit
YIL045w	<i>PIG2</i>	Protein interacting with Gsy2p	YDL037c	strong similarity to glucan 14-glucosidase	YBR253w	<i>SRB6</i>	DNA-directed RNA polymerase II suppressor protein
YIL085c	<i>KTR7</i>	putative α -1,2-mannosyltransferase	YDR516c	strong similarity to glucokinase	YOR047c	<i>STD1</i>	dosage-dependent modulator of glucose repression
YNL029c	<i>KTR5</i>	putative mannosyltransferase	YOR299w	strong similarity to hypothetical protein YMR237w and similarity to Chs6p	YJL155c	<i>FBP26</i>	fructose-2,6-bisphosphatase
YGR199w	<i>PMT6</i>	putative mannosyltransferase	YMR237w	strong similarity to hypothetical protein YOR299w and similarity to CHS6 protein	YPL037c	<i>EGD1</i>	GAL4 DNA-binding enhancer protein
YGL062w	<i>PYC1</i>	pyruvate carboxylase, isozyme 1	YNL009w	strong similarity to isocitrate dehydrogenase	YDR009w	<i>GAL3</i>	galactokinase
YBR218c	<i>PYC2</i>	pyruvate carboxylase, isozyme 2	YJL216c	strong similarity to Mal62p	YLL016w	<i>SDC25</i>	GDP/GTP exchange factor
YDR081c	<i>PDC2</i>	pyruvate decarboxylase regulatory protein	YOR089w	strong similarity to maltase	YLR310c	<i>CDC25</i>	GDP/GTP exchange factor for Ras1p and Ras2p
YLR044c	<i>PDC1</i>	pyruvate decarboxylase, isozyme 1	YDR368w	strong similarity to mannosyltransferases	YGR070w	<i>ROM1</i>	GDP/GTP exchange protein for Rho1p
YLR134w	<i>PDC5</i>	pyruvate decarboxylase, isozyme 2	KTR1	strong similarity to members of the aldo/keto reductase family	YLR371w	<i>ROM2</i>	GDP/GTP exchange protein for Rho1p
YGR087c	<i>PDC6</i>	pyruvate decarboxylase, isozyme 3	YPR1	strong similarity to phosphoglycerate mutase Gpm1p	YDR176w	<i>NNG1</i>	general transcriptional adaptor or co-activator
YER178w	<i>PDA1</i>	pyruvate dehydrogenase (lipoamide) α subunit	GPM2	strong similarity to phosphopyruvate hydratases	YER054c	<i>GIP2</i>	Glc7p-interacting protein
YBR221c	<i>PDB1</i>	pyruvate dehydrogenase (lipoamide) β subunit	YDL021w	strong similarity to polygalacturonases	YNL236w	<i>SIN4</i>	global regulator protein
YGR193c	<i>PDX1</i>	pyruvate dehydrogenase complex protein X	YDL080c	strong similarity to pyruvate decarboxylases	YHL025w	<i>SNF6</i>	global transcription activator
YAL038w	<i>CDC19</i>	pyruvate kinase	YMR323w	strong similarity to rumen fungus β -succinyl-CoA synthetase	YER027c	<i>GAL83</i>	glucose repression protein
YNL048w	<i>ALG11</i>	required for asparagine-linked glycosylation	YJR153w	strong similarity to S. pombe malate oxidoreductase	YNL199c	<i>GCR2</i>	glycolytic genes transcriptional activator
YCR036w	<i>RBK1</i>	ribokinase	YDL080c	strong similarity to S. xylosus glucose kinase	YOR101w	<i>RAS1</i>	GTP-binding protein
YJL137c	<i>GLG2</i>	self-glycosylating initiator of glycogen synthesis	YOR347c	strong similarity to pyruvate kinase	YNL098c	<i>RAS2</i>	GTP-binding protein
YMR306w		similarity to 1,3-glucan synthases	YGR244c	strong similarity to rumen fungus β -succinyl-CoA synthetase	YPR165w	<i>RHO1</i>	GTP-binding protein of the RHO subfamily of RAS-like proteins
YAL060w	<i>FUN49</i>	similarity to alcohol/sorbitol dehydrogenase	YKL029c	strong similarity to S. pombe malate oxidoreductase	YNL090w	<i>RHO2</i>	GTP-binding protein of the RHO subfamily of RAS-like proteins
YAL061w	<i>FUN50</i>	similarity to alcohol/sorbitol dehydrogenase	YBL001c	strong similarity to Y. lipolytica GPR1 gene	YDR420w	<i>HKR1</i>	Hansenula MrakII k9 killer toxin-resistance protein
YMR318c		similarity to alcohol-dehydrogenase	YLR164w	strong similarity to Sdh4p	YGL253w	<i>HXK2</i>	hexokinase II
YDL124w		similarity to aldo reductases	YDL246c	strong similarity to Sor1p	YPL002c	<i>SNF8</i>	involved in glucose derepression
YHR204w		similarity to α -mannosidases	YJL045w	strong similarity to succinate dehydrogenase flavoprotein	YOR125c	<i>CAT5</i>	involved in glucose repression
YPL088w		similarity to aryl-alcohol dehydrogenases	YGR043c	strong similarity to transaldolase	YML048w	<i>EFF2</i>	involved in glucose repression
YML070w		similarity to C. feundi dihydroxyacetone kinase	YNR071c	strong similarity to UDP-glucose 4-epimerase	YNL201c		involved in regulation of carbon metabolism
YIL124w		similarity to C. perfringens nanH protein	YDR384c	strong similarity to Y. lipolytica GPR1 gene	YGR227w	<i>DIE2</i>	ITR1 expression promoting protein
YDR371w		similarity to chitinases	YHR210c	strong similarity to UDP-glucose-4-epimerase	YBR297w	<i>MAL33</i>	maltose fermentation regulatory protein
YIR036c		similarity to E. coli 3-ketoacyl-ACP reductase	YKL148c	strong similarity to succinate dehydrogenase flavoprotein	YGR288w	<i>MAL13</i>	maltose pathway regulatory protein
YBR149w		similarity to Gcy1p and aldose reductases	YDR178w	strong similarity to succinate dehydrogenase membrane anchor subunit for Sdh2p	YLR131c	<i>ACE2</i>	metallothionein expression activator
YBR056w		similarity to glucan 1,3-glucosidase	YIL162w	strong similarity to sucrose hydrolyzing enzyme	YDR422c	<i>SIP1</i>	multicopy suppressor of snf1
YIL169c		similarity to glucan 1,4-glucosidase	YJR075w	strong similarity to pck1	YML051w	<i>GAL80</i>	negative regulator for expression of galactose-induced genes
YOL185c		similarity to glucan 1,4-glucosidase Mal5p	HOC1	suppressor of pck1	YNL076w	<i>MKS1</i>	negative regulator of RAS-cAMP pathway
YNL274c		similarity to glycerate- and formate-dehydrogenases	YLR354c	strong similarity to transaldolase	YIL19c	<i>RPI1</i>	negative regulator of RAS-cAMP pathway
YPL113c		similarity to glycerate dehydrogenases	YPR074c	strong similarity to transketolase 1	YLR025w	<i>SNF7</i>	nuclear protein
YPR184w		similarity to glycogen debranching enzymes	YBL117c	strong similarity to transketolase 2	YGL115w	<i>SNF4</i>	nuclear regulatory protein
YDL131w		similarity to homocitrate synthases and isopropylmalate synthases	YDR050c	strong similarity to triose-phosphate isomerase	YLR273c	<i>PIG1</i>	protein interacting with Gsy2p
YJR096w		similarity to Leishmania reduce	TPI1	strong similarity to UDP-glucose 4-epimerase	YLO45w	<i>PIG2</i>	protein interacting with Gsy2p
YKR096w		similarity to mitochondrial aldehyde dehydrogenase Ald1p	GAL10	strong similarity to UDP-glucose-hexose-1-phosphate uridylyltransferase	YDL006w	<i>PTC1</i>	protein ser/thr phosphatase 2c
YGL257c		similarity to Mn1p	YBR019c	strong similarity to UDP-glucose-starch glucosyltransferase, isoform 1	YDL134c	<i>PPH21</i>	protein ser/thr phosphatase PP2A-1
YIL014w		similarity to Mn1p	YPR018c	strong similarity to UDP-glucose-starch glucosyltransferase, isoform 2	YDL18c	<i>PPH22</i>	protein ser/thr phosphatase PP2A-2
YEL020c		similarity to O. formigenes oxalyl-CoA decarboxylase	YFR015c	strong similarity to UDP-glucose-starch glucosyltransferase, isoform 1	YBL061c	<i>SKT5</i>	protoplast regeneration and killer toxin resistance protein
YDL093w	<i>PMT5</i>	similarity to O-mannosyltransferases Pmt1p-Pmt4p	YLR258w	strong similarity to UDP-glucose-starch glucosyltransferase, isoform 2	YOL110w	<i>SHR5</i>	RAS suppressor
YMR278w		similarity to phosphomannomutases	YBR243c	strong similarity to UDP-N-acetylglucosamine-1-phosphate transferase	YJR095w	<i>ACR1</i>	regulator of acetyl-CoA synthetase activity
YDR307w		similarity to Pmt1p	YKL035w	strong similarity to UDP-glucose-1-phosphate uridylyltransferase	YKL038w	<i>RGT1</i>	regulator of glucose induced genes
YDR380w		similarity to pyruvate decarboxylases	YKR043c	weak similarity to phosphoglycerate mutase	YDR028c	<i>REG1</i>	regulatory subunit for protein phosphatase Glc7p
YDR245w	<i>MNN10</i>	similarity to S. pombe galactosyltransferase	YOR283w	weak similarity to phosphoglycerate mutases	YMR311c	<i>GLC8</i>	regulatory subunit for protein ser/thr phosphatase Glc7p
YLR070c		similarity to sugar dehydrogenases			YBR050c	<i>REG2</i>	regulatory subunit of type I protein phosphatase
YNR059w		similarity to α ,1,3-mannosyltransferase			YDR277c	<i>MTH1</i>	repressor of hexose transport genes
YHL012w		similarity to UDP glucose pyrophosphorylase			YNR052c	<i>POP2</i>	required for glucose derepression
YIR159w	<i>SOR1</i>	sorbitol dehydrogenase			YJR090c	<i>GRR1</i>	required for glucose repression and for glucose and cation transport
YIL099w	<i>SGA1</i>	sporulation specific glucan 1,4-glucosidase			YGL252c	<i>RTG2</i>	retrograde regulation protein
YER096w		sporulation-specific protein			YJR076c	<i>CDC11</i>	septin
YLR307w	<i>CD41</i>	sporulation-specific chitin deacetylase			YHR107c	<i>CDC12</i>	ser/thr phosphoprotein phosphatase 1, catalytic subunit
YLR308w	<i>CD42</i>	sporulation-specific chitin deacetylase			YER133w	<i>GLC7</i>	ser/thr phosphoprotein phosphatase 1, regulatory subunit
YNL331c		strong similarity to aryl-alcohol reductases			YOR178c	<i>GAC1</i>	ser/thr protein kinase of MAP kinase (MAPK) family
YCR107w		strong similarity to aryl-alcohol reductases			YLR113w	<i>HOG1</i>	similarity to 6-phosphofructo-2-kinase
YPL017c		strong similarity to dihydrolipoamide dehydrogenases			YLR345w		similarity to allantoate permease transporter
YBR205w	<i>KTR3</i>	strong similarity to α ,1,2-mannosyltransferase			YCR028c	<i>FEN2</i>	similarity to C. freundii dihydroxyacetone kinase
YBR199w	<i>KTR4</i>	strong similarity to α ,1,2-mannosyltransferase			YFL053w		similarity to C. freundii dihydroxyacetone kinase
YPL053c	<i>KTR6</i>	strong similarity to α ,1,2-mannosyltransferase			YDL225w		similarity to Cdc11p, Cdc3p and human CDC10 protein
YJL221c	<i>FSP2</i>	strong similarity to aryl-alcohol dehydrogenase			YHR193c	<i>EGD2</i>	similarity to human α -NAC
YOL157c		strong similarity to aryl-alcohol dehydrogenase			YDL203c		similarity to Skt5p
YCR105w		strong similarity to aryl-alcohol dehydrogenases			YNL257c	<i>SIP3</i>	Snf1p protein kinase interacting protein
YDL243c		strong similarity to aryl-alcohol dehydrogenase			YLR150w	<i>MPT4</i>	specific affinity for guanine-rich quadruplex nucleic acids
YJR155w		strong similarity to aryl-alcohol dehydrogenase			YFL052w		strong similarity to Mal63p, Mal23p and Mal33p
YFL056c		strong similarity to aryl-alcohol dehydrogenases			YHR155w		strong similarity to Snf1p-interacting protein Sip3p
YFL057c		strong similarity to aryl-alcohol dehydrogenases			YNR002c	<i>FUN34</i>	strong similarity to Y. lipolytica glyoxylate pathway regulator GPR1
YOL165c		strong similarity to aryl-alcohol dehydrogenases			YCR010c		strong similarity to Y. lipolytica GPR1 protein and Fun34p
YKR027w		strong similarity to Chs6p			YIL154c	<i>(IMP2)</i>	sugar utilization regulatory protein
YHR104w		strong similarity to D-xylene 1-dehydrogenase			YPL026c	<i>SKS1</i>	suppressor kinase of snf3
YEL070w		strong similarity to E. coli D-mannonate oxidoreductase			YPL129w	<i>ANC1</i>	TFIIF subunit (transcription initiation factor), 30k
YNR073c		strong similarity to E. coli D-mannonate oxidoreductase, identical to YEL070w			YPL248c	<i>GAL4</i>	transcription factor
					YMR125w	<i>GCR3</i>	transcription factor for glycolytic genes

YMR280c	CAT8	transcription factor involved in gluconeogenesis	YPL069c	BTS1	geranylgeranyl diphosphate synthase	YGL162w	SUT1	hypoxic protein involved in sterol uptake			
YMR043w	MCM1	transcription factor of the MADS box family	YGL126w	SCS3	inositol phospholipid synthesis protein involved in ergosterol biosynthesis	YMR208w	ERG12	mevalonate kinase			
YJL176c	SWI3	transcription regulatory protein	YOR237w	HES1	involved in ergosterol biosynthesis	YHL020c	OPI1	negative regulator of phospholipid biosynthesis pathway			
YPL075w	GCR1	transcriptional activator	YPL145c	KES1	involved in ergosterol biosynthesis	YDR207c	UME6	negative transcriptional regulator			
YOL116w	MSN1	transcriptional activator	YPL117c	IDI1	isopentenyl-diphosphate δ -isomerase lanosterol synthase	YAL051w	OAF1	peroxisome proliferating transcription factor			
YKL062w	MSN4	transcriptional activator	YHR072w	ERG7	long-chain-fatty-acid-CoA ligase	YOR363c	PIP2	peroxisome proliferating transcription factor			
YGL035c	MIG1	transcriptional repressor	YMR246w	FAA4	mannosyltransferase	YNL169c	PSD1	phosphatidylserine decarboxylase 1			
YIL147c	SLN1	two-component signal transducer	YNL219c	ALG9	methylene-fatty-acyl-phospholipid synthase	YAL013w	DEP1	regulator of phospholipid metabolism			
YLR006c	SSK1	two-component signal transducer	YJR073c	OPI3	synthase	YMR207c	HFA1	similarity to acetyl-CoA carboxylase			
YIL128c	PBS2	tyrosine protein kinase of the MAP kinase kinase family	YNR043w	MVD1	mevalonate pyrophosphate decarboxylase	YCR028c	FEN2	similarity to allantate permease transporter			
YLR258w	GSY2	UDP-glucosidase-starch glucosyltransferase, isoform 2	YPL076w	GPI2	N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein	YMR043w	MCM1	transcription factor of the MADS box family			
YDR216w	ADR1	zinc-finger transcription factor	YPL175w	SPT14	N-acetylglucosaminyltransferase	YOL004w	SIN3	transcription regulatory protein			
carbohydrate transport											
YCL040w	GLK1	aldohexose specific glucokinase	YDL142c	PGS1	phosphatidylglycerophosphate synthase	lipid and fatty-acid transport					
YKL217w	JEN1	carboxylic acid transporter protein	YNL169c	PSD1	phosphatidylserine decarboxylase 1	YGR037c	ACB1	acyl-CoA-binding protein (diazepam-binding inhibitor)			
YBR291c	CTP1	citrate transport protein, mitochondrial (MCF)	YGR170w	PSD2	phosphatidylserine decarboxylase 2	YNL130c	CPT1	diacylglycerol cholinophosphotransferase			
YLR348c		dicarboxylate carrier protein	YCL004w	PEL1	phosphatidylserine synthase	YBR041w	FAT1	long-chain-fatty-acid transporter			
YLR081w	GAL2	galactose (and glucose) permease	YMR220w	ERG8	phosphomevalonate kinase	YPL188c	PAT1	long-chain-fatty-acid transporter			
YGR289c	AGT1	general α -glucoside permease	YCR034w	GNS1	probable 1,3-glucan synthase subunit	YPL147w	PXA1	long-chain-fatty-acid transporter			
YLL043w	FPS1	glycerol channel protein	YGL196c	ELO1	putative 3-hydroxysteroid dehydrogenase required for elongation of fatty acids	YOR317w	FAA1	long-chain-fatty-acid-CoA ligase			
YNL318c	HXT14	hexose transport protein	YGR196c	GPI1	required for N-acetylglucosaminyl phosphatidylinositol synthesis	YER016w	FAA2	long-chain-fatty-acid-CoA ligase			
YJL214w	HXT8	hexose transport protein	YML008c	ERG6	S-adenosyl-methionine 6-24-sterol-c-methyltransferase	YMR246w	FAA4	outer carnitine acetyltransferase, mitochondrial			
YJL219w	HXT9	hexose transport protein	YMR296c	LCB1	serine C-palmitoyltransferase subunit	YAR035w	YAT1	protein disulphide-isomerase			
YFL011w	HXT10	hexose transporter	YDR062w	LCB2	serine C-palmitoyltransferase subunit	YCL043c	PDI1	similarity to carnitine O-acetyltransferase			
YDL194w	SNF3	high-affinity glucose transporter	YLR058c	SHM2	serine hydroxymethyltransferase, cytoplasmic	YER024w		Yat1p			
YEL069c	HXT13	high-affinity hexose transporter	YBR263w	SHM1	serine hydroxymethyltransferase, mitochondrial	YKL174c		similarity to choline transport protein			
YMR011w	HXT2	high-affinity hexose transporter	YMR207c	HFA1	similarity to acetyl-CoA carboxylase	YNR056c		Ctr1p			
YDR343c	HXT6	high-affinity hexose transporter	YDR147w		similarity to choline kinase	YHR123w	EPT1	sn-12-diacylglycerol ethanolamine- and cholinephosphotransferase			
YDR342c	HXT7	high-affinity hexose transporter	YBR159w		similarity to human 17-hydroxysteroid dehydrogenase						
YOL156w	HXT11	low-affinity glucose transporter	YDR376w	ARH1	similarity to human adrenodoxin reductase						
YHR094c	HXT1	low-affinity hexose transporter	YML131w		similarity to human leukotriene b4 12-hydroxydehydrogenase						
YDR345c	HXT3	low-affinity hexose transporter	YAR042w	OSH1	similarity to human oxysterol binding protein						
YDR497c	ITR1	major myo-inositol permease	YDR208w	MSS4	similarity to human PI P 5-kinase						
YBR298c	MAL31	maltose permease	YHR001w		similarity to Kes1p						
YHR092c	HXT4	moderate- to low-affinity glucose transporter	YKR003w		similarity to Kes1p, Hes1p and Osh1p						
YOL103w	ITR2	myo-inositol transport protein	YDL019c		similarity to Osh1p						
YIR035c		similarity to <i>C. lanceolata</i> 3-oxoacyl-[acyl-carrier-protein] reductase	YHR073w		similarity to Osh1p, Hes1p, Kes1p						
YBR241c		similarity to glucose transport proteins	YGR175c	ERG1	squalene monooxygenase						
YGL104c		similarity to glucose transport proteins	YGL055w	OLE1	stearoyl-CoA desaturase						
YPR021c		similarity to human citrate transporter protein	YGL012w	ERG4	sterol 24-reductase						
YDR387c		similarity to It1p1 and It2p2	YLR372w	SUR4	sterol isomerase						
YDL199c		similarity to sugar transporter proteins	YKL192c		strong similarity to acyl-carrier proteins						
YFL040w		similarity to yeast glucose transport proteins	YNL045w		strong similarity to human leukotriene-A4 hydrolase						
YHR096c	HXT5	strong similarity to hexose transporters	breakdown of lipids and phospholipids								
YDL245c	HXT15	strong similarity to Hxt17p and Haxt7p	YPL268w	PLC1	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase						
YJR160c		strong similarity to Mal3Tp	YGL205w	POX1	acyl-CoA oxidase						
YDR536w	STL1	strong similarity to members of the sugar permease family	YMR008c	PLB1	phospholipase B (lysophospholipase)						
YDL247w		strong similarity to sugar transport proteins	YKR031c	SPO14	phospholipase D						
YIL170w	HXT12	strong similarity to sugar transport proteins	YLR020c		similarity to triacylglycerol lipase						
YIL171w	HXT12	strong similarity to sugar transport proteins	YLL012w		similarity to triacylglycerol lipases						
YJR158w	HXT16	strong similarity to sugar transport proteins	YJL068c		strong similarity to human esterase D						
YNR072w	HXT17	sugar transport protein	YOL011w		strong similarity to phospholipases						
YDL138w	RGT2	suppressor of snf3 mutant	YMR006c		strong similarity to Plb1p						
lipid, fatty-acid and sterol metabolism			YKL140w	TGL1	triacylglycerol lipase						
lipid, fatty-acid and sterol biosynthesis			YDR058c	TGL2	triacylglycerol lipase						
YML075c	HMG1	3-hydroxy-3-methylglutaryl-CoA reductase 1	YJR176w		weak similarity to acylglycerol lipase						
YLR450w	HMG2	3-hydroxy-3-methylglutaryl-CoA reductase 2	YBR204c		weak similarity to peroxisomal serine-active lipase						
YML126c	HMG3	3-hydroxy-3-methylglutaryl-CoA synthase	lipid, fatty-acid and sterol utilization								
YPL028w	ERG10	acetyl-CoA C-acetyltransferase, cytosolic	YIL160c	POT1	acetyl-CoA C-acyltransferase, peroxisomal						
YNR016c	ACC1	acetyl-CoA carboxylase	YIL009w	FAA3	acyl-CoA oxidase						
YCR048w	ARE1	acyl-CoA sterol acyltransferase	YMR013c	SEC59	phospholipase B (lysophospholipase)						
YNR019w	ARE2	acyl-CoA sterol acyltransferase	YDR331w	GP18	phospholipase D						
YIL009w	FAA3	acyl-CoA synthase	YDR410c	STE14	similarity to triacylglycerol lipase						
YGR037c	ACB1	acyl-CoA-binding protein (diazepam-binding inhibitor)	YPL172c	COX10	similarity to triacylglycerol lipases						
YBR222c	PCS60	AMP-binding protein, peroxisomal	YOR370c	MSI4	strong similarity to human esterase D						
YER061c	CEM1	β -keto- α -ACP synthase	YGL155w	CDC43	strong similarity to phospholipases						
YNL280c	ERG24	C-14 sterol reductase	YPR176c	BET2	strong similarity to Plb1p						
YMR015c	ERG5	C-22 sterol desaturase	YJL031c	BET4	triacylglycerol lipase						
YGR060w	ERG25	C-4 sterol methyl oxidase	YFL014w	HSP12	triacylglycerol desaturase						
YLR056w	ERG3	C-5 sterol desaturase	YBL003w	COQ1	sterol 24-reductase						
YMR202w	ERG2	C-8 sterol isomerase	YKR009c	FOX2	sterol isomerase						
YML042w	CAT2	carnitine O-acetyltransferase	YOR317w	FAA1	strong similarity to acyl-carrier proteins						
YPR113w	PIS1	CDP diacylglycerol-inositol 3-phosphatidyltransferase	YER015w	FAA2	strong similarity to human leukotriene-A4 hydrolase						
YER026c	CHO1	CDP diacylglycerol serine O-phosphatidyltransferase	YMR246w	FAA4	strong similarity to human esterase D						
YBR29c	CDS1	CDP diacylglycerol synthase	YDL078c	MDH3	strong similarity to Plb1p						
YLR133w	CK11	choline kinase	YLR195c	MM17	triacylglycerol synthase						
YGR007w	MUO1	choline phosphate cytidylyltransferase	YJR066w	TOR1	hexaprenyl pyrophosphate synthetase						
YGR202c	PCT1	cholinephosphate cytidylyltransferase	YKL019w	RAM2	hexaprenyl pyrophosphate synthetase						
YNL111c	CYB5	cytochrome b5	YDL090c	RAM1	hexaprenyl pyrophosphate synthetase						
YHR007c	ERG11	cytochrome P450 lanosterol 14 α -demethylase	YHR013c	ARD1	hexaprenyl pyrophosphate synthetase						
YHR190w	ERG9	farnesyldiphosphate farnesyltransferase	YDL040c	NAT1	hexaprenyl pyrophosphate synthetase						
YJL167w	ERG20	farnesyl-pyrophosphate synthetase	regulation of lipid, fatty-acid and sterol biosynthesis								
YDL052c	SLC1	fatty acyltransferase	YBL015w	ACH1	acyl-CoA hydrolase						
YPL231w	FAS2	fatty acyl-CoA synthase, α subunit	YDR123c	INO2	basic helix-loop-helix transcription factor						
YKL182w	FAS1	fatty acyl-CoA synthase, β subunit	YOL108c	INO4	basic helix-loop-helix transcription factor						
metabolism of vitamins, cofactors and prosthetic groups											
YOL096c	COQ3	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase	YDR232w	HEM1	5-aminolevulinate synthase						
YPR036c	CSG2	calcium dependent regulatory protein	YOL143c	RB4	6,7-dimethyl-8-ribityllumazine synthase						
YMR079w	SEC14	phosphatidylinositol/phosphatidylcholine transfer protein	YGR286c	BIO2	biotin synthetase						
YNL264c		similarity to Sec14p	YGR204w	ADE3	C1-tetrahydrofolate synthase, cytoplasmic						
YKL091c		strong similarity to Sec14p	YBR084w	MIS1	C1-tetrahydrofolate synthase, mitochondrial						
YIL002c		synaptosomal homologue 1	YDR44w	HEM13	coproporphyrinogen III oxidase						
YDR302w		weak similarity to human GPI-anchor biosynthesis protein	YPL132w	COX11	GTP cyclohydrolase I						
biosynthesis of vitamins, cofactors and prosthetic groups											
YOL096c	COQ3	3,4-dihydroxy-5-hexaprenylbenzoate synthase	YNR058w	BIO3	GTP cyclohydrolase II						
YPR036c	CSG2	calcium dependent regulatory protein	YBR003w	COQ1	hexaprenyl pyrophosphate synthetase						
YMR079w	SEC14	phosphatidylinositol/phosphatidylcholine transfer protein	YBR153w	RB7	HTP reductase						
YOL024c		similarity to Kes1p	YOR196c	LIP5	lipoic acid synthase						
YDR44w	HEM13	coproporphyrinogen III oxidase	YHR042w	NCP1	NADPH-cytochrome P450 reductase						
YPL132w	COX11	cytochrome c oxidase assembly protein	YOR209c	NPT1	nicotinate phosphoribosyltransferase						
YNR033w	ABZ1	para-aminobenzoate synthase	YNR041c	COQ2	para-hydroxybenzoate- polypropenyltransferase						
YNR041c		para-hydroxybenzoate-polypropenyltransferase	YGR267c	FOL2	GTP cyclohydrolase II						
YOL033c		phosphoserine transaminase	YBL033c	RB1	hexaprenyl pyrophosphate synthetase						
YBR035c		porphobilinogen deaminase	YBR256c	RB5	riboflavin synthase, α subunit						
YGR040c		porphobilinogen synthase	YER043c	SAH1	S-adenosyl-L-homocysteine hydrolase						
YER044w	HEM14	protoporphyrinogen oxidase, mitochondrial	YNL256w		similarity to bacterial dihydropteroate synthase						
YNR057c		putative dehydrobiotin synthetase	YKL027w		similarity to <i>E. coli</i> molybdopterin-converting factor chln						
YBR035c		pyridoxamine-phosphate oxidase	YIL145c		similarity to <i>E. coli</i> pantothenate synthetase						
YGR040c		riboflavin synthase	YGR255c		similarity to <i>E. coli</i> ubiH protein						
YER044w	HEM14	riboflavin synthase	YMR113w		similarity to <i>E. coli</i> pantothenate synthetase						
YER044w		porphobilinogen oxidase, mitochondrial	YGL125w		similarity to <i>E. coli</i> polyglutamate synthetases and strong similarity to hypothetical protein YKL132c						
YER044w		methylenetetrahydrofolate reductase			similarity to human methylenetetrahydrofolate reductase						

YPL023c	similarity to human methylenetetrahydrofolate reductase	YOR031w	<i>CRS5</i>	suppressor of <i>cup1</i> deletion, metallothionein-like protein	YGR192c	<i>TDH3</i>	glyceraldehyde-3-phosphate dehydrogenase 3						
YFR047c	similarity to human quinolinate phosphoribosyltransferase	YCL037c	<i>SRO9</i>	suppressor of <i>rho3</i>	YOL059w	<i>GPD3</i>	glycerol-3-phosphate dehydrogenase (NAD ⁺), mitochondrial						
YHR111w	similarity to molybdopterin biosynthesis proteins	YMR243c	<i>ZRC1</i>	zinc- and cadmium-resistance protein	YFR053c	<i>HXX1</i>	hexokinase I						
YOL151w	similarity to plant dihydroflavonol-4-reductases	YDL128w	<i>VCX1</i>	Ca ²⁺ -transport (H ⁺ /Ca ²⁺ exchange) protein, vacuolar	YGL253w	<i>HXX2</i>	hexokinase II						
YMR222c	similarity to <i>S. pombe</i> dihydrofolate reductase	YGL006w	<i>PMC1</i>	Ca ²⁺ -transporting P-type ATPase	YCR012w	<i>PGK1</i>	phosphoglycerate kinase						
YOR241w	similarity to tetrahydrofolylpolyglutamate synthase	YGR217w	<i>CCH1</i>	Ca ²⁺ -transporting P-type ATPase	YKL152c	<i>GPM1</i>	phosphoglycerate mutase						
YJR142w	similarity to thiamin pyrophosphokinase	YLR348c		calcium channel protein	YOL056w	<i>GPM3</i>	phosphoglycerate mutase						
YKR069w	similarity to uroporphyrinogen methyltransferases	YKL016c	<i>ATP7</i>	dicarboxylate carrier protein	YER178w	<i>PDA1</i>	pyruvate dehydrogenase (lipoamide)						
YGL039w	similarity to <i>V. vinifera</i> dihydroflavonol reductase	YBL099w	<i>ATP1</i>	F1FO-ATPase complex, F0 D subunit	YBR221c	<i>PDB1</i>	α subunit						
YBR176w	strong similarity to <i>E. coli</i> 3-methyl-2-oxobutanate hydroxymethyltransferase	YJR121w	<i>ATP2</i>	F1FO-ATPase complex, F1 α subunit	YGR193c	<i>PDX1</i>	pyruvate dehydrogenase complex protein X						
YHR003c	strong similarity to molybdopterin-converting factor homologue YKL027w	YDL004w	<i>ATP16</i>	F1FO-ATPase complex, F1 β subunit	YAL038w	<i>CDC19</i>	pyruvate kinase						
YDL036c	strong similarity to Rib2p	YPL078c	<i>ATP4</i>	F1FO-ATPase complex, F1 δ subunit	YLR345w		similarity to 6-phosphofructo-2-kinase						
YOL049w	strong similarity to <i>S. pombe</i> Gsa1p	YPL271w	<i>ATP15</i>	F1FO-ATPase complex, F1 ϵ subunit	YDL021w	<i>GPM2</i>	strong similarity to phosphoglycerate mutase Gpm1p						
YOR143c	<i>THI80</i>	YBR039w	<i>ATP3</i>	F1FO-ATPase complex, F1 γ subunit	YMR323w		strong similarity to phosphopyruvate hydratases						
YPL214c	<i>TH16</i>	YDR298c	<i>ATP5</i>	F1FO-ATPase complex, OSCP subunit	YOR347c		strong similarity to pyruvate kinase						
YDR047w	<i>HEM12</i>	YLR295c	<i>ATP14</i>	F1FO-ATPase complex, subunit h	YKL029c		strong similarity to <i>S. pombe</i> malate oxidoreductase						
YOR278w	<i>HEM4</i>	YCR024c-a	<i>PMP1</i>	H ⁺ -ATPase subunit, plasma membrane	YMR125w	<i>GCR3</i>	transcription factor for glycolytic genes						
		YELO17c-a	<i>PMP2</i>	H ⁺ -ATPase subunit, plasma membrane	YDR050c	<i>TPI1</i>	triose-phosphate isomerase						
		YMR054w	<i>STV1</i>	H ⁺ -ATPase V0 domain 102K subunit, vacuolar	YKR043c		weak similarity to phosphoglycerate mutase						
utilization of vitamins, cofactors and prosthetic groups		YHR039c-a	<i>VMA10</i>	H ⁺ -ATPase V0 domain 13K subunit, vacuolar	YOR283w		weak similarity to phosphoglycerate mutases						
YDL141w	<i>BPL1</i>			H ⁺ -ATPase V0 domain 17K subunit, vacuolar									
YBR092c	<i>PHO3</i>			H ⁺ -ATPase V0 domain 17K subunit, vacuolar									
YAL039c	<i>CYC3</i>			H ⁺ -ATPase V0 domain 36K subunit, vacuolar									
YKL087c	<i>CYT2</i>	YOR270c	<i>VPH1</i>	H ⁺ -ATPase V0 domain 95K subunit, vacuolar									
YML120c	<i>ND11</i>	YGR020c	<i>VMA7</i>	H ⁺ -ATPase V1 domain 14K subunit, vacuolar									
YBR093c	<i>PHO5</i>	YOR332w	<i>VMA4</i>	H ⁺ -ATPase V1 domain 27K subunit, vacuolar									
YKL132c		YEL051w	<i>VMA8</i>	H ⁺ -ATPase V1 domain 32K subunit, vacuolar									
		YKL080w	<i>VMA5</i>	H ⁺ -ATPase V1 domain 42K subunit, vacuolar									
		YPR036w	<i>VMA13</i>	H ⁺ -ATPase V1 domain 54K subunit, vacuolar									
		YBR127c	<i>VMA2</i>	H ⁺ -ATPase V1 domain 60K subunit, vacuolar									
		YDL185w	<i>TFP1</i>	H ⁺ -ATPase V1 domain 69K subunit, vacuolar									
		YGL008c	<i>PMA1</i>	H ⁺ -transporting P-type ATPase									
		YPL036w	<i>PMA2</i>	H ⁺ -transporting P-type ATPase 2									
		YML123c	<i>PHO84</i>	high affinity inorganic phosphate/H ⁺ symporter									
		YJL129c	<i>TRK1</i>	high-affinity potassium transport protein									
		YBR294w	<i>SUL1</i>	high-affinity sulphate transport protein									
		YJL17w	<i>PHO86</i>	inorganic phosphate transporter									
		YLR220w	<i>CCC1</i>	involved in calcium regulation									
		YCR037c	<i>PHO87</i>	member of the phosphate permease family									
		YJL093c	<i>TOK1</i>	outward-rectifier potassium channel									
		YJR077c	<i>MIR1</i>	phosphate transport protein, mitochondrial (MCF)									
		YEL031w	<i>SFP1</i>	P-type ATPase									
		YDR040c	<i>ENA1</i>	P-type ATPase involved in Na ⁺ and Li ⁺ efflux									
		YDR039c	<i>ENA2</i>	P-type ATPase involved in Na ⁺ efflux									
		YDR038c	<i>ENAS</i>	P-type ATPase involved in Na ⁺ efflux									
		YLR138w	<i>NHA1</i>	putative Na ⁺ /H ⁺ antiporter									
		YBR235w		similarity to bumetanide-sensitive Na ⁺ K ⁺ -Cl ⁻ cotransport protein									
		YJL094c		similarity to <i>E. hirae</i> Na ⁺ /H ⁺ -antiporter NapA									
		YNR013c		similarity to membrane protein Pho87p and hypothetical protein YJL198w									
		YDR456w		similarity to NA ⁺ /H ⁺ antiports									
		YPR003c		similarity to sulphate transporter proteins									
		YER053c		strong similarity to mitochondrial phosphate carrier protein									
		YJL198w		strong similarity to Pho87p									
		YBR296c		strong similarity to phosphate-repressible phosphate permease									
		YLR092w	<i>SEL2</i>	strong similarity to Sul1p									
		YHL016c	<i>DUR3</i>	urea transport protein									
		YJR040w	<i>GEF1</i>	voltage-gated chloride channel protein									
ionic homeostasis													
homeostasis of metal ions													
YNL259c	<i>ATX1</i>	antioxidant protein and metal homeostasis factor											
YJR049c	<i>UTR1</i>	associated with ferric reductase activity											
YMR058w	<i>FET3</i>	cell-surface ferroxidase											
YOR316c	<i>COT1</i>	cobalt accumulation protein											
YPL177c	<i>CUP9</i>	copper homeostasis protein											
YDR515w	<i>SLT1</i>	copper homeostasis protein											
YPR124w	<i>CTR1</i>	copper transport protein											
YHR175w	<i>CTR2</i>	copper transport protein											
YLR411w	<i>CTR3</i>	copper transport protein											
YGL166w	<i>CUP2</i>	copper-dependent transcription factor											
YLR212w	<i>FRE1</i>	ferric (and cupric) reductase											
YKL220c	<i>FRE2</i>	ferric (and cupric) reductase											
YOR176w	<i>HEM15</i>	ferrocchelatase											
YGL255w	<i>ZRT1</i>	high-affinity zinc-transport protein											
YLL009c	<i>COX17</i>	interacts genetically with <i>SCO1</i> and <i>SCO2</i> in cytochrome oxidase assembly											
YBR037c	<i>SCO1</i>	involved in stabilization of Cox1p and Cox2p											
YGL071w	<i>RCS1</i>	iron-regulated transcriptional repressor											
YLR130c	<i>ZRT2</i>	low-affinity zinc transporter											
YMR319c	<i>FET4</i>	low-affinity Fe(II) iron transport protein											
YOL122c	<i>SMF1</i>	manganese transporter											
YBR290w	<i>BSD2</i>	metal homeostasis protein											
YKL064w	<i>MNR2</i>	overexpression overcomes manganese toxicity											
YDR270w	<i>CCC2</i>	probable copper-transporting ATPase											
YBR295w	<i>PCA1</i>	P-type Cu ²⁺ -transporting ATPase											
YGL096w		similarity to copper homeostasis protein Cup9p											
YDR506c		similarity to Fet3p											
YOL152w		similarity to Fre1p and Fre2p											
YGL160w		similarity to hypothetical protein YLR047c and Fre2p											
YJR126c		similarity to transferrin receptor protein											
YFL041w		strong similarity to cell-surface ferroxidase Fet3p											
YLL051c		strong similarity to ferric reductase Fre2p											
YOR381w		strong similarity to ferric reductase Fre2p											
YNR060w		strong similarity to Fre2p and hypothetical protein YOR381w, and similarity to Fre1p											
YBR024w	<i>SCO2</i>	strong similarity to Sco1p											
Energy													
glycolysis													
YGR240c	<i>PFK1</i>	6-phosphofructokinase, α subunit											
YMR205c	<i>PFK2</i>	6-phosphofructokinase, β subunit											
YIL107c	<i>PFK26</i>	6-phosphofructose-2-kinase, isoenzyme 1											
YOL136c	<i>PFK27</i>	6-phosphofructose-2-kinase, isoenzyme 2											
YNL071w	<i>LAT1</i>	dihydrolipoamide S-acetyltransferase											
YGR254w	<i>ENO1</i>	enolase I (2-phosphoglycerate dehydratase)											
YHR174w	<i>ENO2</i>	enolase II (2-phosphoglycerate dehydratase)											
YOR393w	<i>ERR1</i>	enolase-related protein											
YPL212c	<i>ERR2</i>	enolase-related protein											
YKL060c	<i>FBA1</i>	fructose-bisphosphate aldolase											
YBR196c	<i>PG11</i>	glucose-6-phosphate isomerase											
YIL052w	<i>TDH1</i>	glyceraldehyde-3-phosphate dehydrogenase 1											
YJR009c	<i>TDH2</i>	glyceraldehyde-3-phosphate dehydrogenase 2											
respiration													
YMR282c	<i>AEP2</i>	2'-O-ribosyl phosphate transferase											
YGR008c	<i>STF2</i>	ATPase stabilizing factor											
YDL130w-a	<i>STF1</i>	ATPase stabilizing factor, 10K											
YDR377w	<i>ATP17</i>	ATPase synthase subunit f											
YER061c	<i>CEM1</i>	β -ketothiacyl-ACP synthase											
YIL043c	<i>CBR1</i>	cytochrome b5 reductase											
YKL150w	<i>MCR1</i>	cytochrome b5 reductase											
YKL141w	<i>SDH3</i>	cytochrome b560 subunit of respiratory complex II											
YJR048w	<i>CYC1</i>	cytochrome c isoform 1											
YEL039c	<i>CYC7</i>	cytochrome c isoform 2											

YML129c	<i>COX14</i>	cytochrome c oxidase assembly protein	YLR134w	<i>PDC5</i>	pyruvate decarboxylase, isozyme 2	YHR179w	<i>OYE2</i>	NADPH dehydrogenase (old yellow enzyme), isoform 1
YDR079w	<i>PET100</i>	cytochrome c oxidase assembly protein	YGR087c	<i>PDC6</i>	pyruvate decarboxylase, isozyme 3	YPL171c	<i>OYE3</i>	NADPH dehydrogenase (old yellow enzyme), isoform 3
YGL187c	<i>COX4</i>	cytochrome c oxidase subunit IV	YAL060w	<i>FUN49</i>	similarity to alcohol/sorbitol dehydrogenase	YPR006c	<i>ICL2</i>	non-functional isocitrate lyase
YNL052w	<i>COX5A</i>	cytochrome c oxidase subunit V.A	YAL061w	<i>FUN50</i>	similarity to alcohol/sorbitol dehydrogenase	YOL079w		similarity to NADH dehydrogenase
YIL111w	<i>COX5B</i>	cytochrome c oxidase subunit V.b	YMR318c		similarity to alcohol-dehydrogenase	YEL020c		similarity to <i>O. formigenes</i> oxalyl-CoA decarboxylase
YHR051w	<i>COX6</i>	cytochrome c oxidase subunit VI	YHR039c		similarity to aldehyde dehydrogenases	YDR384c		strong similarity to <i>Y. lipolytica</i> <i>GPR1</i> gene
YGL191w	<i>COX13</i>	cytochrome c oxidase subunit VIa	YPL088w		similarity to aryl-alcohol dehydrogenases			
YLR038c	<i>COX12</i>	cytochrome c oxidase subunit VIb	YMR285c		similarity to Ccr4p			
YMR256c	<i>COX7</i>	cytochrome c oxidase subunit VII	YHL008c		similarity to <i>M. formicicum</i> formate dehydrogenase			
YDL067c	<i>COX9</i>	cytochrome c oxidase subunit VIIA	YKR096w		similarity to mitochondrial aldehyde dehydrogenase Ald1p			
YLR395c	<i>COX8</i>	cytochrome c oxidase subunit VIII	YDR380w		similarity to pyruvate decarboxylases			
YOR065w	<i>CYT1</i>	cytochrome c1	YNL331c		strong similarity aryl-alcohol reductase			
YER154w	<i>OXA1</i>	cytochrome oxidase biogenesis protein	YCR107w		strong similarity aryl-alcohol reductases			
YGR207c	<i>ETF-B</i>	electron-transferring flavoprotein, β subunit	YCR105w		strong similarity to alcohol dehydrogenases			
YKL016c	<i>ATP7</i>	F1FO-ATPase complex, F0 D subunit	YMR169c	<i>ALD4</i>	strong similarity to aldehyde dehydrogenase			
YBL099w	<i>ATP1</i>	F1FO-ATPase complex, F1 α subunit	YDL243c		strong similarity to aryl-alcohol dehydrogenase			
YJR121w	<i>ATP2</i>	F1FO-ATPase complex, F1 β subunit	YJR155w		strong similarity to aryl-alcohol dehydrogenase			
YDL004w	<i>ATP16</i>	F1FO-ATPase complex, F1 δ subunit	YFL056c		strong similarity to aryl-alcohol dehydrogenases			
YPL078c	<i>ATP4</i>	F1FO-ATPase complex, F1 ϵ subunit	YFL057c		strong similarity to aryl-alcohol dehydrogenases			
YPL271w	<i>ATP15</i>	F1FO-ATPase complex, F1 γ subunit	YOL165c		strong similarity to aryl-alcohol dehydrogenases			
YBR039w	<i>ATP3</i>	F1FO-ATPase complex, OSCP subunit	YOR388c		strong similarity to <i>H. polymorpha</i> formate dehydrogenase			
YDR298c	<i>ATP5</i>	F1FO-ATPase complex, subunit h						
YLR295c	<i>ATP14</i>	glucose-repressible protein						
YEL053c	<i>MAK10</i>	interacts genetically with <i>SCO1</i> and <i>SCO2</i> in cytochrome oxidase assembly						
YLL009c	<i>COX17</i>	involved in assembly of cytochrome oxidase						
YJR034w	<i>PET191</i>	involved in plasmid maintenance, respiration and cell proliferation						
YMR165c	<i>SMP2</i>	lactate dehydrogenase cytochrome b2 mitochondrial carrier protein (MCF) protease of the <i>SEC18/CDC48/PAS1</i> family of ATPases (AAA)						
YML054c	<i>CYB2</i>	pyruvate decarboxylase, isozyme 1						
YBR192w	<i>RIM2</i>	required for activity of mitochondrial cytochrome oxidase						
YMR089c	<i>YTA12</i>	similar to <i>M. domestica</i> NADPH-ferredoxin reductase and mammalian nitric-oxide synthases						
YLR044c	<i>PDC1</i>	similar to <i>N. crassa</i> cytochrome c oxidase subunit V						
YGR062c	<i>CCX18</i>	similarity to NCA3 and SUN4 protein						
YBR185c	<i>MBA1</i>	respiratory chain assembly protein ser/thr protein kinase						
YDL107w	<i>MSS2</i>	similarity to <i>M. domestica</i> NADPH-ferredoxin reductase and mammalian nitric-oxide synthases						
YPR048w		similar to <i>N. crassa</i> cytochrome c oxidase subunit V						
YGL226w		similar to NCA3 and SUN4 protein						
YMR244w		strong similarity to cytochrome b5- and nitrate reductases						
YML087c		strong similarity to cytochrome b5- and nitrate reductases						
YML125c		strong similarity to cytochrome b5- and nitrate reductases						
YPR004c		strong similarity to electron transfer flavoproteins α subunit						
YOR356w		strong similarity to human electron transfer flavoprotein-ubiquinone oxidoreductase						
YDL085w		strong similarity to NADH dehydrogenase (ubiquinone)						
YMR145c		strong similarity to NADH dehydrogenase (ubiquinone)						
YDL080c		strong similarity to pyruvate decarboxylases						
YDR178w	<i>SDH4</i>	succinate dehydrogenase membrane anchor subunit for Sdh2p						
YNL118c	<i>PSU1</i>	suppressor protein of a yeast <i>pet</i> mutant						
YFR033c	<i>QCR6</i>	ubiquinol-cytochrome c reductase 17K protein						
YPR191w	<i>QCR2</i>	ubiquinol-cytochrome c reductase 40K subunit II						
YBL045c	<i>COR1</i>	ubiquinol-cytochrome c reductase 44K core protein						
YHR001w-a	<i>QCR10</i>	ubiquinol-cytochrome c reductase 8.5K subunit						
YGR174c	<i>CBP4</i>	ubiquinol-cytochrome c reductase assembly factor						
YGL119w	<i>ABC1</i>	ubiquinol-cytochrome c reductase complex assembly protein						
YEL024w	<i>RIP1</i>	ubiquinol-cytochrome c reductase iron-sulphur protein						
YDR529c	<i>QCR7</i>	ubiquinol-cytochrome c reductase subunit 7						
YGR183c	<i>QCR9</i>	ubiquinol-cytochrome c reductase subunit 9						
YJL166w	<i>QCR8</i>	ubiquinol-cytochrome c reductase subunit VIII						
YMR073c		weak similarity to C-terminal part of cytochrome b5 and b2						
YNL237w	<i>YTP1</i>	weak similarity to mitochondrial electron transport proteins						
<i>fermentation</i>								
YOL086c	<i>ADH1</i>	alcohol dehydrogenase I	YIL160c	<i>POT1</i>	acetyl-CoA C-acyltransferase, peroxisomal acyl-CoA oxidase	YPL268w	<i>PLC1</i>	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
YMR303c	<i>ADH2</i>	alcohol dehydrogenase II	YGL205w	<i>POX1</i>	aldehyde dehydrogenase 2 (NAD $^+$)	YCR088w	<i>ABP1</i>	actin-binding protein
YMR083w	<i>ADH3</i>	alcohol dehydrogenase III	YMR170c	<i>ALD5</i>	mitochondrial	YDL029w	<i>ACT2</i>	actin-like protein
YGL256w	<i>ADH4</i>	alcohol dehydrogenase IV				YOL052c	<i>SPE2</i>	adenosylmethionine decarboxylase
YBR145w	<i>ADH5</i>	alcohol dehydrogenase V				YNL138w	<i>SRV2</i>	adenylate cyclase-associated protein, 70K
YER073w		aldehyde dehydrogenase (NAD $^+$)				YER170w	<i>ADK2</i>	adenylate kinase, mitochondrial
YPL061w	<i>ALD6</i>	aldehyde dehydrogenase, cytosolic				YBR109c	<i>CMD1</i>	calmodulin
YDL174c	<i>DLD1</i>	D-lactate ferricytochrome c oxidoreductase (D-LCR)						
YML004c	<i>GLO1</i>	glyoxalase I						
YOR126c	<i>EST2</i>	isoamyl acetate hydrolytic enzyme						
YPL275w		putative formate dehydrogenase/putative pseudogene						
YPL276w		putative formate dehydrogenase/putative pseudogene						
YDR081c	<i>PDC2</i>	pyruvate decarboxylase regulatory protein						
YLR044c	<i>PDC1</i>	pyruvate decarboxylase, isozyme 1						
<i>other energy-generation activities</i>								
YOL086c								
YER154w								
YGR207c								
YML129c								
YDR079w								
YGL187c								
YNL052w								
YIL111w								
YHR051w								
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YAL161w								

YDL159w	<i>STE7</i>	ser/thr/tyr protein kinase of MAP kinase kinase family	YBR078w	strong similarity to sporulation-specific Sps2p	YJR094c	<i>IME1</i>	transcription factor required for sporulation
YOL068c	<i>HST1</i>	silencing protein	YCL048w	strong similarity to sporulation-specific Sps2p	YGR044c	<i>RME1</i>	zinc-finger transcription factor
YBL052c	<i>SAS3</i>	silencing protein	YDR055w	strong similarity to Sps2p			
YKR101w	<i>SIR1</i>	silencing regulatory protein	YOR075w	<i>UFE1</i> syntaxis (T-SNARE) of the ER			
YDL042c	<i>SIR2</i>	silencing regulatory protein	YMR043w	<i>MCM1</i> transcription factor of the MADS box family			
YLR442c	<i>SIR3</i>	silencing regulatory protein	YJR094c	<i>IME1</i> transcription factor required for sporulation			
YDR227w	<i>SIR4</i>	silencing regulatory protein	YNL330c	<i>RPD3</i> transcription modifier protein	YKL112w	<i>ABF1</i> ARS-binding factor	
YNL283c		similarity to α-agglutinin core protein Aga1p	YLO044w	<i>SIN3</i> transcription regulatory protein	YFL009w	<i>CDC4</i> cell division control protein	
YDL225w		similarity to Cdc11p, Cdc3p and human CDC10 protein	YNL012w	<i>SPO1</i> transcriptional regulator involved in sporulation	YDR364c	<i>CDC40</i> cell division control protein	
YDR191w	<i>HST4</i>	similarity to Hst3p, Hst1p and Sir2p	YLL039c	<i>UBI4</i> ubiquitin	YLR274w	<i>CDC46</i> cell division control protein	
YGR023w		similarity to Mid2p	YGL058w	<i>RAD6</i> ubiquitin-conjugating enzyme	YBR202w	<i>CDC47</i> cell division control protein	
YHR146w		similarity to pheromone-response G-protein YNL173c	YDR177w	<i>UBC1</i> ubiquitin-conjugating enzyme	YIL194w	<i>CDC6</i> cell division control protein	
YKL117w		Ste6p-associated protein	YER125w	<i>RSP5</i> ubiquitin-protein ligase	YML102w	<i>CAC2</i> chromatin assembly complex, subunit p50	
YGL106w		strong similarity to calmodulins	YML115c	<i>VAN1</i> vanadate resistance protein	YBR195c	<i>MS11</i> chromatin assembly complex, subunit p50	
YIL212c		strong similarity to <i>S. pombe</i> ipsp4 protein			YPR018w	<i>RLF2</i> chromatin assembly complex, subunit p90	
YDR312w	<i>SSF2</i>	strong similarity to SSF1 protein			YPR120c	<i>CLB5</i> cyclin, B-type	
YPL129w	<i>ANC1</i>	TFIIF subunit (transcription initiation factor), 30K			YGR109c	<i>CLB6</i> cyclin, B-type	
YDR146c	<i>SWI5</i>	transcription factor			YPL256c	<i>CLN2</i> cyclin, G1/S specific	
YMR043w	<i>MCM1</i>	transcription factor of the MADS box family			YBR160w	<i>CDC28</i> cyclin-dependent protein kinase	
YNL330c	<i>RPD3</i>	transcription modifier protein	YPR103w	<i>PRE2</i> 26S proteasome subunit	YER176w	DNA dependent ATPase/DNA helicase B	
YOL004w	<i>SIN3</i>	transcription regulatory protein	YGR253c	<i>PUP2</i> 26S proteasome subunit	YHR164c	DNA helicase	
YIL176c	<i>SWI3</i>	transcription regulatory protein	YKL112w	<i>ABF1</i> ARS-binding factor	YDL164c	<i>CDC9</i> DNA ligase	
YHR084w	<i>STE12</i>	transcriptional activator	YFL037w	<i>TUB2</i> β-tubulin	YIL173c	<i>RFA3</i> DNA replication factor A, 13K subunit	
YER068w	<i>MOT2</i>	transcriptional repressor	YOR265w	<i>RBL2</i> β-tubulin binding protein	YNL312w	<i>RFA2</i> DNA replication factor A, 36K subunit	
YOL079c	<i>TPM1</i>	tropomyosin 1	YPL204w	<i>HRR25</i> casein kinase I, ser/thr/tyr protein kinase	YAR007c	<i>RFA1</i> DNA replication factor A, 69K subunit	
YOR219c	<i>STE13</i>	type IV dipeptidyl aminopeptidase	YBR136w	<i>ESR1</i> cell cycle checkpoint protein	YOL094c	<i>RFC4</i> DNA replication factor C, 37K subunit	
YMR022w	<i>QRI8</i>	ubiquitin-conjugating enzyme	YLP255w	<i>BPP1</i> cell division control protein	YNL290w	<i>RFC3</i> DNA replication factor C, 40K subunit	
YBR082c	<i>UBC4</i>	ubiquitin-conjugating enzyme	YDL220c	<i>CDC13</i> cell division control protein	YBR087w	<i>RFC5</i> DNA replication factor C, 40K subunit	
YDR059c		ubiquitin-conjugating enzyme	YPO42c	<i>SSN3</i> cyclin-dependent ser/thr protein kinase	YJR068w	<i>RFC2</i> DNA replication factor C, 41K subunit	
YER100w	<i>UBC6</i>	ubiquitin-conjugating enzyme	YOR368w	<i>RAD17</i> DNA damage checkpoint control protein	YOR217w	<i>RFC1</i> DNA replication factor C, 95K subunit	
YJR117w	<i>STE24</i>	zinc metallo-protease	YMR224c	<i>MRE11</i> DNA repair and meiotic recombination protein	YJR006w	<i>HUS2</i> DNA replication protein	
sporulation and germination							
YGR032w	<i>GSC2</i>	1,3-D-glucan synthase, subunit 26S proteasome subunit	YNL250w	<i>RAD50</i> DNA repair protein	YOL006c	<i>TOP1</i> DNA topoisomerase I	
YPR103w	<i>PRE2</i>	26S proteasome subunit	YDR076w	<i>RAD55</i> DNA repair protein	YNL088w	<i>TOP2</i> DNA topoisomerase II (ATP-hydrolysing)	
YGR253c	<i>PUP2</i>	26S proteasome subunit	YDR004w	<i>RAD57</i> DNA repair protein	YNL102w	<i>CDC17</i> DNA-directed DNA polymerase α, 180K subunit	
YBL015w	<i>ACH1</i>	acetyl-CoA hydrolase	YDR369c	<i>XRS2</i> DNA repair protein	YIR008c	<i>PRI1</i> DNA-directed DNA polymerase α, 48K subunit (DNA primase)	
YCR048w	<i>ARE1</i>	acyl-CoA sterol acyltransferase	YLR234w	<i>TOP3</i> DNA topoisomerase III	YKL045w	<i>PRI2</i> DNA-directed DNA polymerase α, 58K subunit (DNA primase)	
YNR019w	<i>ARE2</i>	acyl-CoA sterol acyltransferase	YGL163c	<i>RAD54</i> DNA-dependent ATPase of the Snf2p family	YPR135w	<i>POB1</i> DNA-directed DNA polymerase α-binding protein	
YOL052c	<i>SPE2</i>	adenosylmethionine decarboxylase	YKL017c	<i>DIP1</i> Dom34p Interacting Protein	YDL102w	<i>CDC2</i> DNA-directed DNA polymerase δ, catalytic 125K subunit	
YDR173c	<i>ARG82</i>	arginine metabolism transcription factor cAMP dependent protein kinase, regulatory subunit	YLR129w	<i>DIP2</i> Dom34p-interacting protein	YNL262w	<i>POL2</i> DNA-directed DNA polymerase ε, catalytic subunit A	
YIL033c	<i>SR1A</i>	cell division control protein	YBR045c	<i>GIP1</i> Glc7-interacting protein	YPR175w	<i>DPB2</i> DNA-directed DNA polymerase ε, subunit B	
YDR182w	<i>CDC1</i>	cell division control protein	YPL240c	<i>HSP82</i> heat-shock protein	YBR278w	<i>DPB3</i> DNA-directed DNA polymerase ε, subunit C	
YFL009w	<i>CDC4</i>	cell division control protein	YJL146w	<i>ID52</i> IME2-dependent signaling protein	YOR330c	<i>MIP1</i> DNA-directed DNA polymerase γ, catalytic subunit, mitochondrial	
YNL192w	<i>CHS1</i>	chitin synthase I	YOR198c	<i>BFR1</i> maintenance of normal ploidy	YPL167c	<i>REV3</i> DNA-directed DNA polymerase ζ	
YBR023c	<i>CHS3</i>	chitin synthase III	YHL022c	<i>SP011</i> meiosis-specific protein	YFL036w	<i>RPO41</i> DNA-directed RNA polymerase, mitochondrial	
YDR402c	<i>DIT2</i>	cytochrome P450 56	YER179w	<i>DMC1</i> meiosis-specific protein	YMR072w	<i>ABF2</i> high-mobility group protein	
YML110c	<i>DBF2</i>	DBF2 interacting protein	YIL072w	<i>HOP1</i> meiosis-specific protein	YJL090c	<i>DBP11</i> involved in DNA replication and S-phase checkpoint	
YOL051w	<i>GAL11</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YER180c	<i>ISC10</i> meiosis-specific protein	YDR068w	involved in genome stability	
YBR253w	<i>SRB6</i>	DNA-directed RNA polymerase II	YER044c-a	<i>ME14</i> meiosis-specific protein	YMR001c	<i>CDC5</i> involved in regulation of DNA replication	
		suppressor protein	YDL154w	<i>MSH5</i> meiosis-specific protein	YPR019w	member of the Cdc46p/Mcm2p/Mcm3p family	
YMR013c	<i>SEC59</i>	dolichol kinase	YHL124w	<i>NDT80</i> meiosis-specific protein	YBL023c	member of the Mcm2p,Mcm3p,Cdc46p family	
YOR190w	<i>SPR1</i>	exo-1,3-glucanase	YHR157w	<i>REC104</i> meiosis-specific protein	YML065w	origin recognition complex, 104K subunit	
YLR300w	<i>EXG1</i>	exo-1,3-glucanase (I/II), major isoform	YLR263w	<i>RED1</i> meiosis-specific protein	YNL261w	origin recognition complex, 50K subunit	
YDR261c	<i>EXG2</i>	exo-1,3-glucanase minor isoform	YHR079c-a	<i>SAE3</i> meiosis-specific protein	YHR118c	origin recognition complex, 50K subunit	
YBR045c	<i>GIP1</i>	Glc7p-interacting protein	YHR014w	<i>SPO13</i> meiosis-specific protein	YPR162c	origin recognition complex, 56K subunit	
YNL236w	<i>SIN4</i>	global regulator protein	YPL121c	<i>ME15</i> meiotic protein	YLL004w	origin recognition complex, 62K subunit	
YDL240w	<i>LRG1</i>	GTPase-activating protein of the RHO/RAC family	YBR057c	<i>MUM2</i> meiotic protein	YBR060c	origin recognition complex, 72K subunit	
YNL098c	<i>RAS2</i>	GTP-binding protein	YAL009w	<i>SP07</i> meiotic protein	YGR132c	prohibitin, antiproliferative protein	
YPL240c	<i>HSP82</i>	heat-shock protein	YNL210w	<i>MER1</i> meiotic recombination protein	YBR088c	proliferating cell nuclear antigen (PCNA)	
YJL146w	<i>ID52</i>	IME2-dependent signaling protein	YHR086w	<i>NAM8</i> meiotic recombination protein	YLR017w	protein kinase	
YER044c-a	<i>ME14</i>	meiosis-specific protein	YLR329w	<i>REC102</i> meiotic recombination protein	YFR028c	protein-tyrosine-phosphatase	
YBR057c	<i>MUM2</i>	meiotic protein	YJR021c	<i>REC107</i> meiotic recombination protein	YDR052c	regulatory subunit for Cdc7p protein kinase	
YAL009w	<i>SPO1</i>	meiotic protein	YMR133w	<i>REC114</i> meiotic recombination protein	YEL032w	replication initiation protein	
YLR025w	<i>SNF7</i>	nuclear protein	YGL175c	<i>SAE2</i> meiotic recombination protein	YIL139c	required for DNA damage-induced mutagenesis	
YKR031c	<i>SPO14</i>	phospholipase D	YHL027w	<i>RIM101</i> meiotic regulatory protein	YLR103c	required for minichromosome maintenance and initiation of chromosomal DNA replication	
YGL192w	<i>IME4</i>	positive transcription factor for IME2	YDR207c	<i>UME6</i> negative transcriptional regulator	YIL150c	required for S-phase initiation or completion	
YCR034w	<i>GNS1</i>	probable 1,3-glucan synthase subunit	YBR058w	<i>SHP1</i> potential regulatory subunit for Glc7p	YER070w	ribonucleoside-diphosphate reductase, large subunit	
YIRO26w	<i>YVH1</i>	protein tyrosine phosphatase	YMR076c	<i>PDS5</i> precocious dissociation of sister chromatids	YJL026w	<i>RNR2</i> ribonucleoside-diphosphate reductase, small subunit	
YOR208w	<i>PTP2</i>	protein-tyrosine-phosphatase	YDL017w	<i>CDC7</i> protein kinase	YIL066c	<i>RNR3</i> ribonucleotide reductase, repair inducible	
		putative transcription factor	YIR026c	<i>YVH1</i> protein tyrosine phosphatase	YIL150c	similarity to DNA-directed DNA polymerase II subunit C	
YER052c	<i>POP2</i>	required for glucose derepression	YOR208w	<i>PTP2</i> protein tyrosine phosphatase	YOR005c	similarity to EST1 protein	
YDR218c	<i>SPR28</i>	septin-related sporulation protein	YBR073w	<i>RDH54</i> required for meiosis	YDR206w	similarity to human mRNA for DNA ligase IV	
YIL106w	<i>IME2</i>	ser/thr protein kinase	YER133w	<i>GLC7</i> ser/thr phosphoprotein phosphatase 1, catalytic subunit	YOL095c	similarity to <i>S. aureus</i> DNA helicase PCRA	
YDR523c	<i>SPS1</i>	ser/thr protein kinase	YJL106w	<i>IME2</i> ser/thr protein kinase	YGL201c	similarity with rat intestinal DNA replication protein	
YNL307c	<i>MCK1</i>	ser/thr/tyr protein kinase	YMR139w	<i>MDS1</i> ser/thr protein kinase	YKL113c	ssDNA endonuclease and 5'-3' exonuclease	
YDR403w	<i>DIT1</i>	spore-wall maturation protein	YOR351c	<i>MEK1</i> ser/thr protein kinase	YCR028c-a	ssDNA-binding protein, mitochondrial	
YLR148w	<i>YSW1</i>	spore-specific protein	YDR523c	<i>SPS1</i> ser/thr protein kinase	YGR231c	strong similarity to prohibitins	
YKL165c		sporulation protein	YNL307c	<i>MCK1</i> ser/thr/tyr protein kinase	YBL035c	subunit of DNA polymerase α-primase complex	
YLR399c	<i>BDF1</i>	sporulation protein	YDL028c	<i>MPS1</i> ser/thr/tyr protein kinase	YLR233c	telomere elongation protein	
YHR152w	<i>SPO12</i>	sporulation protein	YNL001w	<i>DOM34</i> similarity to <i>D. melanogaster</i> pelota protein	YCR077c	topoisomerase II-associated protein	
YHR153c	<i>SPO16</i>	sporulation protein			YOL115w	topoisomerase I-related protein	
YIL099w	<i>SGA1</i>	sporulation specific glucan 1,4-glucosidase	YFL003c	<i>MSH4</i> similarity to MSH proteins			
YDR108w	<i>GSG1</i>	sporulation-specific protein	YHR152w	<i>SPO12</i> sporulation protein			
YER096w	<i>SHC1</i>	sporulation-specific protein	YHR153c	<i>SPO16</i> sporulation protein			
YLR307w	<i>CDA1</i>	sporulation-specific chitin deacetylase	YDR108w	<i>GSG1</i> sporulation-specific protein			
YLR308w	<i>CDA2</i>	sporulation-specific chitin deacetylase	YNL202w	<i>SPS19</i> sporulation-specific protein			
YPR054w	<i>SMK1</i>	sporulation-specific MAP kinase	YDR522c	<i>SPS2</i> sporulation-specific protein			
YER115c	<i>SPR6</i>	sporulation-specific protein	YNL204c	<i>SPS18</i> sporulation-specific zinc-finger protein			
YNL202w	<i>SPS19</i>	sporulation-specific protein	YBR078w	<i>Spes2p</i> strong similarity to sporulation-specific Spes2p			
YDR522c	<i>SPS2</i>	sporulation-specific protein	YCL048w	strong similarity to sporulation-specific Spes2p			
YOR313c	<i>SPS4</i>	sporulation-specific protein	YDR055w	strong similarity to Spes2p			
YGR059w	<i>SPR3</i>	sporulation-specific septin	YGR258c	<i>RAD2</i> structure-specific nucleases of the nucleotide excision repairosome			
YHR139c	<i>SPS100</i>	sporulation-specific wall maturation protein	YJR285w	<i>ZIP1</i> synaptonemal complex protein			
YNL204c	<i>SPS18</i>	sporulation-specific zinc-finger protein					

YLR182w	<i>SWI6</i>	transcription factor	YOR026w	<i>BUB3</i>	cell-cycle arrest protein	YGR140w	<i>CBF2</i>	kinetochore protein complex CBF3, 110K subunit
YDR054c	<i>CDC34</i>	ubiquitin-conjugating enzyme	YPL178w	<i>SAE1</i>	cell-cycle block in meiotic prophase	YMR094w	<i>CTF13</i>	kinetochore protein complex CBF3, 58K subunit
YGL058w	<i>RAD6</i>	ubiquitin-conjugating enzyme	YBR136w	<i>ESR1</i>	cell-cycle checkpoint protein	YMR168c	<i>CEP3</i>	kinetochore protein complex CBF3, 71K subunit
<i>recombination and DNA repair</i>								
YGL127c	<i>SOH1</i>	allows <i>hpr1</i> null mutant to grow at 37°C	YOR373w	<i>NUD1</i>	cell-cycle regulatory protein	YDR328c	<i>SKP1</i>	kinetochore protein complex CBF3, subunit D
YBR136w	<i>ESR1</i>	cell-cycle checkpoint protein	YPL256w	<i>BBP1</i>	cell division control protein	YOR198c	<i>BFR1</i>	maintenance of normal ploidy
YER173w	<i>RAD24</i>	cell-cycle checkpoint protein	YDR182w	<i>CDC1</i>	cell division control protein	YLR332w	<i>MID2</i>	matting process protein
YDR182w	<i>CDC1</i>	cell-division control protein	YCR002c	<i>CDC10</i>	cell division control protein	YER179w	<i>DMC1</i>	meiosis-specific protein
YMR106c	<i>HDF2</i>	component of DNA end-joining repair pathway	YDL220c	<i>CDC13</i>	cell division control protein	YHR079c-a	<i>SAE3</i>	meiosis-specific protein
YKL011c	<i>CCE1</i>	cruciform-cutting endonuclease, mitochondrial	YGL116w	<i>CDC20</i>	cell division control protein	YPR019w	<i>CDC54</i>	member of the Cdc46p/Mcm2p/Mcm3p family
YER176w		DNA-dependent ATPase/DNA helicase B	YLR314c	<i>CDC3</i>	cell division control protein	YDL126c	<i>CDC48</i>	microsomal protein of CDC48/PAS1/SEC18 family of ATPases
YLR032w	<i>RAD5</i>	DNA helicase	YDR168w	<i>CDC37</i>	cell division control protein	YOR058c	<i>ASE1</i>	microtubule-associated protein
YMR190c	<i>SGS1</i>	DNA helicase	YFL009w	<i>CDC4</i>	cell division control protein	YNL064c	<i>YD1</i>	mitochondrial and ER import protein
YML061c	<i>PIF1</i>	DNA helicase involved in mitochondrial DNA repair and telomere length	YDR364c	<i>CDC40</i>	cell division control protein	YGR029w	<i>ERV1</i>	mitochondrial biogenesis and regulation of cell cycle
YDL164c	<i>CDC9</i>	DNA ligase	YLR274w	<i>CDC46</i>	cell division control protein	YBL016w	<i>FUS3</i>	mitogen-activated protein kinase (MAP kinase)
YMR167w	<i>MHL1</i>	DNA mismatch repair protein	YBR202w	<i>CDC47</i>	cell division control protein	YMR294w	<i>JNM1</i>	mitosis protein, involved in nuclear migration
YOL090w	<i>MSH2</i>	DNA mismatch repair protein	YJL194w	<i>CBF5</i>	centromere/microtubule binding protein	YMR036c	<i>MIH1</i>	M-phase inducing protein tyrosine phosphatase
YNL082w	<i>MSM1</i>	DNA mismatch repair protein	YDR254w	<i>CHL4</i>	chromosome segregation protein	YGL178w	<i>MPT5</i>	multicopy suppressor of <i>pop2</i>
YHR120w	<i>MSH1</i>	DNA mismatch repair protein, mitochondrial	YOR349w	<i>CIN1</i>	chromosome segregation protein	YML109w	<i>ZDS2</i>	multicopy suppressor of <i>sin4</i>
YCR014c	<i>POL4</i>	DNA polymerase	YFL008w	<i>SMC1</i>	chromosome segregation protein	YGL173c	<i>KEM1</i>	multifunctional nuclease
YMR224c	<i>MRE11</i>	DNA repair and meiotic recombination protein	YFR031c	<i>SMC2</i>	chromosome segregation protein	YDR207c	<i>UME6</i>	negative transcriptional regulator
YJR035w	<i>RAD26</i>	DNA repair and recombination protein	YMR028w	<i>TAP42</i>	component of the Tor signalling pathway	YBL020w	<i>RFT1</i>	nuclear division protein
YEL019c	<i>MMS21</i>	DNA repair protein	YIL106w	<i>MOB1</i>	conditional mutants arrest in late mitosis	YLN299w	<i>TRF5</i>	nuclear division protein
YML095c	<i>RAD10</i>	DNA repair protein	YDL132w	<i>CDC53</i>	controls G1/S transition	YML031w	<i>NDC1</i>	nuclear envelope protein
YCR066w	<i>RAD18</i>	DNA repair protein	YPR120c	<i>CLB5</i>	cyclin, B-type	YJR112w	<i>NNF1</i>	nuclear envelope protein
YNL250w	<i>RAD50</i>	DNA repair protein	YGR109c	<i>CLB6</i>	cyclin, B-type	YLC029c	<i>BIK1</i>	nuclear fusion protein
YER095w	<i>RAD51</i>	DNA repair protein	YMR199w	<i>CLN1</i>	cyclin, G1/S specific	YJO134w	<i>KAR2</i>	nuclear fusion protein
YDR076w	<i>RAD55</i>	DNA repair protein	YPL256c	<i>CLN2</i>	cyclin, G1/S specific	YDR150w	<i>NUM1</i>	nuclear migration protein
YDR004w	<i>RAD57</i>	DNA repair protein	YAL040c	<i>CLN3</i>	cyclin, G1/S specific	YAL025c	<i>MAK16</i>	nuclear viral propagation protein
YDR369w	<i>XRS2</i>	DNA repair protein	YNL289w	<i>PCL1</i>	cyclin, G1/S specific	YKR048c	<i>NAP1</i>	nucleosome assembly protein 1
YAR007c	<i>RFA1</i>	DNA replication factor A, 69K subunit	YDL127w	<i>PCL2</i>	cyclin, G1/S specific	YLR079w	<i>SIC1</i>	p40 inhibitor of Cdc28p-Clb protein kinase complex
YOL006c	<i>TOP1</i>	DNA topoisomerase I	YGR108w	<i>CLB1</i>	cyclin, G2/M-specific	YJR066w	<i>TOR1</i>	phosphatidylinositol 3-kinase
YNL088w	<i>TOP2</i>	DNA topoisomerase II (ATP-hydrolysing)	YPR119w	<i>CLB2</i>	cyclin, G2/M-specific	YKL203c	<i>TOR2</i>	phosphatidylinositol 3-kinase
YGL163c	<i>RAD54</i>	DNA-dependent ATPase of the Sfn2p family	YDL155w	<i>CLB3</i>	cyclin, G2/M-specific	YLR305c	<i>STT4</i>	phosphatidylinositol 4-kinase
YFR023w	<i>PES4</i>	DNA-directed DNA polymerase ε suppressor	YLR210w	<i>CLB4</i>	cyclin, G2/M-specific	YCL004w	<i>PEL1</i>	phosphatidylserine synthase
YPL167c	<i>REV3</i>	DNA-directed DNA polymerase ζ	YBR135w	<i>CKS1</i>	cyclin-dependent kinase regulatory subunit	YBL058w	<i>SHP1</i>	potential regulatory subunit for Glc7p
YCR092c	<i>MSH3</i>	DNA-repair protein	YBR160w	<i>CDC28</i>	cyclin-dependent protein kinase	YGL238w	<i>CSE1</i>	probable kinetochore protein
YKR056w	<i>RNC1</i>	endo-exonuclease	YPL031c	<i>PHO85</i>	cyclin-dependent protein kinase	YGR132c	<i>PHB1</i>	prohibitin, antiproliferative protein
YOR033c	<i>DHS1</i>	exonuclease, interacting with Msh2p	YDL108w	<i>KIN28</i>	cyclin-dependent ser/thr protein kinase	YDL017w	<i>CDC7</i>	protein kinase
YLR288c	<i>MEC3</i>	G2-specific checkpoint protein	YGL215w	<i>CLG1</i>	cyclin-like protein	YOR149c	<i>SMP3</i>	protein kinase C pathway protein
YMR284w	<i>HDF1</i>	high-affinity DNA-binding protein	YOR368w	<i>RAD17</i>	DNA damage checkpoint control protein	YPL140c	<i>MKK2</i>	protein kinase of the MAP kinase kinase (MEK) family
YDR138w	<i>HPR1</i>	hyperrecombination protein related to Top1p	YDR217c	<i>RAD9</i>	DNA repair checkpoint protein	YAR019c	<i>CDC15</i>	protein kinase of the MAP kinase kinase (MEK) family
YHL022c	<i>SPO11</i>	meiosis-specific protein	YOR217c	<i>RFC1</i>	DNA replication factor C, 95K subunit	YHR013c	<i>ARD1</i>	protein N-acetyltransferase subunit
YER179w	<i>DMC1</i>	meiosis-specific protein	YLR234w	<i>TOP3</i>	DNA topoisomerase III	YPL008w	<i>CHL1</i>	protein of the DEAH box family
YIL072w	<i>HOP1</i>	meiosis-specific protein	YKL017c	<i>DIP1</i>	Dom34p-interacting protein	YDL047w	<i>SIT4</i>	protein ser/thr phosphatase
YHR157w	<i>REC104</i>	meiosis-specific protein	YLR129w	<i>DIP2</i>	Dom34p-interacting protein	YDL134c	<i>PPH21</i>	protein ser/thr phosphatase PP2A-1
YLR263w	<i>RED1</i>	meiosis-specific protein	YNL053w	<i>MSG5</i>	dual-specificity protein phosphatase	YBR267w	<i>PPS1</i>	protein ser/thr phosphatase PP2A-2
YPL122c	<i>ME15</i>	meiotic protein	YKR054c	<i>DYN1</i>	dynein heavy chain, cytosolic	YFR028c	<i>CDC14</i>	protein tyrosine phosphatase
YNL210w	<i>MER1</i>	meiotic recombination protein	YDR172w	<i>SUP35</i>	eukaryotic peptide chain release factor	YOL021c	<i>DIS3</i>	Ran binding protein
YHR086w	<i>NAM8</i>	meiotic recombination protein	YNL292w	<i>EXM1</i>	GTP-binding subunit	YDR137w	<i>RGP1</i>	reduced growth phenotype protein
YLR329w	<i>REC102</i>	meiotic recombination protein	YDL087c	<i>EXM2</i>	exit from mitosis	YDR052c	<i>DBF4</i>	regulatory subunit for Cdc7p protein kinase
YJR021c	<i>REC107</i>	meiotic recombination protein	YJL157c	<i>FAR1</i>	exit from mitosis	YKL193c	<i>SDS22</i>	regulatory subunit for the mitotic function of type I protein phosphatase
YGL175c	<i>SAE2</i>	meiotic recombination protein	YLR212c	<i>TUB4</i>	factor arrest protein	YMR078c	<i>CHL12</i>	required for accurate chromosome transmission in mitosis and maintenance of normal telomere length
YBR114w	<i>RAD16</i>	nucleotide excision repair protein	YLR288c	<i>MEC3</i>	γ tubulin	YOL145c	<i>CTR9</i>	required for G1 cyclin expression
YGL025c	<i>PGD1</i>	probable transcription factor	YAL024c	<i>LTE1</i>	G2-specific checkpoint protein	YLR103c	<i>CDC45</i>	required for minichromosome maintenance and initiation of chromosomal DNA replication
YBR088c	<i>POL30</i>	proliferating cell nuclear antigen (PCNA)	YLL016w	<i>SDC25</i>	GDP/GTP exchange factor	YKL089w	<i>MIF2</i>	required for normal chromosome segregation and spindle integrity
YML032c	<i>RAD52</i>	recombination and DNA repair protein	YAL041w	<i>CDC24</i>	GDP/GTP exchange factor for Cdc42p	YGR098c	<i>ESP1</i>	required for normal spindle structure
YDL059c	<i>RAD59</i>	recombination and DNA repair protein	YLR310c	<i>CDC25</i>	GDP/GTP exchange factor for Ras1p and Ras2p	YIL150c	<i>DNA43</i>	required for S-phase initiation or completion
YLR338w	<i>RHC18</i>	recombination repair protein	YGL207w	<i>SPT16</i>	general chromatin factor	YJL074c	<i>SMC3</i>	required for structural maintenance of chromosomes
YBR073w	<i>RDH54</i>	required for meiosis	YGL155w	<i>CDC43</i>	geranylgeranyltransferase type I β subunit	YGR078c	<i>PAC10</i>	required in the absence of Cin8p
YIL066c	<i>RNH3</i>	ribonuclease reductase, repair inducible RNA polymerase specific factor, mitochondrial	YER151c	<i>BEM1</i>	G1Pase-activating protein	YDR488c	<i>PAC11</i>	required in the absence of Cin8p
YMR228w	<i>MTF1</i>	mitochondrial	YMR138w	<i>CIN4</i>	GTP-binding protein	YLR075w	<i>GRC5</i>	ribosomal protein
YOR351c	<i>MEK1</i>	ser/thr protein kinase	YNL098c	<i>RAS2</i>	GTP-binding protein	YJL076c	<i>CDC11</i>	septin
YPL164c		similarity to mismatch repair protein Mlh1p	YLR229c	<i>CDC42</i>	GTP-binding protein of RAS superfamily	YHR107c	<i>CDC12</i>	septin
YOR077w	<i>RTS2</i>	similarity to mouse KIN17 protein	YML064c	<i>TEM1</i>	GTP-binding protein of the RAS superfamily	YAL016w	<i>TPD3</i>	ser/thr phosphatase 2A, regulatory subunit A
YFL003c	<i>MSH4</i>	similarity to MSH proteins	YNL007c	<i>SIS1</i>	heat-shock protein	YER133w	<i>GLC7</i>	ser/thr phosphoprotein phosphatase 1, catalytic subunit
YDR097c	<i>MSH6</i>	similarity to MSH proteins	YBR133c	<i>HSL7</i>	histone synthetic lethality	YOR178c	<i>GAC1</i>	ser/thr phosphoprotein phosphatase 1, regulatory subunit
YHR031c		similarity to Pif1p	YJL080c	<i>SCP160</i>	histone-like protein	YGR188c	<i>BUB1</i>	ser/thr protein kinase
YGL040w	<i>DST1</i>	TFIIS (transcription elongation factor)	YOL076w	<i>DEC1</i>	interacts genetically with CIN8	YKL048c	<i>ELM1</i>	ser/thr protein kinase
YCR077c	<i>(PAT1)</i>	topoisomerase II-associated protein	YOR156c	<i>NF1</i>	interacts with Cdc12p in 2-hybrid assay	YJL106w	<i>IME2</i>	ser/thr protein kinase
YGR063c	<i>SPT7</i>	transcription initiation protein	YNR010w	<i>CSE2</i>	interacts with centromeric element CDEII	YPL209c	<i>IPL1</i>	ser/thr protein kinase
YGR116w	<i>SPT6</i>	transcription initiation protein	YML104c	<i>MDM1</i>	intermediate filament protein	YOR231w	<i>MKK1</i>	ser/thr protein kinase
YML021c	<i>UNG1</i>	uracil-DNA glycosylase	YKR072c	<i>SIS2</i>	involved in cell cycle-specific gene expression	YBL105c	<i>PKC1</i>	ser/thr protein kinase
<i>cell-cycle control and mitosis</i>			YKR063c	<i>LAS1</i>	involved in cell morphogenesis, cytoskeletal regulation and bud formation	YPR161c	<i>SGV1</i>	ser/thr protein kinase
YFR052w	<i>NIN1</i>	26S proteasome regulatory subunit	YPL241c	<i>CIN2</i>	involved in chromosome segregation	YJL141c	<i>YAK1</i>	ser/thr protein kinase
YPR103w	<i>PRE2</i>	26S proteasome subunit	YPL018w	<i>CTF19</i>	involved in chromosome segregation	YMR104c	<i>YPK2</i>	ser/thr protein kinase
YGL048c	<i>SUG1</i>	26S proteasome subunit	YJL090c	<i>DPB11</i>	involved in DNA replication and S-phase checkpoint	YHR030c	<i>SLT2</i>	ser/thr protein kinase of MAP kinase family
YKL145w	<i>YTA3</i>	26S proteasome subunit	YMR273c	<i>ZDS1</i>	involved in negative regulation of cell polarity	YJL095w	<i>BCK1</i>	ser/thr protein kinase of the MEKK family
YJL005w	<i>CYR1</i>	adenylate cyclase	YMR052w	<i>FAR3</i>	involved in pheromone-mediated cell cycle arrest	YER167w	<i>BCK2</i>	ser/thr protein kinase of the protein kinase C pathway
YPL239w	<i>YAR1</i>	ankyrin repeat-containing protein	YMR052w	<i>FAR3</i>	involved in pheromone-mediated cell cycle arrest	YGR092w	<i>DBF2</i>	ser/thr protein kinase related to Dbf20p
YHR101c	<i>BIG1</i>	big cells phenotype	YER123w	<i>TWT1</i>	involved in the tolerance to high concentration of Ca ²⁺			
YHR208w	<i>TWT1</i>	branched-chain amino-acid aminotransferase, mitochondrial	YMR001c	<i>CDC5</i>	karyopherin-α or importin			
YFL037w	<i>TUB2</i>	β-tubulin	YMR127c	<i>SAS2</i>	kinесин-related protein			
YBR200w	<i>BEM1</i>	bud emergence mediator	YKR042w	<i>UTH1</i>	kinесин-related protein			
YBR109c	<i>CMD1</i>	calmodulin	YDR293c	<i>SSD1</i>	kinесин-related protein			
YOR061w	<i>CKA2</i>	casein kinase II α' subunit	YER123w	<i>YCK1</i>	kinесин-related protein			
YIL035c	<i>CKA1</i>	casein kinase II, catalytic α subunit	YMR060w	<i>CBF1</i>	kinetochore protein			
YER123w	<i>YCK3</i>	casein kinase, isoform 3						
YLR178c	<i>TF51</i>	cdc25-dependent nutrient- and ammonia-response cell-cycle regulator						
YGR049w	<i>SCM4</i>	cdc4 suppressor						
YFL029c	<i>CAK1</i>	cdc-activating protein kinase						
YMR055c	<i>BUB2</i>	cell-cycle arrest protein						

YHR006w	<i>STP2</i>	involved in pre-tRNA splicing	YIL021w	<i>RPB3</i>	DNA-directed RNA-polymerase II, 45K involved in repair and RNA polymerase transcription	YOR047c	<i>STD1</i>	dosage-dependent modulator of glucose repression			
YLR375w	<i>STP3</i>	involved in pre-tRNA splicing and in uptake of branched-chain amino acids	YIL128w	<i>MMS19</i>	involved in repair and RNA polymerase transcription	YER159c	<i>NCB1</i>	functional homologue of human NC2α			
YDL048c	<i>STP4</i>	involved in pre-tRNA splicing and in uptake of branched-chain amino acids	YMR228w	<i>MTF1</i>	RNA polymerase specific factor, mitochondrial	YDR397c	<i>YNC2β</i>	functional homologue of human NC2β/Dr1			
YCL017c	<i>NFS1</i>	involved in tRNA processing and mitochondrial metabolism	YPR056w		similarity to human transcription factor BTF2/TFIIB subunit p34	YPL037c	<i>EGD1</i>	GAL4 DNA-binding enhancer protein			
YNR034w	<i>SOL1</i>	multicopy suppressor of <i>los1-1</i>	YPL046c		strong similarity to human DNA-directed RNA polymerase II elongation factor SII, p15	YJL110c	<i>G2F3</i>	GATA zinc-finger protein 3			
YCR073w-a	<i>SOL2</i>	multicopy suppressor of <i>los1-1</i>	YDR045c		strong similarity to <i>S. acidocalcarius</i> transcription elongation factor tfs	YIL038c	<i>NOT3</i>	general negative regulator of transcription, subunit 3			
YMR047c	<i>NUP116</i>	nuclear pore protein	YKL058w	<i>TOA2</i>	TFIIB subunit (transcription initiation factor), 13.5K	YBR112c	<i>CYC8</i>	general repressor of transcription			
YGL092w	<i>NUP145</i>	nuclear pore protein	YOR194c	<i>TOA1</i>	TFIIB subunit (transcription initiation factor), 32K	YCR084c	<i>TUP1</i>	general transcription repressor			
YIR042w	<i>NUP85</i>	nuclear pore protein	YPR086w	<i>SUA7</i>	TFIIB subunit (transcription initiation factor), factor E	YDR176w	<i>NGG1</i>	general transcriptional adaptor or co-activator			
YLR430w	<i>SEN1</i>	positive effector of tRNA-splicing endonuclease	YER148w	<i>SPT15</i>	TFIID and TFIIB subunit	YBR045c	<i>GIP1</i>	Glc7-p-interacting protein			
YAL043c	<i>PTA1</i>	pre-tRNA processing protein	YGR274c	<i>TFA145</i>	TFIID subunit (TBP-associated factor), 145K	YNL236w	<i>SIN4</i>	global regulator protein			
YKL205w	<i>LOS1</i>	pre-tRNA splicing protein	YMR236w	<i>TAF17</i>	TFIID subunit (TBP-associated factor), 17K	YHL025w	<i>SNF6</i>	global transcription activator			
YDR463w	<i>STP1</i>	pre-tRNA splicing protein	YML098w	<i>TAF19</i>	TFIID subunit (TBP-associated factor), 19K	YER027c	<i>GAL83</i>	glucose repression protein			
YNL221c	<i>POP1</i>	protein component of ribonuclease P and ribonuclease MRN	YDR167w	<i>TAF23</i>	TFIID subunit (TBP-associated factor), 23K	YNL199c	<i>GCR2</i>	glycolytic genes transcriptional activator			
YML091c	<i>RPM2</i>	ribonuclease P, mitochondrial	YLO155c	<i>TAF40</i>	TFIID subunit (TBP-associated factor), 40K	YGL073w	<i>HSF1</i>	heat shock transcription factor			
YFR004w	<i>MPR1</i>	strong similarity to <i>S. pombe</i> pad1 protein	YGL112c	<i>TAF60</i>	TFIID subunit (TBP-associated factor), 60K	YPR065w	<i>ROX1</i>	heme-dependent transcriptional repressor of hypoxic genes			
YGR248w	<i>SOLA4</i>	strong similarity to Sol3p	YDR145w	<i>TAF61</i>	TFIID subunit (TBP-associated factor), 61K	YDR006c	<i>SOK1</i>	high copy suppressor of a cyclic AMP-dependent protein kinase mutant			
YIL087c	<i>TRL1</i>	tRNA ligase	YMR227c	<i>TAF67</i>	TFIID subunit (TBP-associated factor), 67K	YMR070w	<i>HMS1</i>	high-copy suppressor of <i>mot1 spt3</i> synthetic lethality			
YLR105c	<i>SEN2</i>	tRNA splicing endonuclease β subunit	YBR198c	<i>TAF90</i>	TFIID subunit (TBP-associated factor), 90K	YGR252w	<i>GCN5</i>	histone acetyltransferase			
YHR163w	<i>SOL3</i>	weak multicopy suppressor of <i>los1-1</i>	YKR062w	<i>TFA2</i>	TFIIE subunit (transcription initiation factor), 43K	YDR225w	<i>HTA1</i>	histone H2A			
<i>tRNA modification</i>											
YGR204w	<i>ADE3</i>	C1-tetrahydrofolate synthase, cytoplasmic initiator tRNA phosphoribosyl-transferase	YKL028w	<i>TFA1</i>	TFIIE subunit (transcription initiation factor), 66K	YBL003c	<i>HTA2</i>	histone H2A.2			
YMR283c	<i>RT11</i>	N2,N2-dimethylguanine tRNA methyltransferase	YGR186w	<i>TFG1</i>	TFIIE subunit (transcription initiation factor), 105K	YDR224c	<i>HTB1</i>	histone H2B			
YDR120c	<i>TRM1</i>	protein with specific affinity for G4 quadruplex nucleic acids	YPL129w	<i>ANC1</i>	TFIIE subunit (transcription initiation factor), 30K	YBL002w	<i>HTB2</i>	histone H2B.2			
YGL105w	<i>G4P1</i>	pseudouridine synthase 1	YGR005c	<i>TFG2</i>	TFIIE subunit (transcription initiation factor), 54K	YBR010w	<i>HTH1</i>	histone H3			
YPL212c	<i>PUS1</i>	pseudouridine synthase 2	YDR311w	<i>TFB1</i>	TFIIE subunit (transcription initiation factor), 75K	YNL031c	<i>HTH2</i>	histone H3			
YGL063w	<i>PUS2</i>	similarity to <i>C. elegans</i> tRNA-guanine transglycosylase	YPR025c	<i>CCL1</i>	TFIIE subunit (transcription initiation factor), cyclin C component	YBR009c	<i>HHF1</i>	histone H4			
YFR010w		similarity to methionyl-tRNA formyltransferase	YLR005w	<i>SSL1</i>	TFIIE subunit (transcription initiation factor), factor B	YNL030w	<i>HHF2</i>	histone H4			
YBL013w		tRNA isopentenyltransferase	YPL122c	<i>TFB2</i>	TFIIE subunit (transcription/repair factor)	YBL008w	<i>HIR1</i>	histone transcription regulator			
YOR274w	<i>MOD5</i>	tRNA nucleotidyltransferase	YDR460w	<i>TFB3</i>	TFIIS (transcription elongation factor)	YOR038c	<i>HIR2</i>	histone transcription regulator			
YER168c	<i>CCA1</i>	nuclear pore protein	YGL043w	<i>DST1</i>	transcription initiation protein	YER161c	<i>SPT2</i>	HMGI-like chromatin protein			
<i>other tRNA-transcription activities</i>			YGR043w	<i>SPT4</i>	transcription initiation protein	YDL106c	<i>GRF10</i>	homeodomain protein			
YOR061w	<i>CKA2</i>	casein kinase II α' subunit	YML100w	<i>SPT5</i>	transcription initiation protein	YDR138w	<i>HPR1</i>	hyperrecombination protein related to Top1p			
YOR039w	<i>CKB2</i>	casein kinase II β' subunit	YGR116w	<i>SPT6</i>	transcription initiation protein	YJL089w	<i>SIP4</i>	interacts with SNF1 protein kinase			
YJL041w	<i>NSP1</i>	nuclear pore protein	<i>mRNA synthesis</i>								
<i>general transcription activities</i>									<i>transcriptional control</i>		
YDL108w	<i>KIN28</i>	cyclin-dependent ser/thr protein kinase	YOR259c	<i>CRL13</i>	26S proteasome subunit	YKR072c	<i>SIS2</i>	involved in cell cycle-specific gene expression			
YIL143c	<i>SSL2</i>	DNA helicase	YJL115w	<i>ASF1</i>	anti-silencing protein	YNL251c	<i>NRD1</i>	involved in regulation of nuclear pre-mRNA abundance			
YER171w	<i>RAD3</i>	DNA helicase/ATPase	YDL197c	<i>ASF2</i>	anti-silencing protein	YIL046w	<i>MET30</i>	involved in regulation of sulphur assimilation genes			
YOR224c	<i>RPB8</i>	DNA-directed RNA polymerase I, II, III 16K subunit	YDR173c	<i>ARG82</i>	arginine metabolism transcription factor	YDL153c	<i>SAS10</i>	involved in silencing			
YPR187w	<i>RPC26</i>	DNA-directed RNA polymerase I, II, III 18K subunit	YKL112w	<i>ABF1</i>	ARS-binding factor	YMR127c	<i>SAS2</i>	involved in silencing at HMR			
YBR154c	<i>RPB5</i>	DNA-directed RNA polymerase I, II, III 25K subunit	YNO123c	<i>INO2</i>	basic helix-loop-helix (BHLH) transcription factor	YGR097w	<i>ASK10</i>	involved in Skn7p-dependent transcription			
YHR143w-a	<i>RPC10</i>	DNA-directed RNA polymerase I, II, III 7.7K subunit	YOL108c	<i>INO4</i>	basic helix-loop-helix transcription factor	YLR039c	<i>RIC1</i>	involved in transcription of ribosomal proteins and ribosomal RNA			
YOR210w	<i>RPB10</i>	DNA-directed RNA polymerase I, II, III 8.3K subunit	YOL067c	<i>RTG1</i>	basic helix-loop-helix transcription factor	YGL071w	<i>RCS1</i>	iron-regulated transcriptional repressor			
YOL051w	<i>GAL11</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YOR344c	<i>TYE7</i>	basic helix-loop-helix transcription factor	YJR060w	<i>CBF1</i>	kinetochore protein			
YDR443c	<i>SCA1</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YBL103c	<i>RTG3</i>	basic helix-loop-helix transcription factor	YDR159w	<i>SAC3</i>	leucine permease transcriptional regulator			
YHR041c	<i>SRB2</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YHL009c		bZip DNA binding protein	YGR100w	<i>MIC1</i>	Mac1p interacting protein			
YER022w	<i>SRB4</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YGL209w	<i>MIG2</i>	C2H2 zinc-finger protein	YBR297w	<i>MAL33</i>	maltoose fermentation regulatory protein			
YGR104c	<i>SRB5</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YKL190w	<i>CNB1</i>	calcineurin B, regulatory subunit	YGR288w	<i>MAL13</i>	maltoose pathway regulatory protein			
YDR308c	<i>SRB7</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YML112w	<i>CTK3</i>	carboxy terminal domain (CTD) kinase, γ subunit	YCR040w	<i>MATα1</i>	mating type regulatory protein (expressed copy at MAT locus)			
YCR081w	<i>SRB8</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YJL006c	<i>CTK2</i>	carboxy-terminal domain (CTD) kinase, β subunit	YCR039c	<i>MATα2</i>	mating type regulatory protein (expressed copy at MAT locus)			
YNL025c	<i>SSN8</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit, cyclin C homologue	YKL139w	<i>CTK1</i>	carboxy-terminal domain (CTD) kinase, α subunit	YCL067c	<i>a2</i>	mating type regulatory protein (silenced copy at HML locus)			
YLR071c	<i>RGR1</i>	DNA-directed RNA polymerase II holoenzyme subunit	YIL035c	<i>CKA1</i>	casein kinase II, catalytic α subunit	YHL027w	<i>RIM101</i>	meiotic regulatory protein			
YBR253w	<i>SRB6</i>	DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit	YGL237c	<i>HAP2</i>	CCAAT-binding factor subunit	YLR216c	<i>CPR6</i>	member of the cyclophilin family			
YOL005c	<i>RPB11</i>	DNA-directed RNA polymerase II, 13.6K subunit	YBL021c	<i>HAP3</i>	CCAAT-binding factor subunit	YJR032w	<i>CPR7</i>	member of the cyclophilin family			
YGL070c	<i>RPB9</i>	DNA-directed RNA polymerase II, 14.2K subunit	YKL109w	<i>HAP4</i>	CCAAT-binding factor subunit	YLR136c	<i>TIS11</i>	member of the inducible coch zinc-finger family			
YOR151c	<i>RPB2</i>	DNA-directed RNA polymerase II, 140K subunit	YOR358w	<i>HAP5</i>	CCAAT-binding factor subunit	YOL148c	<i>SPT20</i>	member of the TBP class of SPT proteins that alter transcription site selection			
YDR404c	<i>RPB7</i>	DNA-directed RNA polymerase II, 19K subunit	YJR122w	<i>CAF17</i>	CCAAT-binding factor subunit	YMR021c	<i>MAC1</i>	metal binding activator			
YDL140c	<i>RPO21</i>	DNA-directed RNA polymerase II, 215K subunit	YKR036c	<i>CAF4</i>	CCR4-associated factor	YLR131c	<i>ACE2</i>	metallothionein expression activator			
YJL140w	<i>RPB4</i>	DNA-directed RNA polymerase II, 32K subunit	YBR215w	<i>HPC2</i>	cell-cycle regulatory protein	YBR026c	<i>(MRF1)</i>	mitochondrial respiratory function protein			
YFL036w	<i>RPO41</i>	DNA-directed RNA polymerase, mitochondrial	YDL220c	<i>CDC13</i>	cell division control protein	YML051w	<i>GAL80</i>	negative regulator for expression of galactose-induced genes			
			YDR073w	<i>SNF11</i>	component of SWI/SNF transcription activator complex	YGL151w	<i>NUT1</i>	negative regulator of HO endonuclease			
			YNR023w	<i>SNF12</i>	component of SWI/SNF transcription activator complex	YPR168w	<i>NUT2</i>	negative regulator of HO endonuclease			
			YOR290c	<i>SNF2</i>	component of SWI/SNF transcription activator complex	YKL185w	<i>ASH1</i>	negative regulator of HO expression			
			YBR289w	<i>SNF5</i>	component of SWI/SNF transcription activator complex	YHL020c	<i>OPI1</i>	negative regulator of phospholipid biosynthesis pathway			
			YPL016w	<i>SWI1</i>	component of SWI/SNF transcription activator complex	YDR44w	<i>SPP41</i>	negative regulator of PRP3 and PRP4 gene expression			
			YCR042c	<i>TSM1</i>	component of TAF(II) complex	YNL076w	<i>MKS1</i>	negative regulator of RAS-cAMP pathway			
			YPL177c	<i>CUP9</i>	copper homeostasis protein	YDR207c	<i>UME6</i>	negative transcriptional regulator			
			YGL166w	<i>CUP2</i>	copper-dependent transcription factor	YGL221c	<i>NIF3</i>	Ngg1p-interacting factor 3			
			YNL167c	<i>SKO1</i>	cre-binding bzip protein	YGL115w	<i>SNF4</i>	nuclear regulatory protein			
			YPL042c	<i>SSN3</i>	cyclin-dependent ser/thr protein kinase	YCR093w	<i>CDC39</i>	nuclear transmembrane protein			
			YLR176c	<i>RFX1</i>	DNA binding protein	YML065w	<i>ORC1</i>	origin recognition complex, 104K subunit			
			YDR217c	<i>RAD9</i>	DNA repair checkpoint protein	YNL261w	<i>ORC5</i>	origin recognition complex, 50K subunit			
			YNL216w	<i>RAP1</i>	DNA-binding protein with repressor and activator activity	YHR118c	<i>ORC6</i>	origin recognition complex, 50K subunit			
			YLR418c	<i>CDC73</i>	DNA-directed RNA polymerase II accessory protein	YLL004w	<i>ORC3</i>	origin recognition complex, 56K subunit			
			YBR279w	<i>PAF1</i>	DNA-directed RNA polymerase II regulator	YBR060c	<i>RRR1</i>	origin recognition complex, 62K subunit			
			YGL208w	<i>SIP2</i>	dominant suppressor of some ts mutations <i>rpo21</i> and <i>prp4</i>	YAL051w	<i>OAF1</i>	peroxisome proliferating transcription factor			
						YOR363c	<i>PIP2</i>	peroxisome proliferating transcription factor			
						YBL005w	<i>PDR3</i>	pleiotropic drug resistance regulatory protein			
						YKL015w	<i>PUT3</i>	positive activator of the proline utilization pathway			
						YGL192w	<i>IME4</i>	positive transcription factor for <i>IME2</i>			

YDR017c	<i>KCS1</i>	potential transcription factor of the BZIP type	YFR037c	<i>RSC8</i>	subunit of the RSC complex	chromatin modification	
YGL025c	<i>PGD1</i>	probable transcription factor	YLR321c	<i>SFH1</i>	subunit of the RSC complex	YBR195c	<i>MSI1</i> chromatin assembly complex, subunit p50
YER108c	<i>FLO8</i>	probable transcriptional activator of Flo1p	YIL126w	<i>STH1</i>	subunit of the RSC complex	YML102w	<i>CAC2</i> chromatin assembly complex, subunit p60
YGL194c	<i>RTL1</i>	putative deacetylase	YGL254w	<i>FZF1</i>	sulphite resistance protein	YPR018w	<i>RLF2</i> chromatin assembly complex, subunit p90
YIL103c		putative regulatory protein	YNL222w	<i>SSU72</i>	suppressor of cs mutant sua ⁷	YGL207w	<i>SPT16</i> general chromatin factor
YBL066c	<i>SEF1</i>	putative transcription factor	YKR099w	<i>BAS1</i>	suppressor of <i>mar1-1</i>	YGR252w	<i>GCN5</i> histone acetyltransferase
YHR056c		putative transcription regulator	YDL165w	<i>CDC36</i>	transcription factor	YGL194c	<i>RTL1</i> putative deacetylase
YBR275c	<i>RIF1</i>	Rap1p-interacting factor 1	YLR098c	<i>CHA4</i>	transcription factor	YHR119w	<i>YTX1</i> regulatory protein
YKL038w	<i>RGT1</i>	regulator of glucose induced genes	YPL248c	<i>GAL4</i>	transcription factor	YBR238c	YBR238c strong similarity to general chromatin factor Spt16p
YDR257c	<i>RMS1</i>	regulatory protein	YFL031w	<i>HAC1</i>	transcription factor	YFR004w	YFR004w strong similarity to <i>S. pombe</i> pad1 protein
YDR392w	<i>SPT3</i>	regulatory protein	YLR256w	<i>HAP1</i>	transcription factor	YOR213c	YOR213c subunit of the RSC complex
YMR016c	<i>SOK2</i>	regulatory protein in the PKA signal transduction pathway	YCR065w	<i>HCM1</i>	transcription factor	YCR052w	YCR052w subunit of the RSC complex
YCL055w	<i>KAR4</i>	regulatory protein required for pheromone induction of karyogamy genes	YLR451w	<i>LEU3</i>	transcription factor	YFR037c	YFR037c subunit of the RSC complex
YNR052c	<i>POP2</i>	required for glucose derepression	YGL013c	<i>PDR1</i>	transcription factor	YLR321c	YLR321c subunit of the RSC complex
YMR179w	<i>SPT21</i>	required for normal transcription at a number of loci	YKL043w	<i>PHD1</i>	transcription factor	YIL126w	YIL126w subunit of the RSC complex
YKL093w	<i>MBR1</i>	required for optimal growth on glycerol silencing protein	YFR034c	<i>PHO4</i>	transcription factor	YGR274c	YGR274c TAF145 TFID subunit (TBP-associated factor), 145K
YOL068c	<i>HST1</i>	silencing protein	YBR049c	<i>REB1</i>	transcription factor	YGR063c	YGR063c <i>SPT4</i> transcription initiation protein
YOR025w	<i>HST3</i>	silencing protein	YBL093c	<i>ROX3</i>	transcription factor	YML010w	YML010w <i>SPT5</i> transcription initiation protein
YBL052c	<i>SAS3</i>	silencing protein	YOR140w	<i>SFL1</i>	transcription factor	YGR116w	YGR116w <i>SPT6</i> transcription initiation protein
YKR101w	<i>SIR1</i>	silencing regulatory protein	YLR055c	<i>SPT8</i>	transcription factor		
YDL042c	<i>SIR2</i>	silencing regulatory protein	YER111c	<i>SWI4</i>	transcription factor		
YLR442c	<i>SIR3</i>	silencing regulatory protein	YDR146c	<i>SWI5</i>	transcription factor		
YDR227w	<i>SIR4</i>	silencing regulatory protein	YLR182w	<i>SWI6</i>	transcription factor		
YKL070w		similarity to <i>B. subtilis</i> transcriptional regulatory protein	YFL021w	<i>GAT1</i>	transcription factor for nitrogen regulation		
YDL070w		similarity to bromodomain protein BDF1	YER040w	<i>GLN3</i>	transcription factor for positive nitrogen regulation		
YIL131c	<i>FKH1</i>	similarity to <i>D. melanogaster</i> fork head protein	YMR042w	<i>ARG80</i>	transcription factor involved in arginine metabolism	YBL074c	YBL074c <i>AAR2</i> A1 cistron splicing factor
YJL056c		similarity to developmental control proteins	YML099c	<i>ARG81</i>	transcription factor involved in arginine metabolism	YHL038c	YHL038c <i>CBP2</i> apo-cytochrome b pre-mRNA processing protein 2
YBR061c		similarity to <i>E. coli</i> ftsJ protein	YMR280c	<i>CAT8</i>	transcription factor involved in gluconeogenesis	YPL119c	YPL119c <i>DBP1</i> ATP-dependent RNA helicase
YJR147w		similarity to heat-shock transcription factors	YGL181w	<i>GTS1</i>	transcription factor of the Gcs1p/Glo3p/Sps18p family	YOR204w	YOR204w <i>DED1</i> ATP-dependent RNA helicase
YGR249w	<i>MGA1</i>	similarity to heat-shock transcription factors	YMR043w	<i>MCM1</i>	transcription factor of the MADS box family	YBR142w	YBR142w <i>MAK5</i> ATP-dependent RNA helicase, mitochondrial
YPL015c	<i>HST2</i>	similarity to Hst1p and Sir2p	YPL089c	<i>RLM1</i>	transcription factor of the MADS box family	YPL029w	YPL029w <i>SUV3</i> ATP-dependent RNA helicase, mitochondrial
YDR191w	<i>HST4</i>	similarity to Hst3p, Hst1p and Sir2p	YLR014c	<i>PPR1</i>	transcription factor regulating pyrimidine pathway	YNL280w	YNL280w <i>CUS2</i> cold sensitive U2 snRNA suppressor involved in mitochondrial RNA splicing of COB mRNA
YNL107w		similarity to human AF-9 protein	YJR094c	<i>IME1</i>	transcription factor required for sporulation	YIRO21w	YIRO21w <i>MRS1</i> involved in mitochondrial RNA splicing of COB mRNA
YHR193c	<i>EGD2</i>	similarity to human α -NAC	YHR206w	<i>SKN7</i>	transcription factor with similarity to Hsf1p	YOR148c	YOR148c <i>SPP2</i> involved in pre-mRNA processing
YAR003w	<i>FUN16</i>	similarity to human RB protein binding protein	YDL056w	<i>MBP1</i>	transcription factor, subunit of the MBF factor	YPR057w	YPR057w <i>BRR1</i> involved in snRNP biogenesis
YER169w		similarity to human retinoblastoma binding protein 2	YNL330c	<i>RPD3</i>	transcription modifier protein	YLR382c	YLR382c <i>NAM2</i> leucine-tRNA ligase, mitochondrial
YJR119c		similarity to human retinoblastoma binding protein 2	YOL004w	<i>SIN3</i>	transcription regulatory protein	YNL210w	YNL210w <i>MER1</i> meiotic recombination protein
YLR116w		similarity to human ZFM1 protein and mouse CW17R protein	YJL127c	<i>SPT10</i>	transcription regulatory protein	YHR086w	YHR086w <i>NAM8</i> meiotic recombination protein
YJL206c		similarity to hypothetical protein YIL130p and Put3p	YJL176c	<i>SWI3</i>	transcription regulatory protein	YMR023c	YMR023c <i>MSS1</i> mitochondrial GTPase involved in expression of <i>COX1</i>
YOL133w		similarity to Lotus RING-finger protein	YPL075w	<i>GCR1</i>	transcriptional activator	YLL036c	YLL036c <i>PRP19</i> non-snRNP sliceosome component required for DNA repair
YER130c		similarity to Msn2p and Msn4p	YOL116w	<i>MSN1</i>	transcriptional activator	YBR237w	YBR237w <i>PRP5</i> pre-mRNA processing RNA-helicase
YER184c		similarity to multidrug resistance protein PDR3	YKL062w	<i>MSN4</i>	transcriptional activator	YKL074c	YKL074c <i>MUD2</i> pre-mRNA splicing factor
YIL050w		similarity to <i>N. crassa</i> regulatory protein preg(+)	YHR084w	<i>STE12</i>	transcriptional activator	YDL043c	YDL043c <i>PRP11</i> pre-mRNA splicing factor
YLR013w		similarity to nitrogen regulatory proteins	YIR023w	<i>DAL81</i>	transcriptional activator for allantoin and GABA catabolic genes	YIL203w	YIL203w <i>PRP21</i> pre-mRNA splicing factor
YDR334w		similarity to nuclear Sth1p, Snf2p and related proteins	YNL314w	<i>DAL82</i>	transcriptional activator for allantoin catabolic genes	YER013w	YER013w <i>PRP22</i> pre-mRNA splicing factor
YPR115w		similarity to probable transcription factor Ask10p, and to hypothetical proteins YNL047c and YIL105c	YDL170w	<i>UGA3</i>	transcriptional activator for GABA catabolic genes	YMR268c	YMR268c <i>PRP24</i> pre-mRNA splicing factor
YIL130w		similarity to Put3p and to hypothetical protein YJL206c	YML007w	<i>YAP1</i>	transcriptional activator involved in oxidative stress response	YGR075c	YGR075c <i>PRP38</i> pre-mRNA splicing factor
YCR020c	<i>PET18</i>	similarity to regulatory protein	YEL009c	<i>GCN4</i>	transcriptional activator of amino acid biosynthetic genes	YML046w	YML046w <i>PRP39</i> pre-mRNA splicing factor
YBR182c		similarity to Rlm1p, Mcm1p, and hMEF2	YDR034c	<i>LYS14</i>	transcriptional activator of lysine pathway genes	YDL300w	YDL300w <i>PRP9</i> pre-mRNA splicing factor (snRNA-associated protein)
YKR008w		similarity to <i>S. pombe</i> bromodomain protein	YIR017c	<i>MET28</i>	transcriptional activator of sulphur amino acid metabolism	YDR088c	YDR088c <i>SLU7</i> pre-mRNA splicing factor affecting 3' splice site choice
YGL150c		similarity to Snf2p and human SNF2 α	YNL103w	<i>MET4</i>	transcriptional activator of sulphur metabolism	YDR243c	YDR243c <i>PRP28</i> pre-mRNA splicing factor RNA helicase of DEAD box family
YLR228c		similarity to transcription activator Lys14p	YPR104c	<i>FHL1</i>	transcriptional activator of the forkhead/hnf3 family	YGR091w	YGR091w <i>PRP31</i> pre-mRNA splicing protein
YLL054c		similarity to transcription factor Pip2p	YDR448w	<i>ADA2</i>	transcriptional adaptor	YDL044c	YDL044c <i>MTF2</i> protein involved in mRNA splicing and protein synthesis, mitochondrial
YLR266c		similarity to transcription factors	YMR039c	<i>SUB1</i>	transcriptional coactivator	YBR091c	YBR091c <i>MRS5</i> regulator of intron splicing, mitochondrial
YLR278c		similarity to transcription factors	YAL021c	<i>CCR4</i>	transcriptional regulator	YDR028c	YDR028c <i>REG1</i> regulatory subunit for protein phosphatase Glc7p
YDR303c		similarity to transcriptional regulator proteins	YER164w	<i>CHD1</i>	transcriptional regulator	YDR478w	YDR478w <i>SNM1</i> RNA binding protein of RNase MRP
YMR019w	<i>STB4</i>	sin3 binding protein	YIL084c	<i>SDS3</i>	transcriptional regulator	YDR194c	YDR194c <i>MSS116</i> RNA helicase of the DEAD box family, mitochondrial
YHR178w	<i>STB5</i>	sin3 binding protein	YNL012w	<i>SPO1</i>	transcriptional regulator involved in sporulation	YER172c	YER172c <i>BRR2</i> RNA helicase-related protein
YKL072w	<i>STB6</i>	sin3 binding protein	YGL035c	<i>MIG1</i>	transcriptional repressor	YOR334w	YOR334w <i>MRS2</i> RNA splicing protein and member of the mitochondrial carrier family (MCF)
YNL309w	<i>STB1</i>	sin3p binding protein	YER068w	<i>MOT2</i>	transcriptional repressor	YJL133w	YJL133w <i>MRS3</i> RNA splicing protein and member of the mitochondrial carrier family (MCF)
YMR063c	<i>STB2</i>	sin3p binding protein	YKR034w	<i>DAL80</i>	transcriptional repressor for allantoin and GABA catabolic genes	YKR052c	YKR052c <i>MRS4</i> RNA splicing protein and member of the mitochondrial carrier family (MCF)
YLR399c	<i>BDF1</i>	sporulation protein	YMR182c	<i>GRM1</i>	transcriptional repressor	YKR086w	YKR086w <i>PRP16</i> RNA-dependent ATPase
YNL204c	<i>SPS18</i>	sporulation-specific zinc-finger protein	YOL083w	<i>TEC1</i>	transcriptional silencing protein	YNR011c	YNR011c <i>PRP2</i> RNA-dependent ATPase of DEAH box family
YMR037c		stress responsive regulatory protein	YOR337w	<i>TEA1</i>	Ty3 enhancer activator	YHR004c-a	YHR004c-a similarity to mitochondrial splicing protein Mrs5p
YDR026c		strong similarity to DNA-binding protein Reb1p	YER151c	<i>UBP3</i>	ubiquitin-specific proteinase	YKR024c	YKR024c similarity to pre-mRNA processing protein Prp5p
YDR252w	<i>BTT1</i>	strong similarity to Egd1p and to human Btf3 protein	YER088c		weak similarity human transforming proteins (B-myb)	YGR074w	YGR074w <i>SMD1</i> snRNA-associated protein
YHR211w	<i>FLO5</i>	strong similarity to Flo1p	YBR240c		weak similarity to regulatory proteins	YPR182w	YPR182w <i>SMX3</i> snRNA-associated protein of the SM family
YOR304w		strong similarity to human Snf2p homologue	YML076w		weak similarity to transcription factor	YBR055c	YBR055c <i>PRP6</i> snRNP(U4/U6)-associated splicing factor
YOL055c		strong similarity to hypothetical proteins YPL258c, YPR121w, similarity to <i>B. subtilis</i> transcriptional activator tenA	YCR106w		weak similarity to transcription factor	YKL012w	YKL012w <i>PRP40</i> splicing factor
YFL052w		strong similarity to Mal63p, Mal23p and Mal33p	YBR033w		weak similarity to transcription factors	YPR134w	YPR134w <i>MSS18</i> splicing protein
YPR196w		strong similarity to regulatory protein Mal63p	YKR064w		weak similarity to transcription factors	YGR222w	YGR222w <i>PET54</i> splicing protein and translational activator, mitochondrial
YBR245c		strong similarity to SNF2/SWI2 DNA binding regulatory protein	YLO89c		weak similarity to transcription factors, similarity to finger proteins YOR162c, YOR172w and YLR266c	YKL078w	YKL078w strong similarity to ATP-dependent RNA helicases
YDR253c		strong similarity to zinc-finger proteins	YKL222c		weak similarity to transcription factors, similarity to finger proteins YOR162c, YOR172w and YLR266c	YOR159c	YOR159c <i>SME1</i> strong similarity to human small nuclear ribonucleoprotein E
YML081w		strong similarity to ZMS1 protein	YBL054w		weak similarity transforming protein (B-myb)	YLR275w	YLR275w strong similarity to human snRNP subunit D2 involved in systemic lupus erythematosus
YEL056w	<i>HAT2</i>	subunit of the major yeast histone acetyltransferase	YER122c	<i>GLO3</i>	zinc-finger protein	YPL060w	YPL060w strong similarity to Mrs2p
YOR213c		subunit of the RSC complex	YDR216w	<i>ADR1</i>	zinc-finger transcription factor	YGL120c	YGL120c strong similarity to Prp22p
YCR052w	<i>RSC6</i>	subunit of the RSC complex	YGR044c	<i>RME1</i>	zinc-finger transcription factor	YLR147c	YLR147c strong similarity to small nuclear ribonucleoprotein D3

YPR178w	<i>PRP4</i>	U4/U6 snRNP 52K protein
YGR006w	<i>PRP18</i>	U5 snRNA-associated protein
YHR165c	<i>PRP8</i>	U5 snRNP protein, pre-mRNA splicing factor
YER112w	<i>USS1</i>	U6 snRNA associated protein
<i>mRNA processing (5'-end, 3'-end processing and mRNA degradation)</i>		
YJL209w	<i>CBP1</i>	apo-cytochrome b pre-mRNA processing protein
YBR120c	<i>CBP6</i>	apo-cytochrome b pre-mRNA processing protein
YPL178w	<i>SAE1</i>	cell cycle block in meiotic prophase component of Pab1p-stimulated poly(A) ribonuclease
YGL094c	<i>PAN2</i>	component of pre-mRNA 3'-end processing factor
YMR061w	<i>RNA14</i>	component of pre-mRNA 3'-end processing factor
YGL044c	<i>RNA15</i>	component of pre-mRNA 3'-end processing factor
YJR093c	<i>FIP1</i>	component of pre-mRNA polyadenylation factor
YKL025c	<i>PAN3</i>	component of the Pab1p-dependent poly (A)
YOL149w	<i>DCP1</i>	component of the yeast decapping enzyme
YGL097w	<i>SRM1</i>	GDP/GTP exchange factor for Gsp1/Gsp2p
YGR158c	<i>MTR3</i>	involved in mRNA transport
YBR236c	<i>ABD1</i>	methyltransferase
YGL130w	<i>CEG1</i>	mRNA guanylyltransferase (mRNA capping enzyme, α subunit)
YER165w	<i>PAB1</i>	mRNA polyadenylate-binding protein
YLR277c	<i>BRR5</i>	mRNA processing protein
YKR002w	<i>PAP1</i>	poly(A) polymerase
YGL122c	<i>NAB2</i>	poly(A)-binding protein
YPL190c	<i>NAB3</i>	polyadenylated RNA-binding protein
YDR301w	<i>CFT1</i>	pre-mRNA 3'-end processing factor
YJR017c	<i>ESS1</i>	processing/termination factor 1
YDR195w	<i>REF2</i>	RNA 3'-end formation protein
YOR179c		similarity to BRR5 protein
YOR319w	<i>HSH49</i>	similarity to human SAP49 and RNA-binding proteins
YHR015w		similarity to PES4 PAB-like protein
YOR159c	<i>SME1</i>	strong similarity to human small nuclear ribonucleoprotein E

other mRNA-transcription activities

YGL171w	<i>ROK1</i>	ATP-dependent RNA helicase
YOL006c	<i>TOP1</i>	DNA topoisomerase I
YGL251c	<i>HFM1</i>	DNA/RNA helicase
YNL037c	<i>IDH1</i>	isocitrate dehydrogenase (NAD ⁺) subunit 1, mitochondrial
YOR136w	<i>IDH2</i>	isocitrate dehydrogenase (NAD ⁺) subunit 2, mitochondrial
YNL016w	<i>PUB1</i>	major polyadenylated RNA-binding protein of nucleus and cytoplasm
YHR170w	<i>NMD3</i>	nonsense-mediated mRNA decay protein
YMR064w	<i>AEP1</i>	nuclear control of ATPase messenger RNA expression protein
YOL123w	<i>HRP1</i>	polyadenylated RNA-binding protein required for stability and translation of COX1 mRNA
YLR067c	<i>PET309</i>	ser/thr phosphatase 2A, regulatory subunit A
YOL042w		similarity to CCR4 protein
YER146w		similarity to human snRNP E
YER029c		similarity to human snRNP-associated protein B
YER028c		similarity to Mig1p
YDR429c		similarity to nuclear RNA binding proteins
YJR127c	<i>ZMS1</i>	similarity to regulatory protein ADR1
YDL031w		similarity to RNA helicases
YNL147w		similarity to snRNP proteins
YNL021w		similarity to transcription factor Rpd3p
YPR068c		similarity to transcription factor Rpd3p
YPL213w	<i>SNP3</i>	similarity to U2 snRNP protein A'
YBL026w		snRNP-related protein
YDL160c	<i>DHH1</i>	strong similarity to RNA helicases of the DEAD box family
YLR147c	<i>SMD3</i>	strong similarity to small nuclear ribonucleoprotein D3
YLR139c	<i>SL1</i>	suppresses lethality of SSM4 deletion

RNA transport

YGL097w	<i>SRM1</i>	GDP/GTP exchange factor for Gsp1/Gsp2p
YMR235c	<i>RNA1</i>	GTPase activating protein
YOR185c	<i>GSP2</i>	GTP-binding protein
YLR293c	<i>GSP1</i>	GTP-binding protein of the ras superfamily
YOR160w	<i>MTR10</i>	involved in mRNA transport
YGR158c	<i>MTR3</i>	involved in mRNA transport
YJL050w	<i>MTR4</i>	involved in nucleocytoplasmic transport of mRNA
YKL186c	<i>MTR2</i>	mRNA transport protein
YKL068w	<i>NUP100</i>	nuclear pore protein
YKL057c	<i>NUP120</i>	nuclear pore protein
YKR082w	<i>NUP133</i>	nuclear pore protein
YGL092w	<i>NUP145</i>	nuclear pore protein
YDR192c	<i>NUP42</i>	nuclear pore protein
YGL172w	<i>NUP49</i>	nuclear pore protein
YJL061w	<i>NUP82</i>	nuclear pore protein
YDR432w	<i>NPL3</i>	nucleolar protein
YGL122c	<i>NAB2</i>	poly(A)-binding protein
YKL205w	<i>LOS1</i>	pre-tRNA splicing protein

YER110c	<i>KAP123</i>	RAN-binding protein
YDR020w	<i>YRB1</i>	ran-specific GTPase-activating protein required for nuclear pore complex structure and function
YER107c	<i>GLE2</i>	required for transport of Rna15p from the cytoplasm to the nucleus
YIR011c	<i>STS1</i>	RNA export mediator
YDL207w	<i>GLE1</i>	suppressor of <i>rna1</i> -1 mutation

other transcription activities

YGL127c	<i>SOH1</i>	allows <i>hpr1</i> null mutant to grow at 37°C
YOR113w	<i>AZF1</i>	asparagine-rich zinc-finger protein
YPR198w	<i>SGE1</i>	drug resistance protein
YBR212w	<i>NGR1</i>	glucose-repressible RNA-binding protein
YML027w	<i>YOX1</i>	homoeodomain protein
YNL068c	<i>FKH2</i>	homology to <i>D. melanogaster</i> forkhead protein
YIL030c	<i>SSM4</i>	involved in mRNA turnover
YNL282w	(<i>POP2</i>)	involved in processing RNAs
YCR087c-a		nucleic acid-binding protein
YDL051w	<i>YLA1</i>	RNA binding protein
YMR164c		similarity to CYC8 protein
YGL014w		similarity to <i>D. melanogaster</i> pumilio protein and HTR1 protein
YIR001c		similarity to <i>D. melanogaster</i> RNA binding protein
YNL004w	<i>HRB1</i>	similarity to Gbp2p
YBR233w		similarity to human hnRNP-E1 protein
YPR031w		similarity to human zinc-finger protein BR140
YCL033c		similarity to <i>M. capricolum</i> transcription repressor
YIR005w		similarity to RNA-binding proteins
YMR213w		similarity to <i>S. pombe</i> putative transcription factor cdc5
YNL175c		similarity to <i>S. pombe</i> Rnp24p
YOR244w		similarity to SAS2 and SAS3 protein
YPR008w		similarity to transcription factor
YPL230w		similarity to transcription factors
YPR013c		similarity to transcription factors
YPR015c		similarity to transcription factors
YNL027w		similarity to zinc-finger proteins
YPL038w		similarity to zinc-finger proteins
YDR169c	<i>STB3</i>	SN3 protein-binding protein
YPR107c		strong similarity to <i>D. melanogaster</i> zinc-finger protein
YIL105c		strong similarity to hypothetical protein YNL047c, similarity to hypothetical protein YPR116w and to probable transcription factor Ask10p
YNL255c		strong similarity to nucleic acid-binding proteins
YHR169w		strong similarity to RNA helicase
YGL078c		strong similarity to RNA helicase DBP2 protein
YCR004c	<i>YCP4</i>	strong similarity to <i>S. pombe</i> protein obr1
YFL017w-a	<i>SNP2</i>	strong similarity to snRNP E
YDR451c		strong similarity to Yox1p
YML017w	<i>PSP2</i>	suppressor of DNA polymerase α mutation
YKR092c	<i>SRP40</i>	suppressor of mutant AC40 of RNA polymerase I and III
YKL005c		weak similarity to <i>D. melanogaster</i> transcription elongation factor DmS-II
YNR063w		weak similarity to CYC1/CYP3 transcription activator
YJL124c		weak similarity to human Sm protein G
YDR043c		weak similarity to <i>K. marxianus</i> Mig1 and other regulatory proteins
YIR018w		weak similarity to transcription activator Pdr4p
YPR199c		weak similarity to transcription activator Yap1p
YBR239c		weak similarity to transcription factor Put3p
YBR150c		weak similarity to transcription factors
YGR067c		weak similarity to transcription factors
YPL133c		weak similarity to transcription factors zinc-finger protein
YER116c		

Protein synthesis*ribosomal proteins*

YGR214w	<i>NAB1A</i>	40S ribosomal protein p40 homologue A
YLR048w	<i>NAB1B</i>	40S ribosomal protein p40 homologue B
YCR031c	<i>CRY1</i>	40S ribosomal protein S14.e
YGL189c	<i>RPS26A</i>	40S ribosomal protein S26.e.c7
YML009c	<i>MRP39A</i>	60S ribosomal protein, mitochondrial
YDL081c	<i>RPLA1</i>	acidic ribosomal protein a1
YLR340w	<i>RPLA0</i>	acidic ribosomal protein L10.e
YDL130w	<i>RPLA3</i>	acidic ribosomal protein L44prime
YDR382w	<i>RPLA4</i>	acidic ribosomal protein L45
YOL039w	<i>RPLA2</i>	acidic ribosomal protein P2. β
YOR369c	<i>RS12</i>	acidic ribosomal protein S12
YGL068w		probable ribosomal protein L12
YLR325c		putative ribosomal protein L38
YFL034c-a		ribosomal protein
YFR032c-a		ribosomal protein
YLR061w		ribosomal protein
YMR142c		ribosomal protein
YPL183w-a		ribosomal protein
YLR075w	<i>GRC5</i>	ribosomal protein
YIL133c	<i>RPL22</i>	ribosomal protein
YNL069c	<i>RP23</i>	ribosomal protein

YOR096w	<i>RP30</i>	ribosomal protein
YKL006w	<i>RPL14A</i>	ribosomal protein
YHL001w	<i>RPL14B</i>	ribosomal protein
YMR242c	<i>RPL18A</i>	ribosomal protein
YOR312c	<i>RPL18B</i>	ribosomal protein
YDR471w	<i>RPL27B</i>	ribosomal protein
YLR344w	<i>RPL33A</i>	ribosomal protein
YMR194w	<i>RPL39A</i>	ribosomal protein
YDL184c	<i>RPL47A</i>	ribosomal protein
YDL133c-a	<i>RPL47B</i>	ribosomal protein
YPL198w	<i>RPL6B</i>	ribosomal protein
YOL040c	<i>RPS21</i>	ribosomal protein
YLR287c-a	<i>RPS30A</i>	ribosomal protein
YDL191w	<i>SOS1</i>	ribosomal protein
YDL136w	<i>SOS2</i>	ribosomal protein
YPL220w	<i>SSM1A</i>	ribosomal protein
YGL135w	<i>SSM1B</i>	ribosomal protein
YGL123w	<i>SUP44</i>	ribosomal protein
YIL148w	<i>UBI1</i>	ribosomal protein
YKR094c	<i>UBI2</i>	ribosomal protein
YHL015w	<i>URP2</i>	ribosomal protein
YML073c	<i>YL16A</i>	ribosomal protein
YLR448w	<i>YL16B</i>	ribosomal protein
YDR500c	<i>RPL35B</i>	ribosomal protein L37.e
YPR102c	<i>RPL16A</i>	ribosomal protein L11.e
YDR418w	<i>RPL15A</i>	ribosomal protein L12.e
YEL054c	<i>RPL15B</i>	ribosomal protein L12.e
YDL082w		ribosomal protein L13
YKL170w	<i>MRPL38</i>	ribosomal protein L14, mitochondrial
YLR029c	<i>RPL13A</i>	ribosomal protein L15.e.c12
YMR121c	<i>RPL13B</i>	ribosomal protein L15.e.c13
YJL063c	<i>MRPL8</i>	ribosomal protein L17, mitochondrial
YKL180w		ribosomal protein L17.e
YJL177w	<i>RPL20B</i>	ribosomal protein L17.e
YNL301c	<i>RP28B</i>	ribosomal protein L18.e
YBL027w	<i>RPL19A</i>	ribosomal protein L19.e
YPL079w	<i>URP1B</i>	ribosomal protein L21
YBR191w	<i>URP1A</i>	ribosomal protein L21.e
YBL087c	<i>RPL17A</i>	ribosomal protein L23.e
YER117w	<i>RPL17B</i>	ribosomal protein L23.e
YOL127w	<i>RPL25</i>	ribosomal protein L23.a.e
YGL031c	<i>RPL30A</i>	ribosomal protein L24.e.A
YGR148c	<i>RPL30B</i>	ribosomal protein L24.e.B
YGR034w	<i>RPL33B</i>	ribosomal protein L26
YHR010w	<i>RPL27A</i>	ribosomal protein L27.e
YGL103w	<i>CYH2</i>	ribosomal protein L27.e.A
YBR031w	<i>RPL2A</i>	ribosomal protein L28.e
YOR063w	<i>TCM1</i>	ribosomal protein L3.e
YGL030w	<i>RPL32</i>	ribosomal protein L30.e
YDL075w	<i>RPL43A</i>	ribosomal protein L31.e
YLR406c	<i>RPL34B</i>	ribosomal protein L31.e.c12
YBL092w		ribosomal protein L32.e
YIL052c		ribosomal protein L34.e
YOR234c	<i>RPL37B</i>	ribosomal protein L35.e.c15
YPL143w	<i>RPL37A</i>	ribosomal protein L35.e.c16
YNL162w	<i>RPL41A</i>	ribosomal protein L36.e
YHR141c	<i>RPL41B</i>	ribosomal protein L36.e
YLR185w	<i>RPL35A</i>	ribosomal protein L37.e
YPR043w	<i>RPL46</i>	ribosomal protein L37.e
YDR012w	<i>RPL2B</i>	ribosomal protein L4.e.B
YPL131w	<i>RPL1</i>	ribosomal protein L5.e
YNL002c	<i>RPL7</i>	ribosomal protein L7.e
YGL076c	<i>RPL6A</i>	ribosomal protein L7.e.A
YHL033c	<i>RPL44</i>	ribosomal protein L7.e.A
YLL045c	<i>RPL48</i>	ribosomal protein L7.e.A
YIL018w	<i>RPL6A</i>	ribosomal protein L8.e
YFR031c-a	<i>RPL5B</i>	ribosomal protein L8.e
YGL147c	<i>RPL9A</i>	ribosomal protein L9.e
YNL067w	<i>RPL9B</i>	ribosomal protein L9.e.c14
YGR076c	<i>MRPL25</i>	ribosomal protein m (YML25), mitochondrial
YJR094w-a		ribosomal protein of the large subunit
YOR293w		ribosomal protein S10.e
YDR025w	<i>RPS18A</i>	ribosomal protein S11.e
YPR048w	<i>RPS18B</i>	ribosomal protein S11.e.B
YPR166c	<i>MRP2</i>	ribosomal protein S14
YJL191w	<i>CRY2</i>	ribosomal protein S14.e.B
YJL190c	<i>RPS24A</i>	ribosomal protein S15.e.c10
YLR367w	<i>RPS24B</i>	ribosomal protein S15.e.c12
YPL013c		ribosomal protein S16.e
YMR143w	<i>RPS16A</i>	ribosomal protein S16.e
YDL083c	<i>RPS16B</i>	ribosomal protein S16.e
YML024w	<i>RPS51A</i>	ribosomal protein S17.e.A
YDR447c	<i>RPS51B</i>	ribosomal protein S17.e.B
YOL120c	<i>RPS28A</i>	ribosomal protein S18.e
YML026c	<i>RPS18EB</i>	ribosomal protein S18.e.c13
YDR450w	<i>RPS18EA</i>	ribosomal protein S18.e.c4
YOL121c	<i>RPS55A</i>	ribosomal protein S19.e
YNL302c	<i>RPS55B</i>	ribosomal protein S19.e
YKR057w	<i>RPS25A</i>	ribosomal protein S21.e
YJL136c	<i>RPS25B</i>	ribosomal protein S21.e
YGR118w	<i>RPS28A</i>	ribosomal protein S23.e
YPR132w	<i>RPS28B</i>	ribosomal protein S23.e
YER074w	<i>RPS50A</i>	ribosomal protein S24.e
YIL069c	<i>RPS50B</i>	ribosomal protein S24.e
YLR333c	<i>RPS31B</i>	ribosomal protein S25.e.c12
YGR027c	<i>RPS31A</i>	ribosomal protein S25.e.c7
YER131w	<i>RPS26B</i>	ribosomal protein S26.e.c5
YKL156w	<i>RPS27A</i>	ribosomal protein S27.e
YHR021c	<i>RPS27B</i>	ribosomal protein S27.e
YDR064w	<i>YS15</i>	

YHR057c	CYP2	peptidyl-prolyl <i>cis-trans</i> isomerase	YBR162w-a	YSY6	secretory pathway protein	YKL134c	(MIP1)	mitochondrial intermediate peptidase			
YCR069w	SCC3	peptidyl-prolyl <i>cis-trans</i> isomerase	YBR097w	VPS15	ser/thr protein kinase	YLR163c	MAS1	mitochondrial processing peptidase			
YDR304c	CYP5	peptidyl-prolyl <i>cis-trans</i> isomerase D (cyclophilin D) of the ER	YPL243w	SRP68	signal recognition particle protein	YHR024c	MAS2	mitochondrial processing peptidase, catalytic 53K (α) subunit			
YNL135c	FPR1	peptidyl-prolyl <i>cis-trans</i> isomerase, FK506-binding protein	YPL210c	SRP72	signal recognition particle protein	YMR150c	IMP1	mitochondrial protease			
YML074c	NPI46	proline <i>cis-trans</i> isomerase	YDR292c	SRP101	signal recognition particle receptor, α subunit	YPR051w	MAK3	N-acetyltransferase			
YDR518w	EUG1	protein disulphide isomerase	YML105c	SEC65	signal recognition particle subunit	YGR147c	NAT2	N-acetyltransferase for N-terminal methionine			
YCL043c	PDI1	protein disulphide-isomerase	YDL092w	SRP14	signal recognition particle subunit	YBR247c	ENP1	N-glycosylation protein			
YIR097w		similarity to CaJ1p	YKL122c	SRP21	signal recognition particle subunit	YLR195c	NMT1	N-myristoyltransferase			
YBR044c		similarity to chaperonin HSP60 proteins	YPR088c	SRP54	signal recognition particle subunit	YJL002c	OST1	oligosaccharyltransferase α subunit			
YOL088c		similarity to disulphide isomerases and ER60 proteases	YOR285w		similarity to <i>D. melanogaster</i> heat-shock protein 67B2	YELO02c	WBP1	oligosaccharyltransferase β subunit			
YNL077w		similarity to dnaj protein homologue YDJ1	YOR286w		similarity to <i>D. melanogaster</i> heat-shock protein 67B2	YMR149w	SWP1	oligosaccharyltransferase δ subunit			
YMR161w	HJ1	similarity to dnaj proteins	YHR110w		similarity to human gp25L2 protein	YOR103c	OST2	oligosaccharyltransferase ϵ subunit			
YIR004w		similarity to DNAJ-like proteins	YAR002c-a		similarity to mammalian gp25L protein	YOR085w	OST3	oligosaccharyltransferase γ subunit			
YLR090w	XDJ1	similarity to <i>E. coli</i> dnaj	YKL154w		similarity to mouse signal recognition particle receptor β subunit	YDL232w	OST4	oligosaccharyltransferase subunit			
YJL073w		similarity to heat-shock proteins	YKL196c		similarity to Sec22p	YGL022w	STT3	oligosaccharyltransferase subunit			
YNR028w		similarity to peptidyl/prolyl isomerase Scc3p	YMR018w		similarity to tetratricopeptide-repeat protein PAS10	YFL045c	SEC53	phosphomannomutase			
YIL005w		similarity to protein disulphide isomerases	YMR214w	SC1	similarity to <i>E. coli</i> dnaJ	YPR122w	AXL1	protease			
YLR369w		strong similarity to heat-shock protein 70-related proteins	YNL304w		similarity to Ypt1p and other GTP-binding proteins	YELO60c	PRB1	protease B, vacuolar			
YLR449w		strong similarity to peptidyl/prolyl isomerase FRP3	YER101c	AST2	strong similarity to Ast1p	YLR389c	STE23	protease involved in a-factor processing			
YJR064w	CCT5	T-complex protein 1, ϵ subunit	YOR016c		strong similarity to FUN54 protein, similarity to hamster COP-coated vesicle membrane protein	YLC043c	PDI1	protein disulphide-isomerase			
YFR041c		weak similarity to dnaj-like heat-shock proteins	YGL002w		strong similarity to Sec61 β subunit	YKL019w	RAM2	protein farnesyltransferase, α subunit			
YNL227c		weak similarity to dnaj-like proteins	YER087c-a	SEB1	strong similarity to human gp25L2 protein	YDL090c	RAM1	protein farnesyltransferase, β subunit			
<i>protein targeting, sorting and translocation</i>											
YKL073w	LHS1	chaperone of the ER lumen	YCR099c		strong similarity to Pep1p	YHR013c	ARD1	protein N-acetyltransferase subunit			
YGL206c	CHC1	clathrin heavy chain	YCR100c		strong similarity to Pep1p	YDL040c	NAT1	protein N-acetyltransferase subunit			
YOL062c	APM4	clathrin-associate protein YAP54	YCR101c		strong similarity to Pep1p	YILO85c	KTR7	putative α -1-mannosyltransferase			
YPL259c	APM1	clathrin-associated protein	YIL173w		strong similarity to Pep1p	YGL194c	RTL1	putative deacetylase			
YBR288c	APM3	clathrin-associated protein complex, medium subunit	YJL222w		strong similarity to Pep1p	YNL029c	KTR5	putative mannosyltransferase			
YDL212w	SHR3	endoplasmic reticulum membrane protein	YBR283c		strong similarity to Sec61p	YGR199w	PMT6	putative mannosyltransferase			
YBL040c	ERD2	ER lumen protein-retaining receptor	YOR327c	SNC2	strong similarity to synaptobrevin	YKL193c	SDS22	regulatory subunit for the mitotic function of type I protein phosphatase			
YER019c-a	SEB2	ER protein-translocation complex subunit	YOR329c	SCD5	suppressor of clathrin deficiency	YNL048w	ALG11	required for asparagine-linked glycosylation			
YLR373c	SEC61	ER protein-translocation complex subunit	YHR050w	SMF2	suppressor of mitochondrial matrix mutant	YLR088w	GAA1	required for attachment of GPI anchor onto proteins			
YPL094c	SEC62	ER protein-translocation complex subunit	YOR306w	PEP12	syntaxis (T-SNARE)	YPL050c	MNN9	required for complex N-glycosylation			
YOR254c	SEC63	ER protein-translocation complex subunit	YLR148w	PEP3	vacuolar membrane protein	YIRO10c-a	SPC1	signal peptidase 10.8K subunit			
YBR171w	SEC66	ER protein-translocation complex subunit	YBL017c	PEP1	vacuolar protein sorting/targeting protein	YML055w	SPC2	signal peptidase 18K subunit			
YLR292c	SEC72	ER protein-translocation complex subunit	YJL053w	PEP8	vacuolar protein sorting/targeting protein	YIR022w	SEC11	signal sequence processing protein silencing regulatory protein			
YDR086c	SSS1	ER protein-translocation complex subunit	YOR132w	VPS17	vacuolar protein sorting-associated protein	YER005w		similarity to GdA1p			
YOR089c	VPS21	GTP-binding protein	YML095c	VPS45	vacuolar protein sorting-associated protein	YMR223w		similarity to human putative ubiquitin carboxy-terminal hydrolase			
YKR014c	VPT52	GTP-binding protein of the RAB family	YJL164c	VPS35	vacuolar protein-sorting protein	YDR098c		similarity to <i>Legionella</i> glutaredoxin-like protein			
YNL093w	VPT53	GTP-binding protein of the RAB family (RAS superfamily)	YDR323c	PEP7	vacuolar segregation protein	YER174c		similarity to <i>Legionella</i> glutaredoxin-like protein			
YOR270c	VPH1	H-ATPase V0 domain 95K subunit, vacuolar	YPL045w	VPS16	vacuolar sorting protein	YGL257c		similarity to Mnn1p			
YAL005c	SSA1	heat-shock protein of HSP70 family	YDR495c	VPS3	vacuolar sorting protein	YILO14w		similarity to Mnn1p			
YCR075c	ERS1	intracellular protein transport protein	YLR396c	VPS33	vacuolar sorting protein	YPR131c		similarity to N-acetyltransferases			
YGR028w	MSP1	intra-mitochondrial sorting protein	YAL002w	VPS8	vacuolar sorting protein	YDL093w	PMT5	similarity to O-mannosyltransferases			
YOR069w	VPS5	involved in Golgi retention and vacuolar sorting	YML097c	VPS9	vacuolar sorting protein	YDR307w		Pmt1p-Pmt4p			
YLR347c	KAP95	karyopherin- β	<i>protein modification (glycosylation, acylation, myristylation, palmitylation, farnesylation and processing)</i>								
YOL122c	SMF1	manganese transporter	YJL143w	TIM17	mitochondrial inner membrane import translocase subunit	YDR245w	MNN10	similarity to Pmt1p			
YKR001c	VPS1	member of the dynamin family of GTPases	YIL022w	TIM44	mitochondrial inner membrane import translocase subunit	YLR066w		similarity to <i>S. pombe</i> galactosyltransferase			
YOR020c	HSP10	mitochondrial chaperonin	YMR035w	IMP2	mitochondrial inner membrane protease subunit	YNR059w		similarity to signal peptidase			
YNR017w	MAS6	mitochondrial inner membrane import translocase subunit	YOR017w	APE1	arginyl tRNA transferase	YPL003w		similarity to α -1,3-mannosyltransferase			
YJL143w		mitochondrial inner membrane import translocase subunit	YPL154c	PEP4	aspartyl protease	YPR180w		similarity to ubiquitin-activating enzymes			
YIL022w		mitochondrial inner membrane import translocase subunit	YLR120c	YAP3	aspergillipepsin	YGL087c		similarity to ubiquitin-activating enzymes			
YMR035w		mitochondrial inner membrane import translocase subunit	YDL141w	BPL1	biotin holocarboxylase synthetase	YIR039c		similarity to ubiquitin-protein ligase			
YNL131w	TOM22	mitochondrial outer membrane import receptor subunit	YJL110w	ALG1	β -mannosyltransferase	YBR205w	KTR3	strong similarity to α -2-mannosyltransferase			
YGR082w	TOM20	mitochondrial outer membrane import receptor subunit, 20K	YGL203c	KEX1	carboxypeptidase YSC- α	YBR199w	KTR4	strong similarity to α -2-mannosyltransferase			
YMR060c	TOM37	mitochondrial outer membrane import receptor subunit, 37K	YPL227c	ALG5	dolichol-P-glucose synthetase	YPL053c	KTR6	strong similarity to α -2-mannosyltransferase			
YMR203w	TOM40	mitochondrial outer membrane import receptor subunit, 40K	YJR143c	PMT4	dolichyl-phosphate-mannose-protein	YPL051w		strong similarity to ADP-ribosylation factors			
YOR045w	TOM6	mitochondrial outer membrane import receptor subunit, 20K	YDL212w	SHR3	O-mannosyl transferase	YLR121c		strong similarity to aspartyl/proteases			
YNL070w	TOM7	mitochondrial outer membrane import receptor subunit, 6K	YNL238w	KEX2	endoplasmic reticulum membrane protein endoprotease of late Golgi compartment	YOR099w	KTR1	strong similarity to mannosyltransferases			
YNL121c	TOM70	mitochondrial outer membrane specialized import receptor	YDR331w	GPI8	essential for GPI-anchor attachment	YOR339c		strong similarity to thioredoxin			
YMR150c	IMP1	mitochondrial protease	YDR410c	STE14	farnesyl cysteine carboxyl-methyltransferase	YPR066w		strong similarity to ubiquitin-conjugating enzymes			
YJL034w	KAR2	nuclear fusion protein	YOR370c	MS4	geranylgeranyltransferase regulatory subunit	YML111w		strong similarity to ubiquitin-activating enzymes			
YMR091c	NPL6	nuclear protein localization factor	YGL155w	CDC43	geranylgeranyltransferase type I β subunit	YGL226c-a	OST75	strong similarity to ubiquitin-conjugating enzymes			
YBR170c	NPL4	nuclear protein localization factor and ER translocation component	YPR176c	BET2	geranylgeranyltransferase type II β subunit	YEL056w	HAT2	strong similarity to ubiquitin-conjugating enzymes			
YDR432w	NPL3	nucleolar protein	YOR002w	ALG6	geranylgeranyltransferase, α subunit	YJR075w	HOC1	suppressor of pkc1			
YLR191w	PAS20	peroxisomal protein involved in protein import	YOR067c	ALG8	glucosyltransferase	YLR043c	TRX1	thioredoxin I			
YPR047w	MSF1	phenylalanine-tRNA ligase α subunit, mitochondrial	YLE042w	GDA1	guanosine diphosphatase	YGR209c	TRX2	thioredoxin II			
YNL106c	PIE3	phosphatidylinositol phosphate phosphatase	YGR252w	GCN5	histone acetyltransferase	YOR219c	STE13	type IV dipeptidyl aminopeptidase			
YBL069w	AST1	PM1 protein targeting protein probably involved in intramitochondrial protein sorting	YPL001w	HAT1	histone acetyltransferase subunit	YMR275c	BUL1	ubiquitination pathway protein			
YLR168c	(MSF1)		YBR034c	HMT1	hnRNP methyltransferase	YDR054c	CDC34	ubiquitin-conjugating enzyme			
YDR244w	PAS10	putative peroxisomal targeting signal receptor	YAL039c	CYC3	holocytchrome c synthase (cytochrome c heme lyase)	YGR133w	PAS2	ubiquitin-conjugating enzyme			
YCL001w	RER1	required for correct localization of Sec12p	YKL087c	CYT2	holocytchrome c1 synthase	YMR022w	QRI8	ubiquitin-conjugating enzyme			
YDR414c	ERD1	required for retention of luminal ER proteins	YGL065c	ALG2	mannosyltransferase	YGL058w	RAD6	ubiquitin-conjugating enzyme			
YDR005c	MAF1	required for sorting of Mod5p	YDL095w	PMT1	mannosyltransferase	YDR177w	UBC1	ubiquitin-conjugating enzyme			
YMR004w	MVP1	required for vacuolar protein sorting	YAL023c	PMT2	mannosyltransferase	YLR306w	UBC12	ubiquitin-conjugating enzyme			
YDR498c	SEC20	secretory pathway protein	YOR321w	PMT3	mannosyltransferase	YDR092w	UBC13	ubiquitin-conjugating enzyme			
			YBL082c	RHK1	mannosyltransferase	YDR059c	UBC5	ubiquitin-conjugating enzyme			
			YLR244w	MAP1	methionine aminopeptidase, isoform 1	YER100w	UBC6	ubiquitin-conjugating enzyme			
			YBL091c	MAP2	methionine aminopeptidase, isoform 2	YEL012w	UBC8	ubiquitin-conjugating enzyme			
			YMR035w	IMP2	mitochondrial inner membrane protease subunit	YDL064w	UBC9	ubiquitin-conjugating enzyme			
						YDR139c		ubiquitin-like protein			
						YER125w	RSP5	ubiquitin-protein ligase			
						YKL210w	UBA1	ubiquitin-protein ligase			
						YJR099w	YUH1	ubiquitin-specific protease			
						YBR243c	ALG7	UDP-N-acetylglucosamine-1-phosphate transferase			
						YKL035w	UGP1	UTP-glucose-1-phosphate uridylyltransferase			
						YDR495c	VPS3	vacuolar sorting protein			

YJR117w	STE24	zinc metallo-protease assembly of protein complexes	YGR105w	VMA21	vacuolar ATPase assembly integral membrane protein	YDR054c	CDC34	ubiquitin-conjugating enzyme
YLR048w	NAB1A	40S ribosomal protein p40 homologue A	YHR060w	VMA22	vacuolar ATPase assembly protein	YMR022w	QR18	ubiquitin-conjugating enzyme
YLR048w	NAB1B	40S ribosomal protein p40 homologue B	YDR495c	VPS3	vacuolar sorting protein	YDR177w	UBC1	ubiquitin-conjugating enzyme
YPL195w	YSK4	α - or γ adaptin, large subunit of the clathrin-associated protein(AP) complex				YLR306w	UBC12	ubiquitin-conjugating enzyme
YBL037w	APL3	α -adaptin, large subunit of the clathrin-associated protein(AP) complex				YDR092w	UBC13	ubiquitin-conjugating enzyme
YOR094w	ARF3	ADP-ribosylation factor 3	YPL149w	APG5	involved in autophagy and nutrient starvation	YBR082c	UBC4	ubiquitin-conjugating enzyme
YBL022c	PIM1	ATP-dependent protease, mitochondrial	YOL013c	HRD1	involved in degradation of Hmg2p	YDR059c	UBC5	ubiquitin-conjugating enzyme
YKL135c	APL2	β -adaptin	YLR207w	HRD3	involved in degradation of Hmg2p	YER100w	UBC6	ubiquitin-conjugating enzyme
YGR261c	YSK5	β -adaptin, large subunit of the clathrin-associated protein(AP) complex	YMR174c	PAI3	protease A (ysca) inhibitor IA3	YDL064w	UBC9	ubiquitin-conjugating enzyme
YBR195c	MSI1	chromatin assembly complex, subunit p50	YNL015w	PBI2	proteinase B inhibitor 2	YDR139c		ubiquitin-like protein
YPR018w	RLF2	chromatin assembly complex, subunit p90	YCL052c	PBN1	required for Prb1p expression	YER125w	RSP5	ubiquitin-protein ligase
YLR170c	APS1	clathrin-associated protein (AP) complex, small subunit AP19	YHR132c		similarity to carboxypeptidase	YKL210w	UBA1	ubiquitin-protein ligase
YJR058c	APS2	clathrin-associated protein 17, small subunit	YNR069c		similarity to central part of Bul1p	YGR184c	UBR1	ubiquitin-protein ligase
YJR005w	YAP80	clathrin-associated protein complex, β subunit	YBR227c		similarity to <i>E. coli</i> ATP-binding protein cipX	YDR069c	DOA4	ubiquitin-specific protease
YJL024c	APS3	clathrin-associated protein(AP) complex, small subunit	YNL186w		similarity to human putative ubiquitin carboxy-terminal hydrolase	YDL122w	UBP1	ubiquitin-specific protease
YER058w	PET117	cytochrome c oxidase assembly factor	YIL137c		similarity to <i>M. musculus</i> aminopeptidase	YER144c	UBP5	ubiquitin-specific protease
YPL132w	COX11	cytochrome c oxidase assembly protein	YKR038c		similarity to Qri7p	YJR099w	YUH1	ubiquitin-specific protease
YML129c	COX14	cytochrome c oxidase assembly protein	YER047c		similarity to regulatory subunit Yta6p of 26S proteasome	YOR124c	UBP2	ubiquitin-specific protease
YDR079w	PET100	cytochrome c oxidase assembly protein	YCR045c		similarity to serin proteases	YER151c	UBP3	ubiquitin-specific proteinase
YLR038c	COX12	cytochrome c oxidase subunit VIB	YER078c		similarity to X-Pro aminopeptidase II			
YMR256c	COX7	cytochrome c oxidase subunit VII	YBR139w		strong similarity to carboxypeptidase			
YDL067c	COX9	cytochrome c oxidase subunit VIIA	YBL067c	UBP13	ubiquitin carboxy-terminal hydrolase			
YER141w	COX15	cytochrome oxidase assembly factor	YOL11c		weak similarity to human ubiquitin-like protein GDX			
YER154w	OXA1	cytochrome oxidase biogenesis protein						
YBL007c	SLA1	cytoskeleton assembly control protein						
YNL243w	SLA2	cytoskeleton assembly control protein						
YLR393w	ATP10	F1FO ATPase complex assembly protein						
YNL315c	ATP11	F1FO-ATPase complex assembly protein						
YJL180c	ATP12	F1FO-ATPase complex assembly protein						
YPL172c	COX10	farnesyl transferase						
YPL231w	FAS2	fatty-acyl-CoA synthase, α subunit						
YPR029c	APL4	γ -adaptin, large subunit of the clathrin-associated protein(AP) complex						
YDL192w	ARF1	GTP-binding protein of the ARF family						
YDL137w	ARF2	GTP-binding protein of the ARF family						
YKL119c	VPH1	H'-ATPase assembly protein, vacuolar						
YPL234c	TFP3	H'-ATPase V0 domain 17K subunit, vacuolar						
YLR447c	VMA6	H'-ATPase V0 domain 36K subunit, vacuolar						
YOR270c	VPH1	H'-ATPase V0 domain 95K subunit, vacuolar						
YOR332w	VMA4	H'-ATPase V1 domain 27K subunit, vacuolar						
YKL080w	VMA5	H'-ATPase V1 domain 42K subunit, vacuolar						
YLL009c	COX17	interacts genetically with SCO1 and SCO2 in cytochrome oxidase assembly						
YJR034w	PET191	involved in assembly of cytochrome oxidase						
YBR037c	SCO1	involved in stabilization of Cox1p and Cox2p						
YDR375c	BCS1	mitochondrial protein of the CDC48/PAS1/SEC18 (AAA) family of ATPases						
YPL085w	SEC16	multidomain vesicle coat protein						
YKR048c	NAP1	nucleosome assembly protein I						
YML102w	CAC2	p60 subunit of the chromatin assembly factor-I (CAF-I)						
YKL197c	PAS1	peroxisomal assembly protein						
YDR265w	PAS4	peroxisomal assembly protein						
YNL329c	PAS8	peroxisomal assembly protein						
YBR237w	PRP5	pre-mRNA processing RNA-helicase						
YJL203w	PRP21	pre-mRNA splicing factor						
YER017c	AFG3	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)						
YPR024w	YME1	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)						
YMR089c	YTA12	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)						
YPL215w	CBP3	required for assembly of cytochrome bc1 complex						
YBR185c	MBA1	respiratory chain assembly protein						
YLL008w	DRS1	RNA helicase of the DEAD box family						
YBR227c		similarity to <i>E. coli</i> ATP-binding protein clpX						
YGR241c		similarity to rat clathrin assembly protein						
YHR161c		similarity to rat clathrin assembly protein AP180						
YGR074w	SMD1	snRNA-associated protein						
YBR024w	SCO2	strong similarity to Sco1p						
YLR327c		strong similarity to STF2p						
YOR134w	BAG7	structural homologue of Sac7p						
YDR389w	SAC7	suppressor of actin mutation						
YOR106w	VAM3	syntaxis related protein						
YDR460w	TFB3	TFIIF subunit (transcription/repair factor)						
YPR178w	PRP4	U4/U6 snRNP 52K protein						
YGL119w	ABC1	ubiquinol cytochrome c reductase complex assembly protein						
YPR191w	QCR2	ubiquinol-cytochrome c reductase 40K subunit II						
YGR174c	CBP4	ubiquinol-cytochrome c reductase assembly factor						
YLL039c	UBI4	ubiquitin						
YGR133w	PAS2	ubiquitin-conjugating enzyme						
YGR105w	VMA21	vacuolar ATPase assembly integral membrane protein						
YHR060w	VMA22	vacuolar ATPase assembly protein						
YDR495c	VPS3	vacuolar sorting protein						
		proteolysis						
YPL149w	APG5	involved in autophagy and nutrient starvation						
YOL013c	HRD1	involved in degradation of Hmg2p						
YLR207w	HRD3	involved in degradation of Hmg2p						
YMR174c	PAI3	protease A (ysca) inhibitor IA3						
YNL015w	PBI2	proteinase B inhibitor 2						
YCL052c	PBN1	required for Prb1p expression						
YHR132c		similarity to carboxypeptidase						
YNR069c		similarity to central part of Bul1p						
YBR227c		similarity to <i>E. coli</i> ATP-binding protein cipX						
YNL186w		similarity to human putative ubiquitin carboxy-terminal hydrolase						
YIL137c		similarity to <i>M. musculus</i> aminopeptidase						
YKR038c		similarity to Qri7p						
YER047c		similarity to regulatory subunit Yta6p of 26S proteasome						
YCR045c		similarity to serin proteases						
YER078c		similarity to X-Pro aminopeptidase II						
YBR139w		strong similarity to carboxypeptidase						
YBL067c	UBP13	ubiquitin carboxy-terminal hydrolase						
YOL11c		weak similarity to human ubiquitin-like protein GDX						
		lysosomal and vacuolar degradation						
YBR286w	APE3	aminopeptidase Y, vacuolar						
YKL103c	LAP4	aminopeptidase ysl, vacuolar						
YPL104w	PEP4	aspartyl protease						
YMR297w	PRC1	carboxypeptidase y, serine-type protease						
YHR028c	DAP2	dipeptidyl aminopeptidase B						
YJL172w	CPS1	Gly-X carboxypeptidase YSCS						
YEL060c	PRB1	protease B, vacuolar						
YOR003w	YSP3	subtilisin-like protease III						
		other subcellular degradation						
YDR144c	MKC7	aspartyl protease of the periplasmic space						
YBL022c	PIM1	ATP-dependent protease, mitochondrial						
YIL010w	BAR1	barrierpepsin						
YBR201w	DER1	involved in degradation proteins in the ER						
YER017c	AFG3	family of ATPases (AAA)						
YPR024w	YME1	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)						
YMR089c	YTA12	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)						
YOL057w	PRD1	family of ATPases (AAA)						
YHR113w		proteinase yscD						
YFR006w		similarity to vacuolar aminopeptidase Lap4p/Ape1p						
		other protein-destination activities						
YDR258c	HSP78	heat-shock protein of clpB family of ATP-dependent proteases, mitochondrial						
YDL104c	QRI7	similar to <i>H. influenzae</i> sialoglycoprotease (gcp)						
YDR415c		strong similarity to bacterial leucyl aminopeptidase						
		Transport facilitation						
		ion channels						
YGR217w	CCH1	calcium channel protein						
YLL052c		member of mip family transmembrane channels						
YJL093c	TOK1	outward-rectifier potassium channel						
YPR192w		similarity to plasma membrane and water channel proteins						
YLL063c		similarity to water channel proteins						
YIL114c	POR2	voltage-dependent anion channel (VDAC2)						
YJR040w	GEF1	voltage-gated chloride channel protein						
		ion transporters						
YNR056c	HOL1	member of major facilitator superfamily multidrug-resistance protein subfamily 1						
YIL048w		similarity to amino-phospholipids-ATPase Drs2p						
		metal ion transporters (Cu, Fe, etc.)						
YOR16c	COT1	cobalt accumulation protein						
YPR124w	CTR1	copper transport protein						
YHR175w	CTR2	copper transport protein						
YLR411w	CTR3	copper transport protein						
YGL087c	ZRT1	high-affinity zinc transport protein						
YPL074w	YTA6	low-affinity Zrt2p						
YOR261c		similarity to human 26S proteasome regulatory subunit, p40						
YOR339c		strong similarity to ubiquitin conjugating enzymes						
YPR066w		strong similarity to ubiquitin-activating enzymes						
YML111w		strong similarity to ubiquitin-activating enzymes						
YHR027c	HRD2	strong similarity to ubiquitin-activating enzymes						
YKL022c	CDC16	ubiquitin						
YOR166c	CDC23	ubiquitin carboxy terminal hydrolase						
YBL084c	CDC27	ubiquitin carboxy-terminal hydrolase						
YLL039c	UBI4	ubiquitin						
YIL156w	UBP7	ubiquitin carboxy terminal hydrolase						
YER098w	UBP9	ubiquitin carboxy-terminal hydrolase						
YKR098c	UBP11	ubiquitin C-terminal hydrolase						
YII197w	UBP12	ubiquitin C-terminal hydrolase						
YGR048w	UFD1	ubiquitin fusion degradation protein						
YDL190c	UFD2	ubiquitin fusion degradation protein						
YBR058c	UBP14	ubiquitin specific protease						
YLR167w	UBI3	ubiquitin/ribosomal protein S27a						
YMR275c	BUL1	ubiquitination pathway protein						
		other cation transporters (Na, K, Ca, NH₄, etc.)						
YGR121c	MEP1	ammonia permease of high capacity and moderate affinity						
YDL128w	VCX1	Ca ²⁺ -transport (H^+/Ca^{2+} exchange) protein, vacuolar						
YGL006w	PMC1	Ca ²⁺ -transporting P-type ATPase						
YGL167c	PMR1	Ca ²⁺ -transporting P-type ATPase						
YCR024c-a	PMP1	H'-ATPase subunit, plasma membrane						
YEL017c-a	SMF1	H'-ATPase subunit, plasma membrane						
YMR054w	STV1	H'-ATPase subunit, plasma membrane						
YHR039c-a	VMA10	H'-ATPase V0 domain 102K subunit, vacuolar						

YEL027w	CUP5	H ⁺ -ATPase V0 domain 17K subunit, vacuolar	YCR098c	GIT1	similarity to phosphate transporter proteins	YOR071c	similarity to allantoin or uracil transport proteins
YPL234c	TFP3	H ⁺ -ATPase V0 domain 17K subunit, vacuolar	YDL199c		similarity to sugar transporter proteins	YOR192c	similarity to allantoin or uracil transport proteins
YLR447c	VMA6	H ⁺ -ATPase V0 domain 36K subunit, vacuolar	YFL040w		similarity to yeast glucose transport proteins	YLR237w	similarity to allantoin transport protein
YOR270c	VPH1	H ⁺ -ATPase V0 domain 95K subunit, vacuolar	YHR096c	HXT5	strong similarity to hexose transporters	YLL056w	similarity to Dal5p
YGR020c	VMA7	H ⁺ -ATPase V1 domain 14K subunit, vacuolar	YDL245c	HXT15	strong similarity to Hxt17p and Hxt7p	YBL042c	strong similarity to allantoin and uracil transport proteins
YOR332w	VMA4	H ⁺ -ATPase V1 domain 27K subunit, vacuolar	YJR160c		strong similarity to Mal3Tp	YAL067c	suppressor of sulphonyde ethionine resistance
YEL051w	VMA8	H ⁺ -ATPase V1 domain 32K subunit, vacuolar	YDR536w	STL1	strong similarity to members of the sugar permease family		
YKL080w	VMA5	H ⁺ -ATPase V1 domain 42K subunit, vacuolar	YOR271c		strong similarity to <i>Rattus</i> tricarboxylate carrier		
YPR036w	VMA13	H ⁺ -ATPase V1 domain 54K subunit, vacuolar	YDL247w		strong similarity to sugar transport proteins		
YBR127c	VMA2	H ⁺ -ATPase V1 domain 60K subunit, vacuolar	YIL171w		strong similarity to sugar transport proteins		
YDL185w	TFP1	H ⁺ -ATPase V1 domain 69K subunit, vacuolar	YIL170w	HXT12	strong similarity to sugar transport proteins		
YGL008c	PMA1	H ⁺ -transporting P-type ATPase	YJR158w	HXT16	strong similarity to sugar transport proteins		
YPL036w	PMA2	H ⁺ -transporting P-type ATPase 2	YRN072w	HXT17	sugar transport protein		
YNL142w	MEP2	high-affinity low-capacity ammonia permease	YDL138w	RG72	suppressor of snf3 mutant		
YJL129c	TRK1	high-affinity potassium transport protein					
YAL026c	DRS2	membrane-spanning P-type amino-phospholipids-ATPase					
YKR050w	TRK2	moderate-affinity potassium transport protein					
YHR026w	PPA1	proteolipid protein of proton-transporting ATPase					
YEL031w	SPF1	P-type ATPase					
YLR138w	NHA1	putative Na ⁺ /H ⁺ antiporter					
YBR235w		similarity to bumetanide-sensitive Na ⁺ -K ⁺ -Cl ⁻ cotransport protein					
YJL094c		similarity to <i>E. hirae</i> Na ⁺ /H ⁺ -antiporter NapA					
YDR456w		similarity to Na ⁺ /H ⁺ antiports					
YPR138c	MEP3	strong similarity to ammonium transport proteins					
YHL016c	DUR3	urea transport protein					
anion transporters (Cl⁻, SO₄²⁻, PO₄³⁻, etc)							
YLR348c		dicarboxylate carrier protein					
YML123c	PHO84	high-affinity inorganic phosphate/H ⁺ symporter					
YBR294w	SUL1	high-affinity sulphate transport protein					
YJL117w	PHO86	inorganic phosphate transporter					
YCR037c	PHO87	member of the phosphate permease family					
YJR077c	MIR1	phosphate transport protein, mitochondrial (MCF)					
YBR235w		similarity to bumetanide-sensitive Na ⁺ -K ⁺ -Cl ⁻ cotransport protein					
YJL094c		similarity to <i>E. hirae</i> Na ⁺ /H ⁺ -antiporter NapA					
YNR013c		similarity to membrane protein Pho87p and hypothetical protein YJL198w					
YCR098c	GIT1	similarity to phosphate transporter proteins					
YPR003c		similarity to sulphate transporter proteins					
YER053c		strong similarity to mitochondrial phosphate carrier protein					
YJL198w		strong similarity to Pho87p					
YBR296c		strong similarity to phosphate-repressible phosphate permease					
YLR092w	SEL2	strong similarity to Sul1p					
sugar and carbohydrate transporters							
YPR021c		similarity to human citrate transporter protein					
YKL217w	JEN1	carboxylic-acid transporter protein					
YBR291c	CTP1	citrate transport protein, mitochondrial (MCF)					
YLR348c		dicarboxylate carrier protein					
YLR081w	GAL2	galactose (and glucose) permease					
YGR289c	AGT1	general α-glucoside permease					
YLL043w	FPS1	glycerol channel protein					
YNL318c	HXT14	hexose transport protein					
YJL214w	HXT78	hexose transport protein					
YJL219w	HXT79	hexose transport protein					
YFL011w	HXT10	hexose transporter					
YDL194w	SNF3	high-affinity glucose transporter					
YEL069c	HXT13	high-affinity hexose transporter					
YMR011w	HXT2	high-affinity hexose transporter					
YDR343c	HXT6	high-affinity hexose transporter					
YDR342c	HXT7	high-affinity hexose transporter					
YML123c	PHO84	high-affinity inorganic phosphate/H ⁺ symporter					
YOL156w	HXT11	low-affinity glucose transporter					
YHR049c	HXT1	low-affinity hexose transporter					
YDR345c	HXT3	low-affinity hexose transporter					
YDR497c	ITR1	major myo-inositol permease					
YBR298c	MAL31	maltose permease					
YDL198c	YHM1	member of the mitochondrial carrier family (MCF)					
YHR092c	HXT4	moderate- to low-affinity glucose transporter					
YOL103w	ITR2	myo-inositol transport protein					
YBR241c		similarity to glucose transport proteins					
YGL104c		similarity to glucose transport proteins					
YDR387c		similarity to mitochondrial citrate transport proteins					
YFR045w							
allantoin and allantoate transporters							
YJR152w	DAL5	allantoate permease					
YLR028w	DAL4	allantoate permease					
YIL166c		similarity to allantoate permease					
YCR028c	FEN2	similarity to allantoate permease					
YGR260w		similarity to allantoate transport protein					
YLR004c		similarity to allantoate transport protein					
transport ATPases							
YGL006w	PMC1	Ca ²⁺ -transporting P-type ATPase					
YGL167c	PMR1	Ca ²⁺ -transporting P-type ATPase					
YKL016c	ATP7	F1FO-ATPase complex, F0 D subunit					
YBL099w	ATP1	F1FO-ATPase complex, F1 α subunit					
YJR121w	ATP2	F1FO-ATPase complex, F1 β subunit					
YDL004w	ATP16	F1FO-ATPase complex, F1 δ subunit					
YPL078c	ATP4	F1FO-ATPase complex, F1 ε subunit					
YPL271w	ATP15	F1FO-ATPase complex, F1 ε subunit					
YBR039w	ATP3	F1FO-ATPase complex, F1 γ subunit					
YDR298c	ATP5	F1FO-ATPase complex, OSCP subunit					
YLR295c	ATP14	F1FO-ATPase complex, subunit h					
YCR024c-a	PMP1	H ⁺ -ATPase subunit, plasma membrane					
YEL017c-a	PMP2	H ⁺ -ATPase subunit, plasma membrane					
YMR054w	STV1	H ⁺ -ATPase V0 domain 102K subunit, vacuolar					
YHR039c-a	VMA10	H ⁺ -ATPase V0 domain 13K subunit, vacuolar					
YEL027w	CUP5	H ⁺ -ATPase V0 domain 17K subunit, vacuolar					
YPL234c	TFP3	H ⁺ -ATPase V0 domain 17K subunit, vacuolar					
YLR447c	VMA6	H ⁺ -ATPase V0 domain 36K subunit, vacuolar					
YOR270c	VPH1	H ⁺ -ATPase V0 domain 95K subunit, vacuolar					
YGR020c	VMA7	H ⁺ -ATPase V1 domain 14K subunit, vacuolar					
YPR036w	VMA13	H ⁺ -ATPase V1 domain 54K subunit, vacuolar					
YOR332w	VMA4	H ⁺ -ATPase V1 domain 27K subunit, vacuolar					
YEL051w	VMA8	H ⁺ -ATPase V1 domain 32K subunit, vacuolar					
YKL080w	VMA5	H ⁺ -ATPase V1 domain 42K subunit, vacuolar					
YPR036w	VMA13	H ⁺ -ATPase V1 domain 54K subunit, vacuolar					
YBR127c	VMA2	H ⁺ -ATPase V1 domain 60K subunit, vacuolar					
YDL185w	TFP1	H ⁺ -ATPase V1 domain 69K subunit, vacuolar					
YGL008c	PMA1	H ⁺ -transporting P-type ATPase					
YPL036w	PMA2	H ⁺ -transporting P-type ATPase 2					
YAL026c	DRS2	membrane-spanning P-type amino-phospholipids-ATPase					
YDR270w	CCC2	probable copper-transporting ATPase					
YHR026w	PPA1	proteolipid protein of proton-transporting ATPase					
YEL031w	SPF1	P-type ATPase					
YDR040c	ENA1	P-type ATPase involved in Na ⁺ and Li ⁺ efflux					
YDR039c	ENA2	P-type ATPase involved in Na ⁺ efflux					
YDR038c	ENA5	P-type ATPase involved in Na ⁺ efflux					
YBR295w	PCA1	P-type Cu ²⁺ -transporting ATPase					
YIL048w		similarly to amino-phospholipids-ATPase Drs2p					
YER166w		similarly to ATPase <i>P. falciparum</i> ATPase 2					
YMR162c		similarity to ATPases					
YDR093w		similarity to <i>P. falciparum</i> ATPase 2					
ABC transporters							
YDR406w	PDR15	ATP-binding cassette protein family member					
YLR188w	MDL1	ATP-binding cassette transporter family member					
YPL270w	MDL2	ATP-binding cassette transporter family member					
YKL209c	STE6	ATP-binding cassette transporter protein					
YGR281w	YOR1	ATP-binding cassette transporter protein required for oligomycin resistance					
YMR301c	ATM1	ATP-binding cassette transporter protein, mitochondrial					
YCR011c	ADP1	ATP-dependent permease glutathione S-conjugate transporter, vacuolar					
YDR135c	YCF1						
YKL188c	PAT1	long-chain-fatty-acid transporter					
YPL147w	PXA1	long-chain-fatty-acid transporter					
YDR011w	SNQ2	multidrug resistance protein					
YPL058c	PDR12	multidrug resistance transporter					
YOR153w	PDR5	pleiotropic drug resistance protein					
YOL075c		similarity to <i>A. gambiae</i> ATP-binding-cassette protein					
YER036c		similarity to members of the ABC transporter family					
YLL015w		similarity to metal resistance proteins					
YHL035c		similarity to multidrug resistance proteins					
YKR103w		similarity to multidrug resistance proteins					
YKR104w		similarity to rat organic anion transporter					
YLL048c		similarity to Snq2p and other ATP-dependent permeases					
YIL013c	PDR11	strong similarity to ABC transporter proteins					
YOR328w	PDR10	strong similarity to ABC transporter proteins					
YOR011w		strong similarity to ATP-dependent permeases					

YJL004c	SYS1	multicopy suppressor of <i>ypt6</i>
YPL085w	SEC16	multidomain vesicle coat protein
YOR326w	MYO2	myosin heavy chain
YFL025c	BST1	negative regulator of COPII vesicle formation
YMR079w	SEC14	phosphatidylinositol/phosphatidylcholine transfer protein
YCR067c	SED4	protein of the endoplasmic reticulum
YIL004c	BET1	protein transport protein
YLR208w	SEC13	protein transport protein
YNL272c	SEC2	protein transport protein
YGR009c	SEC9	protein transport protein
YGL145w	TIP20	required for ER to Golgi transport
YDR498c	SEC20	secretory pathway protein
YBR097w	VPS15	ser/thr protein kinase
YBR264c		similarity to GTP-binding proteins
YKL196c		similarity to Sec22p
YJL193w		similarity to Sly41p
YGL210w	YPT32	small GTP-binding protein
YKL006c-a	SFT1	SNARE-like protein
YPL051w		strong similarity to ADP-ribosylation factors
YDR107c		strong similarity to EMP70 protein
YAL030w	SNC1	strong similarity to synaptic vesicle-associated membrane protein
YOR327c	SNC2	strong similarity to synaptobrevin
YER039c		strong similarity to vanadate resistance protein Van2p
YLR026c	SED5	syntaxin (T-SNARE)
YOR075w	UFE1	syntaxin (T-SNARE) of the ER
YPL232w	SSO1	syntaxin-related protein
YBL050w	SEC17	transport vesicle fusion protein
YLR396c	VPS33	vacuolar sorting protein
YML097c	VPS9	vacuolar sorting protein
YGL225w	GOG5	vanadate-resistance protein
YGL233w	SEC15	vesicular traffic control protein
YBR080c	SEC18	vesicular-fusion protein, functional homologue of NSF
YLR093c		weak similarity to synaptobrevin
YLR078c	BOS1	weak similarity to synaptobrevin (V-SNARE)

peroxisomal transport

YML042w	CAT2	carnitine O-acetyltransferase
YKL18c	PAT1	long-chain-fatty-acid transporter
YPL147w	PXA1	long-chain-fatty-acid transporter
YER015w	FAA2	long-chain-fatty-acid-CoA ligase
YDR329w	PAS3	peroxisomal assembly protein
YJL210w	PAS5	peroxisomal assembly protein
YDR142c	PAS7	peroxisomal import protein
YLR191w	PAS20	peroxisomal protein involved in protein import
YDR244w	PAS10	putative peroxisomal targeting signal receptor

vacuolar transport

YDL128w	VCX1	Ca ²⁺ -transport (H ⁺ /Ca ²⁺ exchange) protein, vacuolar
YGL006w	PMC1	Ca ²⁺ -transporting P-type ATPase
YDR135c	YCF1	glutathione S-conjugate transporter, vacuolar
YOR089c	VPS21	GTP-binding protein
YER031c	YPT31	GTP-binding protein of the RAB family
YKR014c	YPT52	GTP-binding protein of the RAB family
YNL393w	YPT53	GTP-binding protein of the RAB family (RAS superfamily)
YMR054w	STV1	H ⁺ -ATPase V0 domain 102K subunit, vacuolar
YHR039c-a	VMA10	H ⁺ -ATPase V0 domain 13K subunit, vacuolar
YEL027w	CUP5	H ⁺ -ATPase V0 domain 17K subunit, vacuolar
YPL234c	TFP3	H ⁺ -ATPase V0 domain 17K subunit, vacuolar
YLR447c	VMA6	H ⁺ -ATPase V0 domain 36K subunit, vacuolar
YOR270c	VPH1	H ⁺ -ATPase V0 domain 95K subunit, vacuolar
YGR020c	VMA7	H ⁺ -ATPase V1 domain 14K subunit, vacuolar
YOR332w	VMA4	H ⁺ -ATPase V1 domain 27K subunit, vacuolar
YEL051w	VMA8	H ⁺ -ATPase V1 domain 32K subunit, vacuolar
YKL080w	VMA5	H ⁺ -ATPase V1 domain 42K subunit, vacuolar
YPR036w	VMA13	H ⁺ -ATPase V1 domain 54K subunit, vacuolar
YBR127c	VMA2	H ⁺ -ATPase V1 domain 60K subunit, vacuolar
YDL185w	TFP1	H ⁺ -ATPase V1 domain 69K subunit, vacuolar
YPL066w	VPS28	involved in vacuolar traffic
YMR004w	MVP1	required for vacuolar protein sorting
YBR097w	VP-S15	ser/thr protein kinase
YJL222w		strong similarity to Pep1p
YOR036w	PEP12	syntaxin (T-SNARE)
YNR006w	VPS27	vacuolar protein sorting-associated protein
YGL095c	VPS45	vacuolar protein sorting-associated protein
YDR323c	PEP7	vacuolar segregation protein
YPL045w	VPS16	vacuolar sorting protein
YPR173c	VPS4	vacuolar sorting protein
YAL002w	VPS8	vacuolar sorting protein
YML097c	VPS9	vacuolar sorting protein

extracellular transport

YJL085w	EXO70	70K exocyst component protein
YDR129c	SAC6	actin filament bundling protein, fimbrin
YKL209c	STE6	ATP-binding cassette transporter protein
YDL226c	GCS1	cell proliferation zinc-finger protein
YER136w	GDI1	GDP dissociation inhibitor
YLL043w	FPS1	glycerol channel protein
YJL044c	GYP6	GTPase-activating protein
YLR262c	YPT6	GTP-binding protein of the RAB family
YJL205c-a	NCE1	involved in non-classical protein export pathway
YPR149w	NCE2	involved in non-classical protein export pathway
YNL036w	NCE3	involved in non-classical protein export pathway
YOR326w	MYO2	myosin heavy chain
YJL093c	TOK1	outward-rectifier potassium channel
YMR308c	PSE1	protein secretion enhancer
YDR164c	SEC1	protein transport protein
YNL272c	SEC2	protein transport protein
YIL068c	SEC6	protein transport protein
YPR055w	SEC8	protein transport protein
YGR009c	SEC9	protein transport protein
YKL212w	SAC1	recessive suppressor of secretory defect
YLR166c	SEC10	required for exocytosis
YDR166c	SEC5	required for exocytosis
YNR049c	MSD1	secretion protein, multicopy suppressor of sec1
YER008c	SEC3	secretory pathway protein
YOR307c	SLY41	secretory pathway protein
YBR162w-a	SY6	secretory pathway protein
YLR250w	SSP120	secretory protein
YCR032w		similarity to human CDC4L protein
YER006w		similarity to <i>P. polycyathum</i> myosin-related protein mlpA
YGR131w		strong similarity to Nce2p
YNL325c		suppressor of sac1 mutation
YPL232w	SSO1	synctatin-related protein
YGL233w	SEC15	vesicular traffic control protein
YBR080c	SEC18	vesicular-fusion protein, functional homologue of NSF

cellular import

YPL195w	YKS4	α- or γ- adaptin, large subunit of the clathrin-associated protein(AP) complex
YBL037w	APL3	α-adaptin, large subunit of the clathrin-associated protein(AP) complex
YFL039c	ACT1	actin
YDR129c	SAC6	actin filament bundling protein, fimbrin
YDL029w	ACT2	actin-like protein
YCL040w	GLK1	aldohexose specific glucokinase
YJR152w	DAL5	allantoin permease
YIR028w	DAL4	allantoin permease
YBR068c	BAP2	amino-acid permease
YEL063c	CAN1	amino-acid permease
YBR069c	VAP1	amino-acid permease
YGR121c	MEP1	ammonia permease of high capacity and moderate affinity
YKL135c	APL2	β-adaptin
YGR261c	YKS5	β-adaptin, large subunit of the clathrin-associated protein(AP) complex
YBR109c	CMD1	calmodulin
YDL226c	GCS1	cell proliferation zinc-finger protein
YMR058w	FET3	cell surface ferroxidase
YLG077c	HNM1	choline permease
YGL206c	CHC1	clathrin heavy chain
YGR167w	CLC1	clathrin light chain
YLR170c	APS1	clathrin-associated protein (AP) complex, small subunit AP19
YJR058c	APS2	clathrin-associated protein 17, small subunit
YJR005w	YAP80	clathrin-associated protein complex, β subunit
YJL024c	APS3	clathrin-associated protein(AP) complex, small subunit
YPR124w	CTR1	copper transport protein
YHR172w	CTR2	copper transport protein
YNL243w	SLA2	cytoskeleton assembly control protein
YLL001w	DYN1	dynamin-related protein
YDL210w	UGA4	GABA-specific high-affinity permease
YPR029c	APL4	γ-adaptin, large subunit of the clathrin-associated protein(AP) complex
YLR081w	GAL2	galactose (and glucose) permease
YNR026c	SEC12	GDP/GTP exchange factor for Sar1p
YKR039w	GAP1	general amino-acid permease
YLL043w	FPS1	glycerol channel protein
YOR089c	VPS21	GTP-binding protein
YER031c	YPT31	GTP-binding protein of the RAB family
YKR014c	YPT52	GTP-binding protein of the RAB family
YML001w	YPT7	GTP-binding protein of the RAB family
YNL093w	YPT53	GTP-binding protein of the RAB family (RAS superfamily)
YNL318c	HXT14	hexose transport protein
YJL214w	HXT8	hexose transport protein
YJL219w	HXT9	hexose transport protein
YFL011w	HXT10	hexose transporter
YDL194w	SNF3	high-affinity glucose transporter
YER069c	HXT13	high-affinity hexose transporter
YMR011w	HXT2	high-affinity hexose transporter
YDR343c	HXT6	high-affinity hexose transporter
YDR342c	HXT7	high-affinity hexose transporter
YML123c	PHO84	high-affinity inorganic phosphate/H ⁺ symporter
YNL142w	MEP2	high-affinity low capacity ammonia permease
YGR055w	MUP1	high-affinity methionine permease

YNL270c	ALP1	high-affinity permease for basic amino acids
YJL129c	TRK1	high-affinity potassium transport protein
YBR294w	SUL1	high-affinity sulphate transport protein
YOL020w	SCM2	high-affinity tryptophan transport protein histidine permease
YGR191w	HIP1	low-affinity Fe(II) iron transport protein
YMR319c	FET4	low-affinity glucose transporter
YOL156w	HXT11	low-affinity hexose transporter
YHR094c	HXT1	low-affinity hexose transporter
YDR345c	HXT3	lysine-specific high-affinity permease
YNL268w	LYP1	major myo-inositol permease
YDR497c	ITR1	maltose permease
YBR298c	MAL31	manganese transporter
YOL122c	SMF1	moderate-affinity potassium transport protein
YKR050w	TRK2	protein
YHR092c	HXT4	moderate to low-affinity glucose transporter
YOL103w	ITR2	myo-inositol transport protein
YLR240w	VPS34	phosphatidylinositol 3-kinase
YOR348c	PUT4	proline and γ-aminobutyrate permease
YER056c	FCY2	purine-cytosine permease
YLR088w	GAA1	required for attachment of GPI anchor onto proteins
YNL084c	END3	required for endocytosis and cytoskeletal organization
YJR090c	GRR1	required for glucose repression and for glucose and cation transport
YCR009c	RVS161	similarity to human amphiphysin and Rvs167p
YDR046c	(PAP1)	strong similarity to amino-acid transport proteins
YHR096c	HXT5	strong similarity to hexose transporters
YIL170w	HXT12	strong similarity to sugar transport proteins
YJR158w	HXT16	strong similarity to sugar transport proteins
YNR072w	HXT17	sugar transport protein
YOR329c	SCD5	suppressor of clathrin deficiency
YPR129w	SCD6	suppressor of clathrin deficiency
YBR021w	FUR4	uracil permease
YMR231w	PEP5	vacuolar biogenesis protein
YLR337w	VRP1	verprolin
YBR080c	SEC18	vesicular-fusion protein, functional homologue of NSF
YJR040w	GEF1	voltage-gated chloride channel protein
YMR243c	ZRC1	zinc- and cadmium resistance protein

other intracellular-transport activities

YKR054c	DYN1	dynein heavy chain, cytosolic
YER019c-a	SEB2	ER protein-translocation complex subunit
YLR378c	SEC61	ER protein-translocation complex subunit
YLP094c	SEC62	ER protein-translocation complex subunit
YOR254c	SEC63	ER protein-translocation complex subunit
YBR171w	SEC66	ER protein-translocation complex subunit
YLR292c	SEC72	ER protein-translocation complex subunit
YDR066c	SS1	ER protein-translocation complex subunit
YCR075c	ERS1	intracellular protein transport protein
YHL019c	APM2	involved in clathrin-dependent transport processes
YJL034w	KAR2	nuclear fusion protein
YBR170c	NPL4	nuclear protein localization factor and ER translocation component
YKR093w	PTR2	peptide transporter
YKL198c	PTK1	polyamine transport enhancing protein
YDR040c	ENA1	P-type ATPase involved in Na ⁺ and Li ⁺ efflux
YER060w	FCY21	purine-cytosine permease
YNL183c	NPR1	ser/thr protein kinase
YOR100c		similarity to mitochondrial carrier protein YM1
YGL216w		similar similarity to mouse kinesin-related protein KIF3
YPR009w		similarity to sterol uptake protein Sut1p
YHR123w	EPT1	sn-1,2-diacylglycerol ethanolamine- and cholinephosphotransferase
YER060w-a	FCY22	strong similarity to Foy2p
YER087c-a	SEB1	strong similarity to mammalian Sec61β subunit

Cellular organization and biogenesis*organization and biogenesis of cell wall and plasma membrane*

YLR342w	FKS1	1,3-D-glucan synthase, catalytic subunit
YGR032w	GSC2	1,3-D-glucan synthase, subunit
YOR362c	PRE10	26S proteasome subunit C1
YJR004c	SAG1	α-agglutinin
YNR044w	AGA1	α-agglutinin anchor subunit
YGL032c	AGA2	α-agglutinin binding subunit
YDR077w	SED1	abundant cell-surface glycoprotein
YJL005w	CYR1	adenylate cyclase
YLO070c	CWH36	affects the mannoprotein layer of the cell wall
YOR335c	ALA1	alanyl-tRNA synthetase, cytosolic
YPL061w	ALD6	aldehyde dehydrogenase, cytosolic
YIR125w	DAL5	allantoin permease
YIR028w	DAL4	allantoin permease
YBR068c	BAP2	amino-acid permease
YEL063c	CAN1	amino-acid permease
YBR069c	VAP1	amino-acid permease

YML116w	<i>ATR1</i>	aminotriazole and 4-nitroquinoline resistance protein	YHR092c	<i>HXT4</i>	moderate- to low-affinity glucose transporter	YMR138w	<i>CIN4</i>	GTP-binding protein
YGR121c	<i>MEP1</i>	ammonia permease of high capacity and moderate affinity	YGR014w	<i>MSB2</i>	multicopy suppressor of a <i>cdc24</i> bud emergence defect	YOR156c	<i>NF1</i>	interacts with Cdc12p in 2-hybrid assay
YDR144c	<i>MKC7</i>	aspartyl protease of the periplasmic space	YDR011w	<i>SNQ2</i>	multidrug resistance protein	YML104c	<i>MDM1</i>	intermediate filament protein
YLR120c	<i>YAP3</i>	aspartyllopepsin	YOL103w	<i>ITR2</i>	myo-inositol transport protein	YLL021w	<i>SPA2</i>	involved in cell polarity
YKL209c	<i>STE6</i>	ATP-binding cassette transporter protein	YKR093w	<i>PTR2</i>	outward-rectifier potassium channel	YPL241c	<i>CIN2</i>	involved in chromosome segregation
YGR281w	<i>YOR1</i>	ATP-binding cassette transporter protein required for oligomycin resistance	YFL026w	<i>STE2</i>	peptide transporter	YDR085c	<i>AFR1</i>	involved in morphogenesis of the mating projection
YCR011c	<i>ADP1</i>	ATP-dependent permease	YKL178c	<i>STE3</i>	pheromone α -factor receptor	YEL061c	<i>CIN8</i>	kinetochore-related protein
YER123w	<i>YCK3</i>	casein kinase, isoform 3	YMR008c	<i>PLB1</i>	pheromone α -factor receptor	YPR141c	<i>KAR3</i>	kinetochore-related protein
YCL027w	<i>FUS1</i>	cell fusion protein	YCR034w	<i>GNS1</i>	phospholipase B (lysophospholipase)	YBL063w	<i>KIP1</i>	kinetochore-related protein
YMR058w	<i>FET3</i>	cell-surface ferroxidase	YOR348c	<i>PUT4</i>	pleiotropic drug resistance protein	YPL155c	<i>KIP2</i>	kinetochore-related protein
YKL096w	<i>CWP1</i>	cell-wall mannoprotein	YPL140c	<i>MK2</i>	probable 1,3-glucan synthase subunit	YKL079w	<i>SMY1</i>	kinetochore-related protein
YKL096w-a	<i>CWP2</i>	cell-wall mannoprotein	YGR009c	<i>SEC9</i>	proline and γ -aminobutyrate permease	YBR172c	<i>SMY2</i>	kinetochore-related protein
YNL322c	<i>KRE1</i>	cell-wall protein	YER056c	<i>FCY2</i>	protein kinase of the MAP kinase kinase (MEK) family	YOR058c	<i>ASE1</i>	microtubule-associated protein
YAR050w	<i>FLO1</i>	cell-wall protein involved in flocculation	YIL140w	<i>SRO4</i>	protein transport protein	YJL042w	<i>MHP1</i>	microtubule-associated protein
YNL192w	<i>CHS1</i>	chitin synthase I	YCR089w	<i>FIG2</i>	purine-cytosine permease	YMR294w	<i>JNM1</i>	mitosis protein, involved in nuclear migration
YBR038w	<i>CHS2</i>	chitin synthase II	YDR122w	<i>KIN1</i>	required for axial pattern of budding	YBL034c	<i>STU1</i>	mitotic spindle protein
YBR023c	<i>CHS3</i>	chitin synthase III	YLR096w	<i>KIN2</i>	required for efficient mating	YOR326w	<i>MYO2</i>	myosin heavy chain
YGL077c	<i>HMM1</i>	choline permease	YPL176c	<i>YER176c</i>	ser/thr protein kinase	YAL029c	<i>MYO4</i>	myosin heavy chain, unconventional (class V) isoform
YOR010c	<i>TIR2</i>	cold-shock induced protein	YKR102w		ser/thr protein kinase	YMR109w	<i>MYO5</i>	myosin I
YER011w	<i>TIR1</i>	cold-shock induced protein of the <i>Tir1p</i> , <i>Tip1p</i> family	YHL028w		similarity to Chinese hamster transferrin receptor protein	YKL129c	<i>MYO3</i>	myosin type I
YPR124w	<i>CTR1</i>	copper transport protein	YIL013c	<i>PDR11</i>	similarity to <i>Flo1p</i>	YHR023w	<i>MYO1</i>	myosin-1 isoform (type II myosin) heavy chain
YGR282c	<i>BGL2</i>	endo-1,3-glucanase of the cell wall	YJR151c		similarity to mucin and other ser-thr rich proteins	YCL029c	<i>BIK1</i>	nuclear fusion protein
YOR190w	<i>SPR1</i>	exo-1,3-glucanase	YMR317w		similarity to mucin proteins	YOR122c	<i>PFY1</i>	profilin
YDR261c	<i>EXG2</i>	exo-1,3-glucanase minor isoform	YCR098c	<i>GIT1</i>	similarity to mucins, glucan 1,4-glucosidase and exo-sialidase	YDR164c	<i>SEC1</i>	protein transport protein
YLR214w	<i>FRE1</i>	ferric (and cupric) reductase	YIL013c		similarity to phosphate transporter proteins	YDR388w	<i>RVS167</i>	reduced viability upon starvation protein required for endocytosis and cytoskeletal organization
YKL220c	<i>FRE2</i>	ferrous (and cupric) reductase	YIL032w		similarity to Snq2p and other ATP-dependent permeases	YBR130c	<i>SHE3</i>	required for mother cell-specific expression of HO
YDL210w	<i>UGA4</i>	GABA-specific high-affinity permease	YAL063c	<i>FLO9</i>	similarity to Yrp1p and Nup2p	YGR078c	<i>PAC10</i>	required in the absence of Cin8p
YLR081w	<i>GAL2</i>	galactose (and glucose) permease	YLR163c	<i>YRB2</i>	spindle pole body component	YDR488c	<i>PAC11</i>	required in the absence of Cin8p
YLL016w	<i>SDC25</i>	GDP/GTP exchange factor	YNL126w	<i>SPC98</i>	sporulation-specific wall maturation protein	YER007w	<i>PAC2</i>	required in the absence of Cin8p
YLR310c	<i>CDC25</i>	GDP/GTP exchange factor for Ras1p and Ras2p	YHR139c	<i>SPS100</i>	strong similarity to ABC transporter proteins	YJR076c	<i>CDC11</i>	septin
YCR038c	<i>BUD5</i>	GDP/GTP exchange factor for Rsr1p/Bud1p	YOR328w	<i>PDR10</i>	strong similarity to amino-acid transport proteins	YHR107c	<i>CDC12</i>	septin
YKR039w	<i>GAP1</i>	general amino-acid permease	YDR046c	<i>(PAP1)</i>	strong similarity to ABC transporter proteins	YDR218c	<i>SPR28</i>	septin-related sporulation protein
YMR307w	<i>GAS1</i>	glycophospholipid-anchored surface glycoprotein	YDR134c		strong similarity to Flo1p	YNL059c		similarity to actin
YOL081w	<i>IRA2</i>	GTPase-activating protein for RAS proteins	YAL063c		strong similarity to Flo1p	YLR085c		similarity to actin and actin-related proteins
YOR101w	<i>RAS1</i>	GTP-binding protein	YLR343w		strong similarity to Gas1p and <i>C. albicans</i> pH responsive protein	YLR429w		similarity to actin binding protein coronin
YNL098c	<i>RAS2</i>	GTP-binding protein	YOL030w		strong similarity to glycoprotein GAS1	YPR034w		similarity to actins
YHR005c	<i>GPA1</i>	GTP-binding protein α subunit of the pheromone pathway	YHR096c	<i>HXT5</i>	strong similarity to hexose transporters	YGL003c		similarity to <i>C. elegans</i> CDC20 protein and human p55CDC
YOR212w	<i>STE4</i>	GTP-binding protein β subunit of the pheromone pathway	YDR336w	<i>STL1</i>	strong similarity to members of the sugar permease family	YCR009c	<i>RVS167</i>	similarity to human amphiphysin and Rvs167p
YJR086w	<i>STE18</i>	GTP-binding protein γ subunit of the pheromone pathway	YIL170w	<i>HXT12</i>	strong similarity to sugar transport proteins	YER018c		similarity to lamins
YLR229c	<i>CDC42</i>	GTP-binding protein of RAS superfamily	YJR158w	<i>HXT16</i>	strong similarity to sugar transport proteins	YOR367w		similarity to mammalian smooth muscle protein SM22
YCR024c-a	<i>PMP1</i>	H $^+$ -ATPase subunit, plasma membrane	YNR072w	<i>HXT17</i>	sugar transport protein	YIL149c		similarity to Mlp1p and myosin heavy chains
YELO17c-a	<i>PMP2</i>	H $^+$ -ATPase subunit, plasma membrane	YPL232w	<i>SSO1</i>	syntatin-related protein	YGL216w		similarity to mouse kinesin-related protein Kif3
YGL008c	<i>PM1A</i>	H $^+$ -transporting P-type ATPase	YBR067c	<i>TIP1</i>	temp shock induced protein of the Srp1p/Tip1p family	YKL179c		similarity to Nuf1p
YPL036w	<i>PM12</i>	H $^+$ -transporting P-type ATPase 2	YJR007w		translation initiation factor eif2, α subunit	YJR134c		similarity to paramyosin, myosin similar to Smy2p
YDR420w	<i>HKR1</i>	Hansenula MraII k9 killer toxin-resistance protein	YAL020c	<i>SU12</i>	two-component signal transducer	YLP105c		spindle pole body component
YLL024c	<i>SSA2</i>	heat-shock protein of HSP70 family, cytosolic	YIL147c	<i>SLN1</i>	ubiquitin-protein ligase	YDR356w	<i>NUF1</i>	spindle pole body component
YNL318c	<i>HXT14</i>	hexose transport protein	YER125w	<i>RSP5</i>	uracil permease	YNL126w	<i>SPC98</i>	spindle pole body component
YJL214w	<i>HXT8</i>	hexose transport protein	YBR021w	<i>FUR4</i>	urea transport protein	YOL069w	<i>NUF2</i>	spindle pole body protein
YJL219w	<i>HXT9</i>	hexose transport protein	YHL016c	<i>DUR3</i>	vesicular traffic control protein	YGR059w	<i>SPR3</i>	sporulation-specific septin
YFL011w	<i>HXT10</i>	hexose transporter	YLG233w	<i>SEC15</i>	voltage-gated chloride channel protein	YEL071w		strong similarity to Aip2p
YDL194w	<i>SNF3</i>	high-affinity glucose transporter	YJR040w	<i>GEF1</i>	zinc- and cadmium resistance protein	YOR134w	<i>BAG7</i>	structural homologue of Sac7p
YEL069c	<i>HXT13</i>	high-affinity hexose transporter	YMR243c	<i>ZRC1</i>		YAL047c	<i>SP16</i>	Stu2p Interactant
YMR011w	<i>HXT2</i>	high-affinity hexose transporter	YOL032w			YKL022c	<i>CDC16</i>	subunit of anaphase-promoting complex (cyclosome)
YDR343c	<i>HXT6</i>	high-affinity hexose transporter	YHR072w	<i>HXT17</i>	sugar transport protein	YHR166c	<i>CDC23</i>	subunit of anaphase-promoting complex (cyclosome)
YDR342c	<i>HXT7</i>	high-affinity hexose transporter	YPL232w	<i>SSO1</i>	syntatin-related protein	YBL084c	<i>CDC27</i>	subunit of anaphase-promoting complex (cyclosome)
YML123c	<i>PHO84</i>	high-affinity inorganic phosphate/H $^+$ symporter	YBR067c	<i>TIP1</i>	temp shock induced protein of the Srp1p/Tip1p family	YDR484w	<i>SAC2</i>	suppressor of actin mutation
YNL142w	<i>MEP2</i>	high-affinity low-capacity ammonia permease	YJR007w	<i>SU12</i>	translation initiation factor eif2, α subunit	YDR389w	<i>SAC7</i>	suppressor of actin mutation
YGR055w	<i>MUP1</i>	high-affinity methionine permease	YAL020c	<i>ATS1</i>	two-component signal transducer	YNL079c	<i>TPM1</i>	tropomyosin 1
YNL270c	<i>ALP1</i>	high-affinity permease for basic amino acids	YER016w	<i>BIM1</i>	ubiquitin-protein ligase	YIL138c	<i>TPM2</i>	tropomyosin 2
YIL129c	<i>TRK1</i>	high-affinity potassium transport protein	YDL029w	<i>ACT2</i>	uracil permease	YPL045w	<i>VPS16</i>	vacuolar sorting protein
YBR294w	<i>SUL1</i>	high-affinity sulphate transport protein	YDR106w	<i>ARP10</i>	actin-related protein	YLR337w	<i>VRP1</i>	verprolin
YLO020w	<i>SCM2</i>	high-affinity tryptophan transport protein	YNL059c	<i>ARP5</i>	actin-related protein			
YGR191w	<i>HIP1</i>	histidine permease	YLR085c	<i>ARP6</i>	actin-related protein			
YBR140c	<i>IRA1</i>	inhibitory regulator protein of the RAS-cyclic AMP pathway	YOR141c	<i>ARP8</i>	actin-related protein			
YNL291c	<i>MID1</i>	involved in Ca $^{2+}$ influx during mating	YNR033w	<i>ARP9</i>	actin-related protein			
YHL019c	<i>APM2</i>	involved in clathrin-dependent transport processes	YLN138w	<i>SRV2</i>	adenylyl cyclase-associated protein, 70K			
YLR452c	<i>SST2</i>	involved in desensitization to α -factor pheromone	YAL020c	<i>ATS1</i>	α -tubulin suppressor	YLR450w	<i>HMG2</i>	3-hydroxy-3-methylglutaryl-CoA reductase
YCL051w	<i>LRE1</i>	involved in laminarinase resistance	YER016w	<i>BIM1</i>	binding to microtubules	YJR131w	<i>MNS1</i>	α -D-mannosidase
YER118c	<i>SSU81</i>	involved in the <i>HOG1</i> high-osmolarity signal transduction pathway	YFL037w	<i>TUB2</i>	β -tubulin	YDR483w	<i>KRE2</i>	α -D-mannosyltransferase
YMR183c	<i>SSO2</i>	involved in vesicle transport from Golgi to plasma membrane	YOR265w	<i>RBL2</i>	β -tubulin binding protein	YER001w	<i>MNN1</i>	α -D-mannosyltransferase
YLR155c	<i>ASP3A</i>	L-asparaginase II	YBR200w	<i>BEM1</i>	bud emergence mediator	YGL038c	<i>OCH1</i>	α -D-mannosyltransferase
YLR157c	<i>ASP3B</i>	L-asparaginase II	YLR319c	<i>BUD6</i>	bud site selection protein	YGL027c	<i>CWH41</i>	β -D-glucan assembly protein
YLR158c	<i>ASP3C</i>	L-asparaginase II	YNL271c	<i>BNI1</i>	budding protein	YBR110w	<i>ALG1</i>	β -mannosyltransferase
YLR160c	<i>ASP3D</i>	L-asparaginase II	YBR109c	<i>CMD1</i>	calmodulin	YMR015c	<i>ERG5</i>	C-22 sterol desaturase
YMR319c	<i>FEI74</i>	low-affinity Fe(II) iron transport protein	YLR175w	<i>CBF5</i>	centromere/microtubule binding protein	YGR060w	<i>ERG25</i>	C-4 sterol methyl oxidase
YOL156w	<i>HXT11</i>	low-affinity glucose transporter	YOR349w	<i>CIN1</i>	chromosome segregation protein	YLR056w	<i>ERG3</i>	C-5 sterol desaturase
YHR094c	<i>HXT1</i>	low-affinity hexose transporter	YLL050c	<i>COF1</i>	cofilin, actin binding and severing protein	YMR202w	<i>ERG2</i>	C-8 sterol isomerase
YDR345c	<i>HXT3</i>	low-affinity hexose transporter	YBL007c	<i>SLA1</i>	cytoskeleton assembly control protein	YGL167c	<i>PMR1</i>	Ca $^{2+}$ -transporting P-type ATPase
YNL268w	<i>LYP1</i>	lysine-specific high-affinity permease	YNL243w	<i>SLA2</i>	cytoskeleton assembly control protein	YBR036c	<i>CSG2</i>	calcium dependent regulatory protein
YDR497c	<i>ITR1</i>	major myo-inositol permease	YLL001w	<i>DNM1</i>	dynamin-related protein	YGL203c	<i>KEX1</i>	carboxypeptidase (YSC- α)
YBR298c	<i>MAL31</i>	maltose permease	YKR054c	<i>DYN1</i>	dynein heavy chain, cytosolic	YPR113w	<i>PIS1</i>	CDP-diacylglycerol-inositol
YOL122c	<i>SMF1</i>	manganese transporter	YDR454c	<i>YER312c</i>	dynein light chain 1, cytosolic	YER026c	<i>CHO1</i>	3-phosphatidyltransferase
YIL047c	<i>SYG1</i>	member of the major facilitator superfamily	YKL007w	<i>CAP1</i>	F-actin capping protein, α subunit	YBR029c	<i>CDS1</i>	CDP-diacylglycerol-serine
YKR050w	<i>TRK2</i>	moderate-affinity potassium transport protein	YIL034c	<i>CAP2</i>	F-actin capping protein, β subunit	YKL073w	<i>LHS1</i>	O-phosphatidyltransferase
			YLR212c	<i>TUB4</i>	γ -tubulin	YGR202c	<i>PCT1</i>	CDP-diacylglycerol synthase
						YOL062c	<i>APM4</i>	CDP-diacylglycerol synthase
						YPL259c	<i>APM1</i>	clathrin-associated protein

YDL195w	<i>SEC31</i>	component of the COPII coat of ER-Golgi vesicles	YDR245w	<i>MNN10</i>	similarity to <i>S. pombe</i> galactosyltransferase	YGR274c	<i>TAF145</i>	TFIID subunit (TBP-associated factor), 145K
YGL200c	<i>EMP24</i>	component of the COPII-coated vesicles, 24K	YMR214w	<i>SCJ1</i>	similarity to to <i>E. coli</i> dnaJ	YGR187c	<i>HGH1</i>	weak similarity to human Hmg1p and Hmg2p
YML012w	<i>ERV25</i>	component of the COPII-coated vesicles, 25K	YHR123w	<i>EPT1</i>	sn-1,2-diacylglycerol ethanolamine- and cholinophosphotransferase	YGR285c	<i>ZUO1</i>	zutoin (Z-DNA binding protein)
YHR007c	<i>ERG11</i>	cytochrome P450 lanosterol 14α-demethylase	YKL006c-a	<i>SFT1</i>	SNARE-like protein	mitochondrial organization and biogenesis		
YNL130c	<i>CPT1</i>	diacylglycerol cholinophosphotransferase	YGR175c	<i>ERG1</i>	squalene monooxygenase	YHR037w	<i>PUT2</i>	1-pyrroline-5-carboxylate dehydrogenase
YMR013c	<i>SEC59</i>	dolichol kinase	YGL055w	<i>OLE1</i>	stearoyl-CoA desaturase	YNL104c	<i>LEU4</i>	2-isopropylmalate synthase
YPL227c	<i>ALG5</i>	dolichol-P-glucose synthetase	YLR080w		strong similarity to Emp47p	YMR282c	<i>AEP2</i>	2'-O-ribosyl phosphate transferase
YPR183w	<i>DPM1</i>	dolichol-phosphate	YER087c-a	<i>SEB1</i>	strong similarity to mammalian Sec61β subunit	YIL125w	<i>KGD1</i>	2-oxoglutarate dehydrogenase complex E1 component
YJR143c	<i>PMT4</i>	β-D-mannosyltransferase	YOR099w	<i>KTR1</i>	strong similarity to mannosyltransferases	YDR148c	<i>KGD2</i>	2-oxoglutarate dehydrogenase complex E2 component
		dolichyl-phosphate-mannose-protein O-mannosyl transferase	YGL226c-a	<i>OST75</i>	subunit of N-oligosaccharyltransferase, ζ subunit	YOL096c	<i>COQ3</i>	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase
YDL212w	<i>SHR3</i>	endoplasmic reticulum membrane protein	YDR297w	<i>SUR2</i>	suppressor of <i>rvs161</i> and <i>rvs167</i> mutations	YMR287c	<i>MSU1</i>	3'-5' exonuclease for RNA 3' ss-tail, mitochondrial
YNL238w	<i>KEX2</i>	endoprotease of late Golgi compartment	YBL102w	<i>SFT2</i>	suppressor of <i>sed5</i> ts mutants	YDR232w	<i>HEM1</i>	5-aminolevulinic synthase
YBL040c	<i>ERD2</i>	ER lumen protein-retaining receptor	YLR026c	<i>SED5</i>	syntaxin (T-SNARE) of the ER type IV dipeptidyl aminopeptidase	YML009c	<i>MRPL39</i>	60S ribosomal protein, mitochondrial
YLR378c	<i>SEC61</i>	ER protein-translocation complex subunit	YOR075w	<i>UFE1</i>	ubiquitin-conjugating enzyme	YMR108w	<i>ILV2</i>	acetolactate synthase
YPL094c	<i>SEC62</i>	ER protein-translocation complex subunit	YOR219c	<i>STE13</i>	ubiquitin-conjugating enzyme	YLC009c	<i>ILV6</i>	acetolactate synthase, regulatory subunit
YOR254c	<i>SEC63</i>	ER protein-translocation complex subunit	YER100w	<i>UBC6</i>	UDP-N-acetylglucosamine-1-phosphate transferase	YAL054c	<i>ACS1</i>	acetyl-CoA synthetase
YBR171w		ER protein-translocation complex subunit	YBR243c	<i>ALG7</i>	vacuolar ATPase assembly integral membrane protein	YER069w	<i>ARG56</i>	acetylglutamate kinase and acetylglutamyl-phosphate reductase
YLR292c	<i>SEC72</i>	ER protein-translocation complex subunit	YGR105w	<i>VMA21</i>	vacuolar protein sorting/targeting protein vanadate-resistance protein	YOL140w	<i>ARG8</i>	acetylornithine aminotransferase
YDR086c	<i>SSS1</i>	ER protein-translocation complex subunit	YBL017c	<i>PEP1</i>		YLR304c	<i>ACO1</i>	aconitate hydratase
YDR331w	<i>GP18</i>	essential for GPI-anchor attachment	YGL225w	<i>GOG5</i>		YDR234w	<i>LYS4</i>	aconitate hydratase
YHR190w	<i>ERG9</i>	farnesyl-diphosphate farnesyltransferase				YER170w	<i>ADK2</i>	adenylate kinase, mitochondrial
YDR519w	<i>FKB2</i>	FK506/rapamycin-binding protein of the ER				YMR056c	<i>AAC1</i>	ADP/ATP carrier protein (MCF)
YJR031c	<i>GEA1</i>	GDP/GTP exchange factor for ARF				YBL030c	<i>AAC2</i>	ADP/ATP carrier protein (MCF)
YEL022w	<i>GEA2</i>	GDP/GTP exchange factor for ARF				YBR085w	<i>AAC3</i>	ADP/ATP carrier protein (MCF)
YNR026i	<i>SEC12</i>	GDP/GTP exchange factor for Sar1p				YMR083w	<i>ADH3</i>	alcohol dehydrogenase III
YPR159w	<i>KRE6</i>	glucan synthase subunit				YER073w		aldehyde dehydrogenase (NAD ⁺)
YGR143w	<i>SKN1</i>	glucan synthase subunit				YMR170c	<i>ALD5</i>	aldehyde dehydrogenase 2 (NAD ⁺), mitochondrial
YOR067c	<i>ALG8</i>	glycosyltransferase				YER086w	<i>ILV1</i>	anabolic serine and threonine dehydratase
YFL048c	<i>EMP47</i>	Golgi membrane protein				YJL209w	<i>CBP1</i>	apo-cytochrome b pre-mRNA processing protein
YDL192w	<i>ARF1</i>	GTP-binding protein of the ARF family				YBR120c	<i>CBP6</i>	apo-cytochrome b pre-mRNA processing protein
YPL218w	<i>SAR1</i>	GTP-binding protein of the ARF family				YHL038c	<i>CBP2</i>	apo-cytochrome b pre-mRNA processing protein 2
YFL038c	<i>YPT1</i>	GTP-binding protein of the RAB family				YHR091c	<i>MSR1</i>	arginyl-tRNA synthetase, mitochondrial
YLR262c	<i>YPT6</i>	GTP-binding protein of the RAB family				YCR024c		asn-tRNA synthetase, mitochondrial
YPR165w	<i>RHO1</i>	GTP-binding protein of the RHO subfamily of RAS-like proteins				YKL106w	<i>AA1</i>	aspartate transaminase, mitochondrial
YNL090w	<i>RHO2</i>	GTP-binding protein of the RHO subfamily of RAS-like proteins				YPL104w	<i>MSD1</i>	aspartate-tRNA ligase, mitochondrial
YEL042w	<i>GDA1</i>	guanosine diphosphatase				YGR008c	<i>STF2</i>	ATPase stabilizing factor
YDR189w	<i>SLY1</i>	hydrophilic suppressor of <i>ypt1</i> and member of the Sec1p family				YDL130w-a	<i>STF1</i>	ATPase stabilizing factor, 10K
YCR075c	<i>ERS1</i>	intracellular protein transport protein				YDR377w	<i>ATP17</i>	ATPase synthase subunit f
YDL058w	<i>USO1</i>	intracellular protein transport protein				YMR301c	<i>ATM1</i>	ATP-binding cassette transporter protein, mitochondrial
YLR220w	<i>CCCI</i>	involved in calcium regulation				YBL022c	<i>PIM1</i>	ATP-dependent protease, mitochondrial
YBR201w	<i>DER1</i>	involved in degradation proteins in the ER				YPL029w	<i>SUV3</i>	ATP-dependent RNA helicase, mitochondrial
YOR069w	<i>VPS5</i>	involved in Golgi retention and vacuolar sorting				YER061c	<i>CEM1</i>	B-keto-acyl-ACP synthase
YOR336w	<i>KRE5</i>	killer toxin-resistance protein				YHR208w	<i>TWT1</i>	branched chain amino-acid aminotransferase, mitochondrial
YHR072w	<i>ERG7</i>	lanosterol synthase				YBR084w	<i>MIS1</i>	C1-tetrahydrofolate synthase, mitochondrial
YKR061w	<i>KTR2</i>	mannosyltransferase				YML042w	<i>CAT2</i>	carnitine O-acetyltransferase
YDL095w	<i>PMT1</i>	mannosyltransferase				YER026c	<i>CH01</i>	CDP-diacylglycerol serine O-phosphatidyltransferase
YAL023c	<i>PMT2</i>	mannosyltransferase				YNR001c	<i>CIT1</i>	citrate (si)-synthase, mitochondrial
YOR321w	<i>PMT3</i>	mannosyltransferase				YPR001w	<i>CIT3</i>	citrate (si)-synthase, mitochondrial
YBL082c	<i>RHK1</i>	mannosyltransferase				YBR291c	<i>CTP1</i>	citrate transport protein, mitochondrial (MCF)
YJL139c	<i>YUR1</i>	mannosyltransferase				YOR316c	<i>COT1</i>	cobalt accumulation protein
YKR001c	<i>VPS1</i>	member of the dynamin family of GTPases				YOR017w	<i>PET127</i>	component of mitochondrial translation system
YJR073c	<i>OP13</i>	methylene-fatty-acyl-phospholipid synthase				YPR155c	<i>NCA2</i>	control of mitochondrial synthesis of Atp6p and Atp8p
YNL064c	<i>YDJ1</i>	mitochondrial and ER import protein				YKL011c	<i>CCE1</i>	cruciform-cutting endonuclease, mitochondrial
YPL085w	<i>SEC16</i>	multidomain vesicle coat protein				YML078w	<i>CPR3</i>	cyclophilin (peptidylprolyl isomerase), mitochondrial
YHR042w	<i>NCP1</i>	NADPH-cytochrome P450 reductase				YDR197w	<i>CBS2</i>	cytochrome b translational activator protein
YFL025c	<i>BST1</i>	negative regulator of COPII vesicle formation				YIL043c	<i>CBR1</i>	cytochrome b5 reductase
YJL034w	<i>KAR2</i>	nuclear fusion protein				YKL150w	<i>MCR1</i>	cytochrome b5 reductase
YJL002c	<i>OST1</i>	oligosaccharyltransferase α subunit				YKL141w	<i>SDH3</i>	cytochrome b560 subunit of respiratory complex II
YEL002c	<i>WBP1</i>	oligosaccharyltransferase β subunit				YJR048w	<i>CYC1</i>	cytochrome c isoform 1
YMR149w	<i>SWP1</i>	oligosaccharyltransferase δ subunit				YEL039c	<i>CYC7</i>	cytochrome c isoform 2
YOR103c	<i>OST2</i>	oligosaccharyltransferase ε subunit				YOR037w	<i>CYC2</i>	cytochrome c mitochondrial import factor
YOR085w	<i>OST3</i>	oligosaccharyltransferase γ subunit				YER058w	<i>PET117</i>	cytochrome c oxidase assembly factor
YGL022w	<i>ST73</i>	oligosaccharyltransferase subunit				YPL132w	<i>COX11</i>	cytochrome c oxidase assembly protein
YHR057c	<i>CYP2</i>	peptidyl-prolyl cis-trans isomerase				YML129c	<i>COX14</i>	cytochrome c oxidase assembly protein
YCR069w	<i>SCC3</i>	peptidyl-prolyl cis-trans isomerase				YDR079w	<i>PET100</i>	cytochrome c oxidase assembly protein
YDR304c	<i>CYP5</i>	peptidyl-prolyl cis-trans isomerase D (cyclophilin D) of the ER				YGL187c	<i>COX4</i>	cytochrome c oxidase subunit IV
YGR157w	<i>CHO2</i>	phosphatidylethanolamine N-methyltransferase				YLN052w	<i>COX5A</i>	cytochrome c oxidase subunit V A
YGR170w	<i>PSD2</i>	protein disulfide decarboxylase 2				YIL11w	<i>COX5B</i>	cytochrome c oxidase subunit V b
YDR518w	<i>EUG1</i>	protein disulfide-isomerase				YHR051w	<i>COX6</i>	cytochrome c oxidase subunit VI
YCL043c	<i>PDI1</i>	protein disulfide-isomerase				YGL191w	<i>COX13</i>	cytochrome c oxidase subunit VIa
YHR079c	<i>IRE1</i>	protein kinase				YLR038c	<i>COX12</i>	cytochrome c oxidase subunit VII B
YEL036c	<i>ANP1</i>	protein of the endoplasmatic reticulum				YMR256c	<i>COX7</i>	cytochrome c oxidase subunit VII C
YCR067c	<i>SEDA4</i>	protein of the endoplasmic reticulum				YDL067c	<i>COX9</i>	cytochrome c oxidase subunit VIIIA
YIL004c	<i>BET11</i>	protein transport protein				YLR395c	<i>COX8</i>	cytochrome c oxidase subunit VIIIA
YDR040c	<i>ENA1</i>	P-type ATPase involved in Na ⁺ and Li ⁺ efflux				YKR066c	<i>COP1</i>	cytochrome c peroxidase
YKL212w	<i>SAC1</i>	recessive suppressor of secretory defect				YOR065w	<i>CYT1</i>	cytochrome c1
YLR088w	<i>GAA1</i>	required for attachment of GPI anchor onto proteins				YER141w	<i>COX15</i>	cytochrome oxidase assembly factor
YPL050c	<i>MNN9</i>	required for complex N-glycosylation				YER154w	<i>OXA1</i>	cytochrome oxidase biogenesis protein
YCL001w	<i>RER1</i>	required for correct localization of Sec12p				YOR386w	<i>PHR1</i>	cytochrome oxidase photo-lyase
YGL145w	<i>TIP20</i>	required for ER to Golgi transport				YLR348c		dicarboxylate carrier protein
YDR414c	<i>ERD1</i>	required for retention of luminal ER proteins				YFL018c	<i>LPD1</i>	dihydrolipoamide dehydrogenase
YMR004w	<i>MVP1</i>	required for vacuolar protein sorting				YNL071w	<i>LAT1</i>	dihydrolipoamide S-acetyltransferase
YDR498c	<i>SEC20</i>	secretory pathway protein						
YIR010c-a	<i>SPC1</i>	signal peptidase 10.8K subunit						
YML055w	<i>SPC2</i>	signal peptidase 18K subunit						
YDR292c	<i>SRP101</i>	signal recognition particle receptor, α subunit						
YIR022w	<i>SEC11</i>	signal sequence processing protein						
YAL058w	<i>CNE1</i>	similarity to calnexin						

YJR016c	<i>ILV3</i>	dihydroxy-acid dehydratase	YNL131w	<i>TOM22</i>	mitochondrial outer membrane import receptor subunit	YBL038w	<i>MRPL16</i>	ribosomal protein, mitochondrial
YDL174c	<i>DLD1</i>	D-lactate ferricytochrome c oxidoreductase (D-LCR)	YGR082w	<i>TOM20</i>	mitochondrial outer membrane import receptor subunit, 20K	YMR193w	<i>MRPL24</i>	ribosomal protein, mitochondrial
YML061c	<i>PIF1</i>	DNA helicase involved in mitochondrial DNA repair and telomere length	YMR060c	<i>TOM37</i>	mitochondrial outer membrane import receptor subunit, 37K	YMR024w	<i>MRPL3</i>	ribosomal protein, mitochondrial
YHR120w	<i>MSH1</i>	DNA mismatch repair protein, mitochondrial	YMR203w	<i>TOM40</i>	mitochondrial outer membrane import receptor subunit, 40K	YMR286w	<i>MRPL33</i>	ribosomal protein, mitochondrial
YOR330c	<i>MIP1</i>	DNA-directed DNA polymerase γ , catalytic subunit, mitochondrial	YOR045w	<i>TOM6</i>	mitochondrial outer membrane import receptor subunit, 6K	YLR439w	<i>MRPL4</i>	ribosomal protein, mitochondrial
YFL036w	<i>RPO41</i>	DNA-directed RNA polymerase, mitochondrial	YNL070w	<i>TOM7</i>	mitochondrial outer membrane import receptor subunit, 7K	YHR147c	<i>MRPL6</i>	ribosomal protein, mitochondrial
YBR252w	<i>DUT1</i>	dUTP pyrophosphatase, mitochondrial	YNL055c	<i>POR1</i>	mitochondrial outer membrane porin	YGR220c	<i>MRPL9</i>	ribosomal protein, mitochondrial
YOR211c	<i>MGM1</i>	dynamin-like protein	YNL121c	<i>TOM70</i>	mitochondrial outer membrane specialized import receptor	YDR337w	<i>MRPS28</i>	ribosomal protein, mitochondrial
YGR207c	<i>ETF-β</i>	electron-transferring flavoprotein, β subunit	YGL143c	<i>MRF1</i>	mitochondrial peptide chain release factor	YNL137c	<i>NAM9</i>	ribosomal protein, mitochondrial
YLR393w	<i>ATP10</i>	F1FO-ATPase complex assembly protein	YLR163c	<i>MAS1</i>	mitochondrial processing peptidase	YOR158w	<i>PET123</i>	ribosomal protein, mitochondrial
YNL315c	<i>ATP11</i>	F1FO-ATPase complex assembly protein	YHR024c	<i>MAS2</i>	mitochondrial processing peptidase, catalytic 53K (α) subunit	YCR046c	<i>PETCR46</i>	ribosomal protein, mitochondrial
YJL180c	<i>ATP12</i>	F1FO-ATPase complex assembly protein	YMR150c	<i>IMP1</i>	mitochondrial protease	YFR049w	<i>YMR31</i>	ribosomal protein, mitochondrial
YKL016c	<i>ATP7</i>	F1FO-ATPase complex, F0 D subunit	YDR375c	<i>BCS1</i>	mitochondrial protein of the CDC48/PAS1/SEC18 (AAA) family of ATPases	YDR194c	<i>MSS116</i>	RNA helicase of the DEAD box family, mitochondrial
YBL099w	<i>ATP1</i>	F1FO-ATPase complex, F1 α subunit	YDR120c	<i>TRM1</i>	N2,N2-dimethylguanine tRNA methyltransferase	YMR228w	<i>MTF1</i>	RNA polymerase specific factor, mitochondrial
YJR121w	<i>ATP2</i>	F1FO-ATPase complex, F1 β subunit	YML120c	<i>NDI1</i>	NADH-ubiquinone-6 oxidoreductase	YOR334w	<i>MRS2</i>	RNA splicing protein and member of the mitochondrial carrier family (MCF)
YDL004w	<i>ATP16</i>	F1FO-ATPase complex, F1 δ subunit	YOR355w	<i>GDS1</i>	name9-1' suppressor	YJL133w	<i>MRS3</i>	RNA splicing protein and member of the mitochondrial carrier family (MCF)
YPL078c	<i>ATP4</i>	F1FO-ATPase complex, F1 ϵ subunit	YJL208c	<i>NUC1</i>	nuclease, mitochondrial	YKR052c	<i>MRS4</i>	RNA splicing protein and member of the mitochondrial carrier family (MCF)
YPL271w	<i>ATP15</i>	F1FO-ATPase complex, F1 γ subunit	YAR035w	<i>YAT1</i>	outer carnitine acetyltransferase, mitochondrial	YOR201c	<i>PET56</i>	rRNA (guanosine-2'-O)-methyltransferase
YBR039w	<i>ATP3</i>	F1FO-ATPase complex, F1 γ subunit	YNR041c	<i>COQ2</i>	para-hydroxybenzoate-polypropylene transferase	YBR263w	<i>SHM1</i>	serine hydroxymethyltransferase, mitochondrial
YDR298c	<i>ATP5</i>	F1FO-ATPase complex, OSCP subunit	YPR047w	<i>MSF1</i>	phenylalanine-tRNA ligase α subunit, mitochondrial	YPR037c		similarity to Erv1p and rat ALR protein
YLR295c	<i>ATP14</i>	F1FO-ATPase complex, subunit h	YJR077c	<i>MIR1</i>	phosphate transport protein, mitochondrial (MCF)	YDR376w	<i>ARH1</i>	similarity to human adrenodoxin reductase
YIL134w	<i>FLX1</i>	FAD carrier protein, mitochondrial (MCF)	YNL169c	<i>PSD1</i>	phosphatidylserine decarboxylase 1 possibly involved in translational activation of COX1 and COB mRNA	YBL013w		similarity to methionyl-tRNA formyltransferase
YPL172c	<i>COX10</i>	farnesyl transferase	YLR203c	<i>MSS51</i>	probable ribosomal protein L12	YJR113c		similarity to mitochondrial ribosomal protein S7
YOR176w	<i>HEM15</i>	ferrochelatase	YGL068w	(MSF1)	probably involved in intramitochondrial protein sorting	YKL120w	<i>PMT</i>	similarity to mitochondrial uncoupling protein (MCF)
YPL262w	<i>FUM1</i>	fumarate hydratase	YLR168c	(MSF1)	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)	YMR244w		similarity to NCA3 and SUN4 protein
YOL033w	<i>MSE1</i>	glutamyl-tRNA synthetase, mitochondrial	YLR142w	<i>PUT1</i>	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)	YOR150w		similarity to ribosomal protein L13
YOL059w	<i>GPD3</i>	glycerol-3-phosphate dehydrogenase (NAD $^+$), mitochondrial	YER017c	<i>AFG3</i>	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)	YPR134w	<i>MSS18</i>	splicing protein
YIL155c	<i>GUT2</i>	glycerol-3-phosphate dehydrogenase, mitochondrial	YPR024w	<i>YME1</i>	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)	YGR222w	<i>PET54</i>	splicing protein and translational activator, mitochondrial
YMR189w	<i>GSD2</i>	glycine decarboxylase subunit	YMR089c	<i>YTA12</i>	protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)	YCR028c-a	<i>RIM1</i>	ss-DNA-binding protein, mitochondrial
YDL019c	<i>GCV1</i>	glycine decarboxylase T subunit	YDL044c	<i>MTF2</i>	protein involved in mRNA splicing and protein synthesis, mitochondrial	YKL192c		strong similarity to acyl-carrier proteins
YFL016c	<i>MDJ1</i>	heat-shock protein - chaperone	YIL136w	<i>OM45</i>	protein of the outer mitochondrial membrane	YBR024w	<i>SCO2</i>	strong similarity to Sco1p
YOR232w	<i>MGE1</i>	heat-shock protein - chaperone	YAL011w	<i>FUN36</i>	protein of unknown function	YHR117w	<i>Tom70p/Mas70p</i>	strong similarity to Tom70p/Mas70p
YLR259c	<i>HSP60</i>	heat-shock protein - chaperone, mitochondrial	YJL023c	<i>PET130</i>	protein synthesis protein, mitochondrial	YKL148c	<i>SDH1</i>	succinate dehydrogenase flavoprotein
YJR045c	<i>SSC1</i>	heat-shock protein 70-related protein, mitochondrial	YER014w	<i>HEM14</i>	protoporphyrinogen oxidase, mitochondrial	YLL041c	<i>SDH2</i>	succinate dehydrogenase iron-sulphur protein subunit
YDR258c	<i>HSP78</i>	heat-shock protein of clp family of ATP-dependent proteases, mitochondrial	YER178w	<i>PDA1</i>	pyruvate dehydrogenase (lipoamide) α subunit	YDR178w	<i>SDH4</i>	succinate dehydrogenase membrane
YBR003w	<i>COQ1</i>	hexenaphenyl pyrophosphate synthetase	YBR221c	<i>PDB1</i>	pyruvate dehydrogenase (lipoamide) β subunit	YHR008c	<i>SOD2</i>	anchor subunit for Sdh2p
YMR072w	<i>ABF2</i>	high mobility group protein	YGR193c	<i>PDX1</i>	pyruvate dehydrogenase complex protein X	YHR050w	<i>SMF2</i>	superoxide dismutase (Mn), mitochondrial
YAL039c	<i>CYC3</i>	holocytochrome c synthase (cytochrome c haem lyase)	YER095w	<i>ACR1</i>	regulator of acetyl-CoA synthetase activity	YKL194c	<i>MST1</i>	succinate dehydrogenase iron-sulphur protein subunit
YKL087c	<i>CYT2</i>	holocytochrome c1 synthase	YBR091c	<i>MRS5</i>	regulator of mitochondrial intron splicing	YLR069c	<i>MEF1</i>	threonine-tRNA ligase, mitochondrial
YMR038c	<i>LYS7</i>	homocitrate dehydrogenase	YPL215w	<i>CBP3</i>	required for assembly of cytochrome bc1 complex	YER153c	<i>PET122</i>	translation elongation factor G, mitochondrial
YDL181w	<i>INH1</i>	inhibitor of mitochondrial ATPase	YEL059c-a	<i>SOM1</i>	required for mitochondrial Imp1 peptidase function	YPR097w	<i>MSY1</i>	translation initiation factor 2, mitochondrial
YMR267w	<i>PPA2</i>	inorganic pyrophosphatase, mitochondrial	YLL006w	<i>MMM1</i>	required for mitochondrial shape and structure	YOL023w	<i>IFM1</i>	translational activator of cob mRNA
YLL009c	<i>COX17</i>	interacts genetically with <i>SCO1</i> and <i>SCO2</i> in cytochrome oxidase assembly	YKL093w	<i>MBR1</i>	required for optimal growth on glycerol	YDL069c	<i>CBS1</i>	translational activator of cytochrome c oxidase subunit III
YGR028w	<i>MSP1</i>	intra-mitochondrial sorting protein	YLR067c	<i>PET309</i>	required for stability and translation of COX1 mRNA	YER153c	<i>PET122</i>	translational activator, mitochondrial
YJR034w	<i>PET191</i>	involved in assembly of cytochrome oxidase	YEL059c-a	<i>SOM1</i>	required for translation of COX2 mRNA	YPR045w	<i>PET494</i>	tRNA isopentenyltransferase
YMR302c	<i>PRP12</i>	involved in early maturation of pre-rRNA	YER178w	<i>PDA1</i>	required to maintain RHO $^+$ mitochondrial DNA	YOR274w	<i>MOD5</i>	tRNA nucleotidyltransferase
YOL009c	<i>MDM12</i>	involved in mitochondrial inheritance	YBR221c	<i>PDB1</i>	regulator of acetyl-CoA synthetase activity	YER168c	<i>CCA1</i>	tryptophanyl-tRNA synthetase
YAL010c	<i>MDM10</i>	involved in mitochondrial morphology and inheritance	YGR193c	<i>PDX1</i>	regulator of mitochondrial intron splicing	YDR268w	<i>MSW1</i>	ubiquinol-cytochrome c reductase 17K protein
YIR021w	<i>MRS1</i>	involved in mitochondrial RNA splicing of COB mRNA	YER095w	<i>ACR1</i>	required for assembly of cytochrome bc1 complex	YPR191w	<i>QCR2</i>	ubiquinol-cytochrome c reductase 40K subunit II
YBR037c	<i>SCO1</i>	involved in stabilization of Cox1p and Cox2p	YBR091c	<i>MRS5</i>	required for assembly of cytochrome bc1 complex	YBL045c	<i>COR1</i>	ubiquinol-cytochrome c reductase 44K core protein
YNL066w	<i>SUN4</i>	involved in the aging process	YPL215w	<i>CBP3</i>	required for mitochondrial shape and structure	YHR001w-a	<i>QCR10</i>	ubiquinol-cytochrome c reductase 8.5K subunit
YCL017c	<i>NFS1</i>	involved in tRNA processing and mitochondrial metabolism	YER095w	<i>ACR1</i>	required for optimal growth on glycerol	YGR174c	<i>CBP4</i>	ubiquinol-cytochrome c reductase assembly factor
YNL037c	<i>IDH1</i>	isocitrate dehydrogenase (NAD $^+$) subunit 1, mitochondrial	YBR091c	<i>MRS5</i>	required for stability and translation of COX1 mRNA	YGL119w	<i>ABC1</i>	ubiquinol-cytochrome c reductase complex assembly protein
YOR136w	<i>IDH2</i>	isocitrate dehydrogenase (NAD $^+$) subunit 2, mitochondrial	YPL215w	<i>CBP3</i>	required for translation of COX2 mRNA	YEL024w	<i>RIP1</i>	ubiquinol-cytochrome c reductase iron-sulphur protein
YDL066w	<i>IDP1</i>	isocitrate dehydrogenase (NADP $^+$), mitochondrial	YER095w	<i>PET111</i>	required to maintain RHO $^+$ mitochondrial DNA	YDR529c	<i>QCR7</i>	ubiquinol-cytochrome c reductase subunit 7
YPL040c	<i>ISM1</i>	isoleucine-tRNA ligase, mitochondrial	YBR185c	<i>MBA1</i>	respiratory chain assembly protein	YGR183c	<i>QCR9</i>	ubiquinol-cytochrome c reductase subunit 9
YLR355c	<i>ILV6</i>	ketol-acid reducto-isomerase	YML091c	<i>RP2</i>	ribonuclease P, mitochondrial	YJL166w	<i>QCR8</i>	ubiquinol-cytochrome c reductase subunit VIII
YML054c	<i>YMC1</i>	lactate dehydrogenase cytochrome b2	YKL170w	<i>MRPL38</i>	ribosomal protein L14, mitochondrial	YML021c	<i>UNG1</i>	uracil-DNA glycosylase
YLR382c	<i>NAM2</i>	leucine-tRNA ligase, mitochondrial	YJL063c	<i>MRPL8</i>	ribosomal protein L17, mitochondrial	YGR094w	<i>VAS1</i>	valyl-tRNA synthetase
YOR196c	<i>LIP5</i>	lipoyl acid synthase	YPR166c	<i>MRP2</i>	ribosomal protein S14	YIL114c	<i>POR2</i>	voltage-dependent anion channel (YVDAC2)
YNL073w	<i>MSK1</i>	lysyl-tRNA synthetase, mitochondrial	YPL013c	<i>MRP2</i>	ribosomal protein S16, mitochondrial	YNL237w	<i>YTP1</i>	weak similarity to mitochondrial electron transport proteins
YKL085w	<i>MDH1</i>	malate dehydrogenase, mitochondrial	YBR251w	<i>MRP55</i>	ribosomal protein S5, mitochondrial			
YOR130c	<i>ARG11</i>	member of the mitochondrial carrier family (MCF)	YPR146w	<i>MRP9</i>	ribosomal protein S9, mitochondrial			
YDL198c	<i>YHM1</i>	member of the mitochondrial carrier family (MCF)	YKR006c	<i>MRPL13</i>	ribosomal protein Yml13, mitochondrial			
YGR171c	<i>MSM1</i>	methionyl-tRNA synthetase	YNL005c	<i>MRPL2</i>	ribosomal protein Yml2, mitochondrial			
YGR029w	<i>ERV1</i>	mitochondrial biogenesis and regulation of cell cycle	YKR085c	<i>MRPL20</i>	ribosomal protein Yml20, mitochondrial			
YBR192w	<i>RIM2</i>	mitochondrial carrier protein (MCF)	YBR282w	<i>MRPL27</i>	ribosomal protein Yml27, mitochondrial			
YPR058w	<i>YMC1</i>	mitochondrial carrier protein (MCF)	YDR462w	<i>MRPL37</i>	ribosomal protein Yml28, mitochondrial			
YBR104w	<i>YMC2</i>	mitochondrial carrier protein (MCF)	YNL252c	<i>MRPL25</i>	ribosomal protein Yml30, mitochondrial			
YOR202c	<i>HSP10</i>	mitochondrial chaperonin	YKL138c	<i>MRPL31</i>	ribosomal protein Yml31, mitochondrial			
YJR144w	<i>MGM101</i>	mitochondrial genome maintenance protein	YCR003w	<i>MRPL32</i>	ribosomal protein Yml32, mitochondrial			
YMR023c	<i>MSS1</i>	mitochondrial GTPase involved in expression of COX1	YBR122c	<i>MRPL36</i>	ribosomal protein Yml36, mitochondrial			
YNR017w	<i>MAS6</i>	mitochondrial inner membrane import translocase subunit	YBR268w	<i>MRPL37</i>	ribosomal protein Yml37, mitochondrial			
YJL143w	<i>TIM17</i>	mitochondrial inner membrane import translocase subunit	YPL173w	<i>MRPL25</i>	ribosomal protein Yml40, mitochondrial			
YIL022w	<i>TIM44</i>	mitochondrial inner membrane import translocase subunit	YGR076c	<i>MRPL25</i>	ribosomal protein Yml426 (YML25), mitochondrial			
YMR035w	<i>IMP2</i>	mitochondrial inner membrane protease subunit	YMR225c	<i>MRPL44</i>	ribosomal protein Ymr44, mitochondrial			
YKL134c	(<i>MIP1</i>)	mitochondrial intermediate peptidase	YML025c	<i>MRPL44</i>	ribosomal protein, mitochondrial			
			YGR347w	<i>MRP1</i>	ribosomal protein, mitochondrial			
			YGR084c	<i>MRP13</i>	ribosomal protein, mitochondrial			
			YKL003c	<i>MRP17</i>	ribosomal protein, mitochondrial			
			YDR405w	<i>MRP20</i>	ribosomal protein, mitochondrial			
			YHL028w	<i>MRP4</i>	ribosomal protein, mitochondrial			
			YKL167c	<i>MRP49</i>	ribosomal protein, mitochondrial			
			YKL142w	<i>MRP8</i>	ribosomal protein, mitochondrial			
			YLR312w-a	<i>MRPL15</i>	ribosomal protein, mitochondrial			

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YIL160c	<i>POT1</i>	acetyl-CoA C-acyltransferase, peroxisomal
YAL054c	<i>AC51</i>	acetyl-CoA synthetase
YGL205w	<i>POX1</i>	acyl-CoA oxidase
YBR222c	<i>PCS60</i>	AMP-binding protein, peroxisomal
YML042w	<i>CAT2</i>	carnitine O-acetyltransferase
YDR256c	<i>CTA1</i>	catalase A, peroxisomal
YCR005c	<i>CIT2</i>	citrate (si)-synthase, peroxisomal
YKR009c	<i>FOX2</i>	hydratase-dehydrogenase-epimerase, peroxisomal
YER065c	<i>ICL1</i>	isocitrate lyase
YKL188c	<i>PAT1</i>	long-chain-fatty-acid transporter

YPL147w	PXA1	long-chain-fatty-acid transporter	YPR036w	VMA13	H ⁺ -ATPase V1 domain 54K subunit, vacuolar	YLR371w	ROM2	GDP/GTP exchange protein for Rho1p
YER015w	FAA2	long-chain-fatty-acid-CoA ligase	YBR127c	VMA2	H ⁺ -ATPase V1 domain 60K subunit, vacuolar	YPL115c	BEM3	GTPase-activating protein for Cdc42p and Rho1p
YDL078c	MDH3	malate dehydrogenase, peroxisomal	YDL185w	TFP1	H ⁺ -ATPase V1 domain 69K subunit, vacuolar	YLR229c	CDC42	GTP-binding protein of RAS superfamily
YNL117w	MLS1	malate synthase 1	YFR019w	FAB1	probable PI P-5-kinase	YPR165w	RHO1	GTP-binding protein of the RHO subfamily of RAS-like proteins
YIR031c	DAL7	malate synthase 2	YEL060c	PRB1	protease B, vacuolar	YNL090w	RHO2	GTP-binding protein of the RHO subfamily of RAS-like proteins
YDR329c	PAS3	peroxisomal assembly protein	YDR481c	PHO8	repressible vacuolar alkaline phosphatase	YPL106c	SSE1	heat-shock protein of HSP70 family
YDR265w	PAS4	peroxisomal assembly protein	YIL099w	SGA1	sporulation specific glucan 14-glucosidase	YOR149c	SMP3	protein kinase C pathway protein
YJL210w	PAS5	peroxisomal assembly protein	YOR036w	PEP12	syntaxis (T-SNARE)	YPL140c	MKK2	protein kinase of the MAP kinase kinase (MEK) family
YNL329c	PAS8	peroxisomal assembly protein	YOR106w	VAM3	syntaxis related protein	YDL135c	RD11	RHO GDP dissociation inhibitor with activity towards Rho1p
YDR142c	PAST7	peroxisomal import protein	YMR231w	PEP5	vacuolar biogenesis protein	YOR231w	MKK1	ser/thr protein kinase
YOL147c	PMP27	peroxisomal membrane protein	YLR148w	PEP3	vacuolar membrane protein	YBL105c	PKC1	ser/thr protein kinase
YLR191w	PAS20	peroxisomal protein involved in protein import	YGL212w	VAM7	vacuolar morphogenesis protein	YHR030c	SLT2	ser/thr protein kinase of MAP kinase family
YDR244w	PAS10	putative peroxisomal targeting signal receptor	YJL053w	PEP8	vacuolar protein-sorting/targeting protein	YJL095w	BCK1	ser/thr protein kinase of the MEKK family
YLR109w		similarity to <i>C. boidinii</i> peroxisomal membrane protein 20K A	YIL154c	VPS35	vacuolar protein-sorting protein	YER167w	BCK2	ser/thr protein kinase of the protein kinase C pathway
YGR077c		similarity to peroxisomal matrix protein Per1p	YDR323c	PEP7	vacuolar segregation protein	YOL113w	SKM1	Ste20p/PAK-like protein kinase
YLR251w		similarity to peroxisomal rat membrane protein MPMP22	YLP045w	VPS16	vacuolar sorting protein	YGL106w		strong similarity to calmodulins
YNL202w	SPS19	sporulation-specific protein	YDR495c	VPS3	vacuolar sorting protein	YKL161c		strong similarity to ser/thr-specific protein kinase Slt2p
YGR133w	PAS2	ubiquitin-conjugating enzyme	YLR396c	VPS33	vacuolar sorting protein	YPL089c	RLM1	transcription factor of the MADS box family
YBR204c		weak similarity to peroxisomal serine-active lipase	YPR173c	VPS4	vacuolar sorting protein	YGL095c	VPS45	vacuolar protein sorting-associated protein
<i>other cellular organization and biogenesis activities</i>								
<i>endosomal organization and biogenesis</i>								
YKL135c	APL2	β -adaptin	YKL157w	APE2	aminopeptidase yscII	YDL202w	GPD1	glycerol-3-phosphate dehydrogenase (NAD ⁺), cytoplasmic
YNL192w	CHS1	chitin synthase I	YLO15w	BAR1	barrier pepsin	YFL014w	HSP12	heat-shock protein
YBR023c	CHS3	chitin synthase III	YJL174w	KRE9	cell wall synthesis protein	YER118c	SSU81	involved in the HOG1 high-osmolarity signal transduction pathway
YIR058c	APS2	clathrin-associated protein 17, small subunit	YBR092c	PHO3	constitutive acid phosphatase	YCR073c	SSK22	MAP kinase kinase kinase
YJR005w	APL1	clathrin-associated protein complex, β subunit	YLR286c	CTS1	endochitinase	YNR031c	SSK2	MAP kinase kinase kinase of the high-osmolarity signal transduction pathway
YBR288c	APM3	clathrin-associated protein complex, medium subunit	YLR300w	EXG1	exo-1,3-glucanase (I/II), major isoform	YDL006w	PTC1	protein ser/thr phosphatase 2c
YLR170c	APS1	clathrin-associated protein complex, small subunit AP19	YIR019c	STA1	extracellular α 1-glucan glucosidase	YLR113w	HOG1	ser/thr protein kinase of MAP kinase (MAPK) family
YDL145c	RET1	coatomer complex α subunit	YPL187w	MFa1	mating pheromone α -1 factor	YHR030c	SLT2	ser/thr protein kinase of MAP kinase family
YDR238c	SEC26	coatomer complex β subunit of secretory pathway vesicles	YGL089c	MFa2	mating pheromone α -2 factor	YKL161c		strong similarity to ser/thr-specific protein kinase Slt2p
YGL137w	SEC27	coatomer complex β' subunit	YDR461w	MFa1	mating pheromone α -factor 1	YIL147c	SLN1	two-component signal transducer
YFR051c	RET2	coatomer complex δ subunit	YNL145w	MFa2	mating pheromone α -factor 2	YLR006c	SSK1	two-component signal transducer
YNL287w	SEC21	coatomer complex γ subunit	YKL163w	PIR3	member of the Pir1p/Pir2p/Pir3p family	YJL128c	PBS2	tyrosine protein kinase of the MAP kinase kinase family
YPL010w	RET3	coatomer complex ζ subunit	YBR093c	PHO5	repressible acid phosphatase	YDR069c	DOA4	ubiquitin-specific protease
YPR181c	SEC23	component of COPII coat of ER-golgi vesicles	YKL164c	PIR1	required for tolerance to heat-shock S-adenosyl-methionine 8-24-stanol-c-methyltransferase			
YDR170c	SEC7	component of non-clathrin vesicle coat	YML008c	ERG6	secreted acid phosphatase			
YLR083c	EMP70	endosomal protein	YAR071w	PHO11	secreted acid phosphatase			
YPR017c	DSS4	GDP/GTP exchange factor for Sec4p	YHR215w	PHO12	secreted acid phosphatase			
YOR089c	VPS21	GTP-binding protein	YNL160w	YGP1	secreted glycoprotein			
YDL137w	ARF2	GTP-binding protein of the ARF family	YLR250w	SSP120	secretory protein			
YML001w	YPT7	GTP-binding protein of the RAB family	YBR046c	ZTA1	similarity to ζ -crystallin			
YFL005w	SEC4	GTP-binding protein of the RAS superfamily	YMR215w	ZTA1	similarity to GAS1 protein			
YLR268w	SEC22	high copy suppressor of ypt1 null mutation	YNL275w	ZTA1	similarity to human band 3 anion transport protein			
YPL085w	SEC16	multidomain vesicle protein	YIL162w	SUC2	sucrose hydrolyzing enzyme			
YLR208w	SEC13	protein transport protein						
YKL196c		similarity to Sec22p						
YLR080w		strong similarity to Emp47p						
YDR107c		strong similarity to Emp70p						
YAL030w	SNC1	strong similarity to synaptic vesicle-associated membrane protein						
YOR327c	SNC2	strong similarity to synaptobrevin						
YBL050w	SEC17	transport vesicle fusion protein						
YNR006w	VPS27	vacuolar protein sorting-associated protein						
YBR080c	SEC18	vesicular-fusion protein, functional homologue of NSF						
YLR078c	BOS1	weak similarity to synaptobrevin (V-SNARE)						
<i>vacuolar and lysosomal organization and biogenesis</i>								
YGL156w	AMS1	α -mannosidase	YDR264c	AKR1	ankyrin repeat-containing protein	YJL005w	CYR1	adenylate cyclase
YBR286w	APE3	aminopeptidase Y, vacuolar	YPL161c	BEM4	bud emergence protein	YLR178c	TFS1	cdc25-dependent nutrient- and ammonia-response cell-cycle regulator
YKL103c	LAP4	aminopeptidase yscI, vacuolar	YCL027w	FUS1	cell fusion protein	YBR195c	MSI1	chromatin assembly complex, subunit p50
YPL154c	PEP4	aspartyl protease	YNL053w	MSG5	dual-specificity protein phosphatase	YLL016w	SDC25	GDP/GTP exchange factor
YDL128w	VCX1	Ca^{2+} -transport ($\text{H}^{+}/\text{Ca}^{2+}$ exchange) protein, vacuolar	YAL041w	CDC24	GDP/GTP exchange factor for Cdc42p	YLR310c	CDC25	GDP/GTP exchange factor for Ras1p and Ras2p
YGL006w	PMC1	Ca^{2+} -transporting P-type ATPase	YHR005c	GPA1	GTP-binding protein α subunit of the pheromone pathway	YOR101w	RAS1	GTP-binding protein
YMR297w	PRC1	carboxypeptidase y, serine-type protease	YOR212w	STE4	GTP-binding protein β subunit of the pheromone pathway	YNR098c	RAS2	GTP-binding protein
YHR028c	DAP2	dipeptidyl aminopeptidase B	YJR086w	STE18	GTP-binding protein γ subunit of the pheromone pathway	YER020w	GPA2	guanine nucleotide-binding regulatory protein
YDR135c	YCF1	glutathione S-conjugate transporter, vacuolar	YLR229c	CDC42	GTP-binding protein of RAS superfamily	YPL106c	SSE1	heat-shock protein of HSP70 family
YJL172w	CPS1	Gly-X carboxypeptidase YSCS	YNL173c	MDG1	GTP-binding protein of the pheromone pathway	YBR140c	IRA1	inhibitory regulator protein of the RAS-cyclic AMP pathway
YKL119c	VPH2	H ⁺ -ATPase assembly protein, vacuolar	YER020w	GPA2	guanine nucleotide-binding regulatory protein	YIL119c	RPI1	negative regulator of RAS-cAMP pathway
YHR039c-a	VMA10	H ⁺ -ATPase V0 domain 13K subunit, vacuolar	YLR452c	SST2	involved in desensitization to α -factor pheromone	YIR026c	YV1H	protein tyrosine phosphatase
YEL027w	CUP5	H ⁺ -ATPase V0 domain 17K subunit, vacuolar	YMR052w	FAR3	involved in pheromone-mediated cell cycle arrest	YOR208w	PTP2	protein-tyrosine-phosphatase
YPL234c	TFP3	H ⁺ -ATPase V0 domain 17K subunit, vacuolar	YDR104w	MFA1	mating pheromone α -factor 1	YOL110w	SHR5	RAS suppressor
YLR447c	VMA6	H ⁺ -ATPase V0 domain 36K subunit, vacuolar	YIL047c	SYG1	member of the major facilitator superfamily	YPL084w	BRO1	required for normal response to nutrient limitation
YOR270c	VPH1	H ⁺ -ATPase V0 domain 95K subunit, vacuolar	YBL016w	FUS3	mitogen-activated protein kinase (MAP kinase)	YLR362w	STE11	ser/thr protein kinase of the MEKK family
YGR020c	VMA7	H ⁺ -ATPase V1 domain 14K subunit, vacuolar	YFL026w	STE2	pheromone α -factor receptor	YDL159w	STE7	ser/thr/tyr protein kinase of MAP kinase kinase family
YOR332w	VMA4	H ⁺ -ATPase V1 domain 27K subunit, vacuolar	YKL178c	STE3	pheromone α -factor receptor	YHR084w	STE12	transcriptional activator
YEL051w	VMA8	H ⁺ -ATPase V1 domain 32K subunit, vacuolar	YCL032w	STE50	pheromone response pathway protein			
YKL080w	VMA5	H ⁺ -ATPase V1 domain 42K subunit, vacuolar	YDR103w	STE5	pheromone signal transduction pathway protein			
<i>Signal transduction</i>								
<i>pheromone response generation</i>								
YGR077c	SEC17	strong similarity to synaptobrevin	YOR212w	STE4	GTP-binding protein β subunit of the pheromone pathway	YJL166c	TPK3	cAMP-dependent protein kinase, catalytic subunit
YPR181c	SEC23	strong similarity to synaptobrevin	YJR086w	STE18	GTP-binding protein γ subunit of the pheromone pathway	YJL164c	SRA3	cAMP-dependent protein kinase, catalytic subunit
YML001w	YPT7	transport vesicle fusion protein	YER020w	GPA2	guanine nucleotide-binding regulatory protein	YMR028w	TAP42	component of the Tor signalling pathway
YFL005w	SEC4	GTP-binding protein of the RAS superfamily	YLR404w	KSS1	ser/thr protein kinase of the MAP kinase family	YML064c	TEM1	GTP-binding protein of the RAS superfamily
YLR268w	SEC22	high copy suppressor of ypt1 null mutation	YLR362w	STE11	ser/thr protein kinase of the MEKK family	YJL146w	IDS2	IME2-dependent signalling protein
YPL085w	SEC16	multidomain vesicle protein	YHL007c	STE20	ser/thr protein kinase of the pheromone pathway	YJR066w	TOR1	phosphatidylinositol 3-kinase
YLR208w	SEC13	protein transport protein	YDL159w	STE7	ser/thr/tyr protein kinase of MAP kinase kinase family	YKL203c	TOR2	phosphatidylinositol 3-kinase
YLR107c		strong similarity to Emp47p	YHR146w	KSS1	similarity to pheromone-response G-protein YNL173c	YLR240w	VPS34	phosphatidylinositol 3-kinase
YAL030w		strong similarity to Emp70p	YHR084w	STE12	transcriptional activator	YNL267w	PIK1	phosphatidylinositol 4-kinase
<i>morphogenesis</i>								
YGR077c	SEC17	strong similarity to synaptobrevin	YBR200w	BEM1	bud emergence mediator	YNL267w	PIE3	phosphatidylinositol phosphate phosphatase
YPR181c	SEC23	strong similarity to synaptobrevin	YPL161c	BEM4	bud emergence protein	YNL106c	DUN1	phosphatidylinositol-4-kinase protein kinase
YML001w	YPT7	transport vesicle fusion protein	YBR109c	CMD1	calmodulin			
YFL005w	SEC4	GTP-binding protein of the RAS superfamily	YAL041w	CDC24	GDP/GTP exchange factor for Cdc42p			
YLR268w	SEC22	high copy suppressor of ypt1 null mutation	YGR070w	ROM1	GDP/GTP exchange protein for Rho1p			
<i>other signal-transduction activities</i>								
YGR077c	SEC17	strong similarity to synaptobrevin						
YPR181c	SEC23	strong similarity to synaptobrevin						
YML001w	YPT7	transport vesicle fusion protein						
YFL005w	SEC4	GTP-binding protein of the RAS superfamily						
YLR268w	SEC22	high copy suppressor of ypt1 null mutation						
YPL085w	SEC16	multidomain vesicle protein						
YLR208w	SEC13	protein transport protein						
YLR107c		strong similarity to Emp47p						
YAL030w		strong similarity to Emp70p						
<i>vacuolar and lysosomal organization and biogenesis</i>								
YGL156w	AMS1	α -mannosidase						
YBR286w	APE3	aminopeptidase Y, vacuolar						
YKL103c	LAP4	aminopeptidase yscI, vacuolar						
YPL154c	PEP4	aspartyl protease						
YDL128w	VCX1	Ca^{2+} -transport ($\text{H}^{+}/\text{Ca}^{2+}$ exchange) protein, vacuolar						
YGL006w	PMC1	Ca^{2+} -transporting P-type ATPase						
YMR297w	PRC1	carboxypeptidase y, serine-type protease						
YHR028c	DAP2	dipeptidyl aminopeptidase B						
YDR135c	YCF1	glutathione S-conjugate transporter, vacuolar						
YJL172w	CPS1	Gly-X carboxypeptidase YSCS						
YKL119c	VPH2	H ⁺ -ATPase assembly protein, vacuolar						
YHR039c-a	VMA10	H ⁺ -ATPase V0 domain 13K subunit, vacuolar						
YEL027w	CUP5	H ⁺ -ATPase V0 domain 17K subunit, vacuolar						
YPL234c	TFP3	H ⁺ -ATPase V0 domain 17K subunit, vacuolar						
YLR447c	VMA6	H ⁺ -ATPase V0 domain 36K subunit, vacuolar						
YOR270c	VPH1	H ⁺ -ATPase V0 domain 95K subunit, vacuolar						
YGR020c	VMA7	H ⁺ -ATPase V1 domain 14K subunit, vacuolar						
YOR332w	VMA4	H ⁺ -ATPase V1 domain 27K subunit, vacuolar						
YEL051w	VMA8	H ⁺ -ATPase V1 domain 32K subunit, vacuolar						
YKL080w	VMA5	H ⁺ -ATPase V1 domain 42K subunit, vacuolar						

YHR079c	<i>IRE1</i>	protein kinase	YGL178w	<i>MPT5</i>	multiplicity suppressor of <i>pop2</i>	YDR059c	<i>UBC5</i>	ubiquitin-conjugating enzyme
YMR016c	<i>SOK2</i>	regulatory protein in the PKA signal transduction pathway	YGR159c	<i>NSR1</i>	nuclear localization sequence binding protein	YER125w	<i>RSP5</i>	ubiquitin-protein ligase
YGR216c	<i>GPI1</i>	required for N-acetylglucosaminyl phosphatidylinositol synthesis	YGL115w	<i>SNF4</i>	nuclear regulatory protein	YKL210w	<i>UBA1</i>	ubiquitin-protein ligase
YPL153c	<i>SPK1</i>	ser/thr/tyr protein kinase	YJR051w	<i>OSM1</i>	osmotic growth protein			
YHR046c		similarity to bovine myo-inositol-1(or 4)-monophosphatase	YMR175w	<i>SIP18</i>	osmotic stress protein			
YBR260c		similarity to <i>C. elegans</i> GTPase-activating protein	YBR070c	<i>SAT2</i>	peptidyl-prolyl cis-trans isomerase			
YGR136w		similarity to chicken growth factor receptor-binding protein GRB2 homologue	YHR057c	<i>CYP2</i>	potential regulatory subunit of protein phosphatase 2A			
YDR379w		similarity to Dbm1p	YOR014w	<i>RTS1</i>	protease A (ysca) inhibitor IA3			
YDR208w	<i>MSS4</i>	similarity to human PI P-5-kinase	YMR174c	<i>PAI3</i>	protein kinase	YER142c	<i>MAG1</i>	3-methyladenine DNA glycosylase
YCR027c		similarity to human Ras-related GTP-binding protein	YHR079c	<i>IKE1</i>		YML060w	<i>OGG1</i>	8-oxoguanine DNA glycosylase
YDR287w		similarity to inositol monophosphatase	YPL140c	<i>MKK2</i>	protein kinase of the MAP kinase kinase (MEK) family	YKL114c	<i>APN1</i>	AP endonuclease
YLR150w	<i>MPT4</i>	specific affinity for guanine-rich quadruplex nucleic acids	YOL064c	<i>MET22</i>	protein ser/thr phosphatase	YJL092w	<i>HPR5</i>	ATP-dependent DNA helicase
YPR054w	<i>SMK1</i>	sporulation-specific MAP kinase	YDL006w	<i>PTC1</i>	protein ser/thr phosphatase 2c	YPL204w	<i>HRR25</i>	caspase kinase I, ser/thr/tyr protein kinase component of the nucleotide excision repairosome
YNL132w		strong similarity to <i>A. ambisexualis</i>	YDR436w	<i>PP2Z</i>	protein ser/thr phosphatase of the PP-1 family	YPL022w	<i>RAD1</i>	
YHR206w	<i>SKN7</i>	antheridial steroid receptor transcription factor with similarity to Hsf1p	YOL084w	<i>BRO1</i>	protein tyrosine phosphatase required for glucose and cation transport	YDL108w	<i>KIN28</i>	
			YKR090c	<i>GRR1</i>	required for normal response to nutrient limitation	YOR386w	<i>PHR1</i>	cyclin-dependent ser/thr protein kinase
			YGL084c	<i>CDC55</i>	required for tolerance to heat-shock	YOR368w	<i>RAD17</i>	deoxyribodipyrimidine photo-lase
			YKL164c	<i>PIR1</i>	subunit B	YER176w		DNA damage checkpoint control protein
			YPR005c	<i>HAL1</i>	secreted glycoprotein	YLR032w	<i>RAD5</i>	DNA dependent ATPase/DNA helicase B
			YNL160w	<i>YGP1</i>	ser/thr phosphatase 2A regulatory	YIL143c	<i>SSL2</i>	DNA helicase
			YGL190c	<i>CDC55</i>	subunit B	YML061c	<i>PIF1</i>	DNA helicase involved in mitochondrial DNA repair and telomere length
			YML016c	<i>PPZ1</i>	ser/thr phosphatase required for normal osmoregulation	YER171w	<i>RAD3</i>	DNA helicase/ATPase
			YJL165c	<i>HAL5</i>	ser/thr protein kinase	YDL164c	<i>CDC9</i>	DNA ligase
			YOR231w	<i>MKK1</i>	ser/thr protein kinase	YEL019c	<i>MMS21</i>	DNA repair protein
			YBL105c	<i>PKC1</i>	ser/thr protein kinase	YAL015c	<i>NTG1</i>	DNA repair protein
			YLR113w	<i>HOG1</i>	ser/thr protein kinase of MAP kinase (MAPK) family	YMR137c	<i>PSO2</i>	DNA repair protein
			YHR030c	<i>SLT2</i>	ser/thr protein kinase of MAP kinase family	YML095c	<i>RAD10</i>	DNA repair protein
			YDL025c		ser/thr protein kinase of the DEAD/DEAH box family	YCR066w	<i>RAD18</i>	DNA repair protein
			YJL095w	<i>BCK1</i>	ser/thr protein kinase of the MEKK family	YER095w	<i>RAD51</i>	DNA repair protein
			YER167w	<i>BCK2</i>	ser/thr protein kinase of the protein kinase C pathway	YDR076w	<i>RAD55</i>	DNA repair protein
			YDR227w	<i>SIR4</i>	silencing regulatory protein	YDR004w	<i>RAD57</i>	DNA repair protein
			YKL088w		similarity to <i>C. tropicalis</i> hal3 protein, to C-term. of Sis2p and to hypothetical protein YOR054c	YOR346w	<i>REV1</i>	DNA repair protein
			YBR044c		similarity to chaperonin HSP60 proteins	YDR369c	<i>XRS2</i>	DNA repair protein
			YJR147w		similarity to heat-shock transcription factors	YGL163c	<i>RAD54</i>	DNA-dependent ATPase of the Snf2p family
			YGR249w	<i>MGA1</i>	similarity to heat-shock transcription factors	YDL102w	<i>CDC2</i>	DNA-directed DNA polymerase δ, catalytic 125K subunit
			YBR054w	<i>YRO2</i>	similarity to HSP30 heat-shock protein	YFR023w	<i>PES4</i>	DNA-directed DNA polymerase ε suppressor
			YAR020c		similarity to members of the Srp1p/Tip1p family	YNL262w	<i>POL2</i>	DNA-directed DNA polymerase ε, catalytic subunit A
			YCR008w	<i>SAT4</i>	similarity to Npr1p and Hal5p protein kinases	YPL167c	<i>REV3</i>	DNA-directed DNA polymerase ζ
			YOR009w		similarity to SRP1 and TIR2 proteins	YKR056w	<i>RNC1</i>	endo-exonuclease
			YCR060w		similarity to stress inducible protein St1p	YOL043c	<i>NTG2</i>	endonuclease III-like glycosylase 2
			YMR037c		stress responsive regulatory protein	YER162c	<i>RAD4</i>	excision repair protein
			YOR027w	<i>ST11</i>	stress-induced protein	YLR288c	<i>MEC3</i>	G2-specific checkpoint protein
			YBL009w		strong similarity to DNA damage responsive Alk1p	YFL014w	<i>HSP12</i>	heat-shock protein
			YLR369w		strong similarity to heat-shock protein 70-related proteins	YIL128w	<i>MMS19</i>	involved in repair and RNA polymerase transcription
			YHL046c		strong similarity to members of the Srp1p/Tip1p family	YMR035w	<i>IMP2</i>	mitochondrial inner membrane protease subunit
			YIL011w		strong similarity to members of the Srp1p/Tip1p family	YKR095w	<i>MLP1</i>	myosin-like protein related to Uso1p
			YOL161c		strong similarity to members of the Srp1p/Tip1p family	YMR201c	<i>RAD14</i>	nucleotide excision repair protein
			YJL223c	<i>PAU1</i>	strong similarity to members of the Srp1p/Tip1p family	YBR114w	<i>RAD16</i>	nucleotide excision repair protein
			YEL049w	<i>PAU2</i>	strong similarity to members of the Srp1p/Tip1p family	YELO37c	<i>RAD23</i>	nucleotide excision repair protein
			YCR104w	<i>PAU3</i>	strong similarity to members of the Srp1p/Tip1p family	YJR052w	<i>RAD7</i>	nucleotide excision repair protein
			YFL020c	<i>PAU5</i>	strong similarity to members of the Srp1p/Tip1p family	YDL200c	<i>MG11</i>	O6-methylguanine DNA repair methyltransferase
			YLR461w	<i>PAU4</i>	strong similarity to members of the Srp1p/Tip1p family	YDL101c	<i>DUN1</i>	protein kinase
			YNR076w	<i>PAU6</i>	strong similarity to members of the Srp1p/Tip1p family	YML032c	<i>RAD52</i>	recombination and DNA repair protein
			YDR033w		strong similarity to putative heat-shock protein Yro2p	YIL139c	<i>REV7</i>	required for DNA damage induced mutagenesis
			YKL161c		strong similarity to ser/thr-specific protein kinase Slt2p	YBR073w	<i>RDH54</i>	required for meiosis
			YOR054c		strong similarity to SIS2 protein and <i>C. tropicalis</i> hal3 protein	YIL066c	<i>RNR3</i>	ribonucleotide reductase, repair inducible large subunit
			YBR067c	<i>TIP1</i>	temp shock induced protein of the Srp1p/Tip1p family	YPL153c	<i>SPK1</i>	ser/thr/tyr protein kinase
			YGR144w	<i>THI4</i>	thiamine-repressed protein	YDR061w		similarity to <i>E. coli</i> deoxyribodipyrimidine photolyase
			YBL093c	<i>ROX3</i>	transcription factor	YAL019w	<i>FUN30</i>	similarity to helicases of the Snf2/Rad54 family
			YGL181w	<i>GTS1</i>	transcription factor of the Gcs1p/Glo3p/Sps18p family	YLR035c		similarity to human mutL protein homologue
			YMR043w	<i>MCM1</i>	transcription factor of the MADS box family	YPR056w		similarity to human transcription factor BTF2/TFIH subunit p34
			YHR206w	<i>SKN7</i>	transcription factor with similarity to Hsf1p	YFR038w		strong similarity to mouse lymphocyte specific helicase
			YKL062w	<i>MSN4</i>	transcriptional activator	YOR206w	<i>Rad4p</i>	strong similarity to Rad4p
			YML007w	<i>YAP1</i>	transcriptional activator involved in oxidative stress response	YGR258c	<i>RAD2</i>	structure-specific nuclelease of the nucleotide excision repairosome
			YIL147c	<i>SLN1</i>	two-component signal transducer	YDL088c	<i>ASM4</i>	suppressor of temperature-sensitive mutations in Pol3p
			YLR026c	<i>SKS1</i>	two-component signal transducer	YDR311w	<i>TFB1</i>	TFIIF subunit (transcription initiation factor), 75K
			YJL128c	<i>PBS2</i>	tyrosine protein kinase of the MAP kinase kinase family	YPR025c	<i>CCL1</i>	TFIIF subunit (transcription initiation factor), cyclin C component
			YLL039c	<i>UBI4</i>	ubiquitin	YLR005w	<i>SSL1</i>	TFIIF subunit (transcription initiation factor), factor B
			YMR022w	<i>QRI8</i>	ubiquitin-conjugating enzyme	YPL122c	<i>TFB2</i>	TFIIF subunit (transcription/repair factor)
			YLR082c	<i>UBC4</i>	ubiquitin-conjugating enzyme	YDR460w	<i>TFB3</i>	TFIIF subunit (transcription/repair factor)
						YGL058w	<i>RAD6</i>	ubiquitin-conjugating enzyme
								<i>detoxification</i>
						YOL052c	<i>SPE2</i>	adenosylmethionine decarboxylase
						YFL050c	<i>ALR2</i>	aluminum resistance protein
						YML116w	<i>ATR1</i>	aminoimidazole and 4-nitroquinoline resistance protein
						YNL259c	<i>ATX1</i>	antioxidant protein and metal homeostasis factor
						YLR398c	<i>SKI2</i>	antiviral protein and putative helicase
						YKL004w	<i>AUR1</i>	aureobasidin-resistance protein
						YDR256c	<i>CTA1</i>	catalase A, peroxisomal
						YGR088w	<i>CTT1</i>	catalase T, cytosolic
						YJR104c	<i>SOD1</i>	copper-zinc superoxide dismutase
						YKR066c	<i>CCP1</i>	cytochrome c peroxidase
						YPR198w	<i>SGE1</i>	drug resistance protein
						YJL101c	<i>GSH1</i>	glutamate-cysteine ligase

YOL093w	similarity to <i>C. elegans</i> hypothetical protein F25H8.1	YLR050c	similarity to human MAC30 C-terminus	YGL228w	similarity to hypothetical protein YFR039c
YDL008w	similarity to <i>C. elegans</i> hypothetical protein F35G12.9	YCR071c	similarity to human NOF1 protein	YBR281c	similarity to hypothetical protein YFR044c
YKL151c	similarity to <i>C. elegans</i> hypothetical protein R1072	YOR001w	similarity to human nucleolar 100K polymyositis-scleroderma protein	YDL001w	similarity to hypothetical protein YFR048w, YDR282c and <i>S. pombe</i> hypothetical protein SPAC12G12.14
YDR196c	similarity to <i>C. elegans</i> hypothetical protein T05G5.5	YEL016c	similarity to human nucleotide pyrophosphatase	YPL216w	similarity to hypothetical protein YGL133w
YJL029c	similarity to <i>C. elegans</i> hypothetical protein T05G5.8	YIL153w	similarity to human phosphotyrosyl phosphatase activator	YPL219w	similarity to hypothetical protein YGL134w
YNL223w	similarity to <i>C. elegans</i> hypothetical protein ZK792.1	YDR280w	similarity to human PMSl-75 autoantigen	YDR444w	similarity to hypothetical protein YGL144c and YDL1009c
YOL003c	similarity to <i>C. elegans</i> hypothetical protein, YDR126w, YNL326c and YLR246w	YPR108w	similarity to human protein GPS1	YLR047c	similarity to hypothetical protein YGL160w
YDR049w	similarity to <i>C. elegans</i> K06H7.3 protein	YLR206w	similarity to human protein KIAA0171 and hypothetical protein YDL161w	YER132c	similarity to hypothetical protein YGL197w
YGR278w	similarity to <i>C. elegans</i> LET-858	YDR096w	similarity to human tyrosine kinase KIAA0174	YFR039c	similarity to hypothetical protein YGL228w
YHR004c	similarity to <i>C. elegans</i> SPA2CF7.02c protein		similarity to human ragA protein	YHR036w	similarity to hypothetical protein YGL247w
YML059c	similarity to <i>C. elegans</i> ZK370.4 protein	YNL265c	similarity to human retinoblastoma binding protein 2	YGR031w	similarity to hypothetical protein YGR015c
YNL168c	similarity to <i>C. elegans</i> ZK68.3 protein and <i>E. coli</i> hpcEp	YGR163w	similarity to human Sm protein F	YGR015c	similarity to hypothetical protein YGR031w
YPR188c	similarity to calmodulin and calmodulin-related proteins	YDL060w	similarity to human SURF-1 protein	YBR105c	similarity to hypothetical protein YGR066c
YPR128c	similarity to carrier protein FLX1	YDR183w	similarity to human tyrosine kinase A6	YLR373c	similarity to hypothetical protein YGR071c
YPL202c	similarity to cell size regulation protein Rcs1p	YDR427w	similarity to hypothetical <i>C. elegans</i> protein	YPR158w	similarity to hypothetical protein YGR142w
YPR154w	similarity to chicken growth factor receptor-binding protein GRB2 homologue	YDR473c	similarity to hypothetical <i>C. elegans</i> protein	YHR149c	similarity to hypothetical protein YGR221c
YNL091w	similarity to chicken h-caldesmon, Uso1p and hypothetical protein YKL201c	YER051w	similarity to hypothetical <i>C. elegans</i> protein	YHR158c	similarity to hypothetical protein YGR238c
YPL176c	similarity to chinese hamster transferrin receptor protein	YGR145w	similarity to hypothetical <i>C. elegans</i> protein	YMR295c	similarity to hypothetical protein YGR273c
YDR259c	similarity to Cin5p	YGR194c	similarity to hypothetical <i>C. elegans</i> protein	YMR310c	similarity to hypothetical protein YGR283c
YGL241w	similarity to Cse1p	YGR245c	similarity to hypothetical <i>C. elegans</i> protein	YGR033c	similarity to hypothetical protein YHR032w
YNL305c	similarity to C-term. of <i>A. nidulans</i> regulatory protein (qtrR)	YHL010c	similarity to hypothetical <i>C. elegans</i> protein	YGR034c	similarity to hypothetical protein YHR036w
YPR127w	similarity to C-term. of <i>N. tabacum</i> auxin-induced protein	YJR070c	similarity to hypothetical <i>C. elegans</i> protein	YLN075w	similarity to hypothetical protein YHR061c
YDL112w	similarity to C-terminus of human TRP-185 protein	YML094w	similarity to hypothetical <i>C. elegans</i> protein	YDR348c	similarity to hypothetical protein YHR088w
YMR304w	similarity to <i>D. melanogaster</i> fat facets gene	YMR002w	similarity to hypothetical <i>C. elegans</i> protein	YER031c	similarity to hypothetical protein YHR097c
YGR003w	similarity to <i>D. melanogaster</i> lin19 protein	YJR072c	similarity to hypothetical <i>C. elegans</i> protein	YLN144c	similarity to hypothetical protein YHR131c
YLL013c	similarity to <i>D. melanogaster</i> pumilio protein	YOL060c	similarity to hypothetical <i>C. elegans</i> protein	YLN156c	similarity to hypothetical protein YHR133c
YNL023c	similarity to <i>D. melanogaster</i> shuttle craft protein	YOL097c	similarity to hypothetical <i>C. elegans</i> protein	YGR221c	similarity to hypothetical protein YHR149c
YKL201c	similarity to <i>D. melanogaster</i> sperm-tail-specific protein	YER004w	similarity to hypothetical <i>C. elegans</i> protein	YOR147w	similarity to hypothetical protein YHR194w
YCL001w-a	similarity to Dom34p	YDL238c	similarity to hypothetical <i>C. elegans</i> protein	YER175c	similarity to hypothetical protein YHR209w
YIL103w	similarity to Dph2 protein	YDL013w	similarity to hypothetical <i>C. elegans</i> protein	YJR108w	similarity to hypothetical protein YIL105w
YGL018c	similarity to <i>E. coli</i> dnaJ homologue	YDR496c	similarity to hypothetical <i>C. elegans</i> protein	YER064c	similarity to hypothetical protein YIL056w
YHL014c	similarity to <i>E. coli</i> GTP-binding protein	YDR524c	similarity to hypothetical <i>C. elegans</i> protein	YLR036c	similarity to hypothetical protein YIL089w
YLR011w	similarity to <i>E. coli</i> hypothetical 20.4K protein	YHR098c	similarity to hypothetical <i>C. elegans</i> protein	YFL034c-b	similarity to hypothetical protein YIL106w
YLF2	similarity to <i>E. coli</i> hypothetical 23K protein	YOL294w	similarity to hypothetical <i>C. elegans</i> protein	YLN058c	similarity to hypothetical protein YIL117c
	similarity to <i>E. coli</i> hypothetical 27K protein	YOR215c	similarity to hypothetical <i>C. elegans</i> protein	YLN074c	similarity to hypothetical protein YIL135c
YGL037c	similarity to <i>E. coli</i> hypothetical 33.7K protein	YDR105c	similarity to hypothetical <i>C. elegans</i> protein	YKR100c	similarity to hypothetical protein YIL158w
YOR131c	similarity to <i>E. coli</i> hypothetical 55.3K protein	YDL193w	similarity to hypothetical <i>C. elegans</i> protein	YKR015c	similarity to hypothetical protein YIL043w
YDR400w	similarity to <i>E. coli</i> hypothetical 55.3K protein in rfaB-rfe intergenic region	YOR324c	similarity to hypothetical <i>C. elegans</i> protein	YBR273c	similarity to hypothetical protein YIL048c
YDR539w	similarity to <i>E. coli</i> hypothetical 55.3K protein in rfaB-rfe intergenic region	YOR371c	similarity to hypothetical <i>C. elegans</i> protein	YLL031c	similarity to hypothetical protein YIL062w
YDR332w	similarity to <i>E. coli</i> hypothetical 55.3K protein in rfaB-rfe intergenic region	YJR115w	similarity to hypothetical <i>C. elegans</i> protein	YKR010c	similarity to hypothetical protein YIL076w
YGR021w	similarity to <i>E. coli</i> hypothetical 55.3K protein in rfaB-rfe intergenic region	YER093c-a	similarity to hypothetical <i>C. elegans</i> protein	YKR019c	similarity to hypothetical protein YIL083w
YJL046w	similarity to <i>E. coli</i> hypothetical 55.3K protein in rfaB-rfe intergenic region	YPR030w	similarity to hypothetical <i>C. elegans</i> protein	YKR029c	similarity to hypothetical protein YIL105p
YIL003w	similarity to <i>E. coli</i> hypothetical 55.3K protein in rfaB-rfe intergenic region	YMR101c	similarity to hypothetical <i>C. elegans</i> protein	YLR149w	similarity to hypothetical protein YIL149w
YOR165w	similarity to <i>E. histolytica</i> surface lectin	YGR066c	similarity to hypothetical <i>C. elegans</i> protein	YER151c	similarity to hypothetical protein YIL151c
YNR015w	similarity to <i>E. histolytica</i> nitrogen fixation regulatory protein-3 homologue	YIL171c	similarity to hypothetical <i>C. elegans</i> protein	YJR162c	similarity to hypothetical protein YIL171c
YER113c	similarity to Emp70p	YER145c	similarity to hypothetical <i>C. elegans</i> protein	YJR030c	similarity to hypothetical protein YIL181w
YDR036c	similarity to enoyl-CoA hydratase	YLR387c	similarity to hypothetical <i>C. elegans</i> protein	YIL181w	similarity to hypothetical protein YIR30c
YOR172w	similarity to finger protein YKL222c, YOR162c and YLR266c, weak similarity to transcription factors	YJR044c	similarity to hypothetical <i>C. elegans</i> protein	YKL002w	similarity to hypothetical protein YKL041w
YOR162c	similarity to finger proteins YKL222c, YOR162c and YLR266c, weak similarity to transcription factors	YDL177c	similarity to hypothetical <i>C. elegans</i> protein	YMR031c	similarity to hypothetical protein YKL050c and human restin
YOR338w	similarity to FUN19 protein	YDR282c	similarity to hypothetical <i>C. elegans</i> protein	YPR086w	similarity to hypothetical protein YKL105c
YLR193c	similarity to <i>G. gallus</i> px19	YDR425w	similarity to hypothetical <i>C. elegans</i> protein	YMR171c	similarity to hypothetical protein YKL124w
YKL054c	similarity to glutenin, high molecular weight subunit	YLR426w	similarity to hypothetical <i>C. elegans</i> protein	YMR115w	similarity to hypothetical protein YKL133c
YOL132w	similarity to glycophospholipid-anchored surface glycoprotein GAS1	YJL151c	similarity to hypothetical <i>C. elegans</i> protein	YLN101w	similarity to hypothetical protein YKL146w
YHR168w	similarity to GTP-binding proteins	YDR233c	similarity to hypothetical <i>C. elegans</i> protein	YJL076w	similarity to hypothetical protein YKR010c
YDL033c	similarity to <i>H. influenzae</i> hypothetical protein H0174	YER139c	similarity to hypothetical <i>C. elegans</i> protein	YJL043w	similarity to hypothetical protein YKR015c
YLL027w	similarity to <i>H. influenzae</i> hypothetical protein H0376	YLN249c	similarity to hypothetical <i>C. elegans</i> protein	YJL083w	similarity to hypothetical protein YKR019c
YLR419w	similarity to helicases	YLR099c	similarity to hypothetical <i>C. elegans</i> protein	YJL105w	similarity to hypothetical protein YKR029c
YMR128w	similarity to helicases	YJL149w	similarity to hypothetical <i>C. elegans</i> protein	YLR158w	similarity to hypothetical protein YKR100c
YGR271w	similarity to Hfmp1p	YLR238w	similarity to hypothetical <i>C. elegans</i> protein	YLR019w	similarity to hypothetical protein YLL010c
YDR080w	similarity to human (clone S53) mRNA, 3' end of cds	YDL204w	similarity to hypothetical <i>C. elegans</i> protein	YNL328c	similarity to hypothetical protein YLR008c
YLR051c	similarity to human acidic 82K protein	YHR061c	similarity to hypothetical <i>C. elegans</i> protein	YPL063w	similarity to hypothetical protein YLR019w and <i>S. pombe</i> hypothetical protein SPAC2F7.02c
YCR026c	similarity to human autotaxin	YHR080c	similarity to hypothetical <i>C. elegans</i> protein	YIL089w	similarity to hypothetical protein YLR036c
YJL059w	similarity to human Batten disease-related protein CLN3	YOR012w	similarity to hypothetical <i>C. elegans</i> protein	YLL023c	similarity to hypothetical protein YLR064w
YHC3	similarity to human DNA-PK	YDL113c	similarity to hypothetical <i>C. elegans</i> protein	YFL043c	similarity to hypothetical protein YLR072w
	similarity to human DS-1 protein	YML018c	similarity to hypothetical <i>C. elegans</i> protein	YNR067c	similarity to hypothetical protein YLR144c
YPR026c	similarity to human E6-associated protein	YML033w	similarity to hypothetical <i>C. elegans</i> protein	YDR501w	similarity to hypothetical protein YLR183c
YJL059w	similarity to human FVT1 protein	YML034w	similarity to hypothetical <i>C. elegans</i> protein	YNL278w	similarity to hypothetical protein YLR187w
YHR099w	similarity to human GT19 (partial ORF)	YOR19w	similarity to hypothetical <i>C. elegans</i> protein	YDR200c	similarity to hypothetical protein YLR238w
YOL114c	similarity to human hypothetical protein	YLR183c	similarity to hypothetical <i>C. elegans</i> protein	YDR262w	similarity to hypothetical protein YLR243w
YJR036c	similarity to human hypothetical protein	YLC036w	similarity to hypothetical <i>C. elegans</i> protein	YDR126w	similarity to hypothetical protein YLR246w and YOL003c
YBR265w	similarity to human hypothetical protein	YNR027w	similarity to hypothetical <i>C. elegans</i> protein	YOR137c	similarity to hypothetical protein YLR361c
YPL120w	similarity to human hypothetical protein	YGL197w	similarity to hypothetical <i>C. elegans</i> protein	YGR071c	similarity to hypothetical protein YLR373c
YPR023c	similarity to human hypothetical protein	YDR066c	similarity to hypothetical <i>C. elegans</i> protein	YPR117w	similarity to hypothetical protein YLR454w
YGL141w	similarity to human hypothetical protein	YBR207w	similarity to hypothetical <i>C. elegans</i> protein	YLN031w	similarity to hypothetical protein YML034w
YPL217c	similarity to human hypothetical protein KIAA0187	YHR209w	similarity to hypothetical <i>C. elegans</i> protein	YPL228w	similarity to hypothetical protein YML047c
YJR125c	similarity to human KIAA0171 protein	YGL262w	similarity to hypothetical <i>C. elegans</i> protein	YGR283c	similarity to hypothetical protein YMR059c
		YPL100w	similarity to hypothetical <i>C. elegans</i> protein	YGR237c	similarity to hypothetical protein YMR295c
			similarity to hypothetical <i>C. elegans</i> protein	YMR119w	similarity to hypothetical protein YMR310c
			similarity to hypothetical <i>C. elegans</i> protein	YIL117c	similarity to hypothetical protein YNL058c
			similarity to hypothetical <i>C. elegans</i> protein	YHR088w	similarity to hypothetical protein YNL075w
			similarity to hypothetical <i>C. elegans</i> protein	YHR131c	similarity to hypothetical protein YNL144c
			similarity to hypothetical <i>C. elegans</i> protein	YHR133c	similarity to hypothetical protein YNL156c
			similarity to hypothetical <i>C. elegans</i> protein	YDL211c	similarity to hypothetical protein YNL176c
			similarity to hypothetical <i>C. elegans</i> protein	YLR187w	similarity to hypothetical protein YNL278w
			similarity to hypothetical <i>C. elegans</i> protein	YDR214w	similarity to hypothetical protein YNL281w
			similarity to hypothetical <i>C. elegans</i> protein	YLR008c	similarity to hypothetical protein YNL328c
			similarity to hypothetical <i>C. elegans</i> protein	YEL029c	similarity to hypothetical protein YNR027w
			similarity to hypothetical <i>C. elegans</i> protein	YER012w	similarity to hypothetical protein YOL019w
			similarity to hypothetical <i>C. elegans</i> protein	YOL083w	similarity to hypothetical protein YOL019w
			similarity to hypothetical <i>C. elegans</i> protein	YDR474c	similarity to hypothetical protein YOR191w

YKR078w	similarity to hypothetical protein YOR069w	YNL006w	similarity to Met30p	YGL164c	similarity to <i>S. pombe</i> hypothetical protein SPAC31A2.10	
YHR194w	similarity to hypothetical protein YOR147w	YNL293w	similarity to Mic1p and human transforming protein tre-2, and strong similarity to hypothetical protein YOL112w	YPL236c	similarity to <i>S. pombe</i> hypothetical protein SPAC3H113	
YAL028w	similarity to hypothetical protein YOR324c	YNR047w	similarity to microtubule-associated ser/thr protein kinases	YAL032c	similarity to <i>S. pombe</i> hypothetical protein SPAC8A4.06	
YLR361c	similarity to hypothetical protein YOR3329c	YPL137c	similarity to microtubule-interacting protein Mhp1p and to hypothetical protein YOR227w	YEL007w	similarity to <i>S. pombe</i> pac2 protein	
YAL034c	FUN19	similarity to hypothetical protein YOR338w	YIL151c	YLR247c	similarity to <i>S. pombe</i> rad8 protein	
YAL056w	similarity to hypothetical protein YOR371c	YGR058w	similarity to mitochondrial aldehyde dehydrogenase Ald1p	YJL062w	similarity to <i>S. pombe</i> SPAC13G6.3 protein	
YFR021w	similarity to hypothetical protein YPL100w	YBL047c	similarity to mouse calcium-binding protein	YHR009c	similarity to <i>S. pombe</i> YAM3 protein	
YML117w	similarity to hypothetical protein YPL184c	YLR200w	similarity to mouse eps15R protein	YBL051c	similarity to <i>S. pombe</i> Z66568_C protein	
YGL133w	similarity to hypothetical protein YPL216w	YIL023c	similarity to mouse KE2 protein	YOR240w	similarity to <i>S. pombe</i> ZK1058.5 protein	
YGL134w	similarity to hypothetical protein YPL219w	YCR033w	similarity to mouse H-2K/t-w5-linked ORF	YPL150w	similarity to ser/thr kinases	
YMR180c	similarity to hypothetical protein YPL228w	YER030w	similarity to mouse nuclear receptor co-repressor N-Cor	YGR052w	similarity to ser/thr protein kinases	
YMR181c	similarity to hypothetical protein YPL229w	YDR060w	similarity to mouse nucleolin	YAL017w	similarity to ser/thr protein kinases	
YJR116w	similarity to hypothetical protein YPR114w	YBR187w	similarity to mouse putative CCAAT binding factor 1	YOR090c	similarity to ser/thr protein phosphatases	
YLR454w	similarity to hypothetical protein YPR117w	YGR284c	similarity to mouse putative transmembrane protein FT27	YBR059c	similarity to ser/thr-specific protein kinase Pak1p	
YOL027c	similarity to hypothetical protein YPR125w	YGR127w	similarity to mouse Surf-4 protein	YBR274w	similarity to ser/thr-specific protein kinases	
YGR142w	similarity to hypothetical protein YPR158w	YMR192w	similarity to mouse T10 protein	YLR118c	similarity to several esterases	
YOL048c	similarity to hypothetical proteins YAL018c and YOL047c	YPL249c	similarity to mouse Tbc1 protein	YMR077c	similarity to SNF7 protein	
YOL047c	similarity to hypothetical proteins YAL018c and YOL048c	YHR181w	similarity to mouse Tbc1 protein	YLR313c	similarity to SPA2 protein	
YMR210w	similarity to hypothetical proteins YBR177c and YPL095c	YDR109c	similarity to mouse TEG-261 protein	YIR033w	similarity to Sp123p	
YML052w	similarity to hypothetical proteins YDL222c and YNL194c	YDL038c	similarity to MPA43p	YBL109w	similarity to subtelomeric encoded proteins	
YLR246w	similarity to hypothetical proteins YDR126w, YNL326w and YOL003c	YER085c	similarity to mucin proteins	YEL074w	similarity to subtelomeric encoded proteins	
YER072w	similarity to hypothetical proteins YFL004w and YPL09c	YJL112w	similarity to myosins	YGL263w	similarity to subtelomeric encoded proteins	
YLR072w	similarity to hypothetical proteins YFL042c, YFL043c, YDR326c and YHR080c	YDR395w	similarity to <i>N. crassa</i> sulphur controller-2	YHL042w	similarity to subtelomeric encoded proteins	
YGL028c	similarity to hypothetical proteins YGR279c and YMR305c	YPR072w	similarity to NMD and CSE1 proteins	YHL043w	similarity to subtelomeric encoded proteins	
YFL042c	similarity to hypothetical proteins YHR080c, YDR326c and YLR072w	YBL024w	similarity to N-terminal part of Cdc39p	YHL044w	similarity to subtelomeric encoded proteins	
YNL097c	similarity to hypothetical proteins YHR090c and YHR090c	YDR071c	similarity to nucleolar Nop2p	YIL177c	similarity to <i>O. aries</i> arylalkylamine N-acetyltransferase	
YJR061w	similarity to hypothetical proteins YKL200c and YKL201c	YOL164w	similarity to <i>P. aeruginosa</i> alkyl sulphatase	YKL219w	similarity to subtelomeric encoded proteins	
YMR313c	similarity to hypothetical proteins YKR089c and YOR081c	YMR099c	similarity to <i>P. ciliare</i> possible apospory-associated protein	YMR326c	similarity to subtelomeric encoded proteins	
YOL019w	similarity to hypothetical proteins YMR063w and YFR012w	YNR029c	similarity to <i>P. denitrificans</i> cobW protein	YLR177w	similarity to suppressor protein Gin5p	
YPR027c	similarity to hypothetical proteins YNL019c and YNL033w	YDR472w	similarity to <i>P. falciparum</i> 41-2 protein antigen	YNL191w	similarity to <i>Synechocystis</i> hypothetical protein	
YNL056w	similarity to hypothetical proteins YNL032w and YNL099c	YNL136w	similarity to <i>P. falciparum</i> mature-parasite-infected erythrocyte surface antigen	YGR036c	similarity to <i>T. denticola</i> phosphatase	
YNL099c	similarity to hypothetical proteins YNL032w, YNL056w and YDR067c	YIL010w	similarity to MESA	YDR485c	similarity to trichohyalin	
YNL032w	similarity to hypothetical proteins YNL099c, YNL056w and YDR067c	YLR107w	similarity to <i>P. falciparum</i> merozoite cap protein-1	YOR195w	similarity to USO1 protein	
YOL101c	similarity to hypothetical proteins YOL002c and YDR492w	YOL065c	similarity to <i>P. troglodytes</i> prot GOR	YPL188w	similarity to Utr1p and hypothetical protein YEL041w	
YNL326c	similarity to hypothetical proteins YOL003c, YLR246w and <i>C. elegans</i> hypothetical protein ZK757.1	YNL047c	similarity to Pie3p and hypothetical proteins YIL002c	POSS5	similarity to UTR2 protein	
YML072c	similarity to hypothetical proteins YOR314c and YNL087w and weak similarity to synaptogamines	YBR125c	similarity to probable transcription factor Ask10p and hypothetical protein YPR115w, and strong similarity to hypothetical protein YIL105c	YLR213c	similarity to Utr2p	
YLR152c	similarity to hypothetical proteins YOR316w and YNL095c	YNR038w	similarity to protein phosphatase 2C	YGR189c	similarity to <i>V. alginolyticus</i> bolA protein	
YNL165w	similarity to hypothetical proteins YOR385w and YMR316w	YER150w	similarity to Prp5p	YGL220w	similarity to <i>X. laevis</i> protein-tyrosin-phosphatase cdc homologue 2 and to hypothetical protein YPR200c	
YMR316w	similarity to hypothetical proteins YOR385w and YNL165w	YGL099w	similarity to putative cell surface glycoprotein Sed1p	YGR203w	similarity to YDR503c	
YDR083w	similarity to hypothetical <i>S. pombe</i> protein	YPR062w	similarity to putative human GTP-binding protein HSR1	YDR284c	similarity to Yke2p	
YDR346c	similarity to hypothetical <i>S. pombe</i> protein	YJL055w	similarity to <i>R. fascians</i> hypothetical protein 6	YELO03w	similarity to Ymk1p	
YGR272c	similarity to hypothetical <i>S. pombe</i> protein	YOR191w	similarity to RAD5 protein	YIL135c	similarity to YOL083w	
YLR241w	similarity to hypothetical <i>S. pombe</i> protein	YGL059w	similarity to rat branched-chain α -ketoacid dehydrogenase kinase	YOL082w	similarity to YOR383c, Sta1p and pig mucin	
YML005w	similarity to hypothetical <i>S. pombe</i> protein	YBR053c	similarity to rat calcineurin	YDR534c	similarity to YPR030w	
YOL098c	similarity to hypothetical <i>S. pombe</i> protein	YDL015c	similarity to rat synaptic glycoprotein SC2	YBL101c	similarity to Ytp1p protein	
YOR091w	similarity to hypothetical <i>S. pombe</i> protein D83992_G	YDR457w	similarity to rat URE-B1	YCR062w	strong similarity hypothetical protein YHR016c	
YOL071w	similarity to hypothetical <i>S. pombe</i> protein SPAC12B10.06c	YBR028c	similarity to ribosomal protein kinases	YFR024c-a	strong similarity to <i>A. thaliana</i> PRL1 and PRL2 proteins	
YFR048w	similarity to hypothetical <i>S. pombe</i> protein SPAC12G12.14 and to YDL001w and YDR282c	YLR276c	similarity to RNA helicases	YOR034c	strong similarity to Akr1p	
YOR322c	similarity to hypothetical <i>S. pombe</i> protein SPAC1F12.05	YPR112c	similarity to RNA-binding proteins	YOR374w	strong similarity to aldehyde dehydrogenase	
YOR250c	similarity to hypothetical <i>S. pombe</i> protein SPAC22H10.05c	YPR016c	similarity to <i>S. acidocaldaricus</i> aa2 ₂ ac protein	YKL013c	strong similarity to <i>C. albicans</i> dual-specificity phosphatase MSG5	
YER143w	similarity to hypothetical <i>S. pombe</i> protein SPAC56F8.08	YOL154w	similarity to <i>S. furnigata</i> Asp FII	YNL288w	strong similarity to <i>C. carbonum</i> toxD protein	
YDR504c	similarity to hypothetical <i>T. brucei</i> protein	YHR029c	similarity to <i>S. lincolnenis</i> lmbX protein	YOL077c	strong similarity to <i>C. elegans</i> hypothetical protein	
YDR223w	similarity to Ifh1p	YFL033c	similarity to <i>S. pombe</i> cek1	YGL080w	strong similarity to <i>C. elegans</i> K12H.4.3 protein	
YAL035w	FUN12	similarity to inositol polyphosphate 5-phosphatases	YIL144w	similarity to <i>S. pombe</i> hypothetical protein	YPR194c	strong similarity to C-term. of <i>S. pombe</i> isp4 protein
YOR109w	similarity to intracellular attachment proteins	YKR051w	similarity to <i>S. pombe</i> hypothetical protein	YAR023c	strong similarity to Fun5p, Fun59p, YGL051w, YCR007c, YGL053w, YAR031w and YAR028w	
YEL013w	similarity to Jsn1p	YOL087c	similarity to <i>S. pombe</i> hypothetical protein	YAR028w	strong similarity to Fun55p, YGL053w, YCR007c, YAR031w, Fun59p and YGL051w	
YPR042c	similarity to ketoreductases	YBR004c	similarity to <i>S. pombe</i> hypothetical protein SPAC18B11.05	YGL051w	strong similarity to Fun59p	
YMR226c	similarity to <i>L. mactans</i> α -latroinsectotoxin	YKR079c	similarity to <i>S. pombe</i> hypothetical protein SPAC1D4.10	YGL236c	strong similarity to gida E. coli protein	
YGR232w	similarity to <i>L. pneumophila</i> dlpA protein	YNL308c	similarity to <i>S. pombe</i> hypothetical protein SPAC22G7.05	YAL036c	strong similarity to GTP-binding proteins	
YER010c	similarity to <i>M. capricolum</i> hypothetical protein SGCS3	YAL042w	similarity to <i>S. pombe</i> hypothetical protein SPAC24B10.08c	YMR290c	strong similarity to helicases of the DEAD/DEAH box family	
YGH210c	similarity to <i>M. leprae</i> hisH protein	YNL310c	similarity to <i>S. pombe</i> hypothetical protein SPAC24H6.02c	YDR276c	strong similarity to <i>Hordeum</i> btt101 protein	
YMR095c	similarity to <i>M. musculus</i> p162 protein	YGR125w	similarity to <i>S. pombe</i> hypothetical protein SPAC24H6.11c	YDL103c	strong similarity to human Agx-1 antigen	
YBR079c	similarity to <i>M. verrucaria</i> cyanamide hydratase, identical to hypothetical protein YFL061w	YMR075w	similarity to <i>S. pombe</i> hypothetical protein SPAC2C70.7c	YDR373w	strong similarity to human BDR-1 protein and other calcium binding proteins	
YNL335w	similarity to mammalian valosin	YDR175c	similarity to <i>S. pombe</i> hypothetical protein SPAC2F7T:15	YNR053c	strong similarity to human breast tumor associated autoantigen	
YLL034c	similarity to members of the mitochondrial carrier protein family	YFL047w	similarity to <i>S. pombe</i> hypothetical protein SPAC2F718c	YDL120w	strong similarity to human frataxin (Friedreich's ataxia)	
YMR166c	similarity to members of the Srp1p/Tip1p family	YLR023c	similarity to <i>S. pombe</i> hypothetical protein SPAC3D11.11	YGR173w	strong similarity to human GTP-binding protein	
YIR041w	similarity to members of the Srp1p/Tip1p family	YDR180w	similarity to <i>S. pombe</i> hypothetical protein SPAC31A2.05c	YKL056c	strong similarity to human IgE-dependent histamine-releasing factor	
				FUN11		
				QRI1		

YPL152w	strong similarity to human phosphotyrosyl phosphatase activator	YDL109c	strong similarity to hypothetical protein YGL144c	YGR004w	strong similarity to hypothetical protein YLR324w
YPR028w	strong similarity to human protein TB2	YER037w	strong similarity to hypothetical protein YGL224c	YGR010w	strong similarity to hypothetical protein YLR328w
YCL059c	strong similarity to human Rev interacting protein Rip-1	YOR387c	strong similarity to hypothetical protein YGL258w	YGR038w	<i>ORM1</i> strong similarity to hypothetical protein YLR350w
YLR146c	strong similarity to human spermidine synthase	YLR324w	strong similarity to hypothetical protein YGR004w	YGR056w	strong similarity to hypothetical protein YLR357w
YNL200c	strong similarity to human TGR-CL10C	YLR328w	strong similarity to hypothetical protein YGR010w	YKL187c	strong similarity to hypothetical protein YLR413w
YBL036c	strong similarity to hypothetical <i>C. elegans</i> protein	YLR350w	strong similarity to hypothetical protein YGR038w	YPR172w	strong similarity to hypothetical protein YLR456w
YBL078c	strong similarity to hypothetical <i>C. elegans</i> protein	YLR357w	strong similarity to hypothetical protein YGR056w	YDR438w	strong similarity to hypothetical protein YML018c
YMR292w	strong similarity to hypothetical <i>C. elegans</i> protein	YPL004c	strong similarity to hypothetical protein YGR086c	YBR002c	strong similarity to hypothetical protein YMR101c
YDR430c	strong similarity to hypothetical <i>C. perfringens</i> protein	YPR157w	strong similarity to hypothetical protein YGR141w	YKL121w	strong similarity to hypothetical protein YMR102c
YOR365c	strong similarity to hypothetical protein YAL053w	YHR162w	strong similarity to hypothetical protein YGR243w	YPL224c	strong similarity to hypothetical protein YMR177w
YHR214w-a	strong similarity to hypothetical protein YAR068w	YBR300c	strong similarity to hypothetical protein YGR293c	YOR295w	strong similarity to hypothetical protein YMR233w
YPR032w	strong similarity to hypothetical protein YBL106c	YHR054c	strong similarity to hypothetical protein YHR056c	YKL046c	strong similarity to hypothetical protein YMR238w
YDR003w	strong similarity to hypothetical protein YBR005w	YDR358w	strong similarity to hypothetical protein YHR108w	YPL264c	strong similarity to hypothetical protein YMR253c
YDR210w	strong similarity to hypothetical protein YBR016w	YNL116w	strong similarity to hypothetical protein YHR115c	YGR279c	strong similarity to hypothetical protein YMR306c
YDL012c	strong similarity to hypothetical protein YBR016w and YDR210w	YGR238c	strong similarity to hypothetical protein YHR158c	YOR385w	strong similarity to hypothetical protein YMR316w
YDR018c	strong similarity to hypothetical protein YBR042c	YGR243w	strong similarity to hypothetical protein YHR162w	YNL034w	strong similarity to hypothetical protein YNL018c
YOL092w	strong similarity to hypothetical protein YBR147w	YHR199c	strong similarity to hypothetical protein YHR198c	YNL033w	strong similarity to hypothetical protein YNL019c
YPL095c	strong similarity to hypothetical protein YBR177c	YHR198c	strong similarity to hypothetical protein YHR199c	YNL019c	strong similarity to hypothetical protein YNL033w
YPL087w	strong similarity to hypothetical protein YBR183w	YAR060c	strong similarity to hypothetical protein YHR212c	YNL018c	strong similarity to hypothetical protein YNL034w
YGL056c	strong similarity to hypothetical protein YBR214w	YAR068w	strong similarity to hypothetical protein YHR214w-a	YIL109c	strong similarity to hypothetical protein YNL049c
YGL060w	strong similarity to hypothetical protein YBR216c	YPR071w	strong similarity to hypothetical protein YIL029c	YOR086c	strong similarity to hypothetical protein YNL087w and weak similarity to synaptogamines
YGL107c	strong similarity to hypothetical protein YBR238c	YER067w	strong similarity to hypothetical protein YIL067c	YOR092w	strong similarity to hypothetical protein YNL095c
YGL101w	strong similarity to hypothetical protein YBR242w	YDL175c	strong similarity to hypothetical protein YIL079c	YOR110w	strong similarity to hypothetical protein YNL108c
YJL058c	strong similarity to hypothetical protein YBR270c	YIL014c-a	strong similarity to hypothetical protein YIL102c	YHR115c	strong similarity to hypothetical protein YNL116w
YGR293c	strong similarity to hypothetical protein YBR300c	YNL049c	strong similarity to hypothetical protein YIL109c	YDL222c	strong similarity to hypothetical protein YNL194c and similarity to YML052w
YDR514c	strong similarity to hypothetical protein YCL036w	YOL162w	strong similarity to hypothetical protein YIL166c	YLR144c	strong similarity to hypothetical protein YNR067c
YGL144c	strong similarity to hypothetical protein YDL109c	YJL038c	strong similarity to hypothetical protein YIL037w	YDR492w	strong similarity to hypothetical protein YOL002c
YIL079c	strong similarity to hypothetical protein YDL175c	YJL037w	strong similarity to hypothetical protein YIL038c	YPR125w	strong similarity to hypothetical protein YOL027c
YNL194c	strong similarity to hypothetical protein YDL222c and similarity to hypothetical protein YML052w	YBR270c	strong similarity to hypothetical protein YIL058c	YBR147w	strong similarity to hypothetical protein YOL092w
YBR005w	strong similarity to hypothetical protein YDR003w	YKR018c	strong similarity to hypothetical protein YIL082w	YDR391c	strong similarity to hypothetical protein YOR013w
YBR042c	strong similarity to hypothetical protein YDR018c	YKR021w	strong similarity to hypothetical protein YIL084c	YAL007c	strong similarity to hypothetical protein YOR016c, similarity to hamster COP-coated vesicle membrane protein
YLR108c	strong similarity to hypothetical protein YDR132c	YKR053c	strong similarity to hypothetical protein YIL134w	YKR089c	strong similarity to hypothetical protein YOR081c
YPL235w	strong similarity to hypothetical protein YDR190c	YML047c	strong similarity to hypothetical protein YJR054w	YNL095c	strong similarity to hypothetical protein YOR092w
YNL281w	strong similarity to hypothetical protein YDR214w	YKL200c	strong similarity to hypothetical protein YJR061w	YNL108c	strong similarity to hypothetical protein YOR110w
YLR225c	strong similarity to hypothetical protein YDR222w	YDR399w	strong similarity to hypothetical protein YJR133w	YLR260w	strong similarity to hypothetical protein YOR171c
YHR032w	<i>ERC1</i> strong similarity to hypothetical protein YDR338c	YMR238w	strong similarity to hypothetical protein YKL046c	YLR270w	strong similarity to hypothetical protein YOR173w
YHR097c	strong similarity to hypothetical protein YDR348c	YMR040w	strong similarity to hypothetical protein YKL065c	YLR284c	strong similarity to hypothetical protein YOR180c
YHR108w	strong similarity to hypothetical protein YDR358w	YMR102c	strong similarity to hypothetical protein YKL121w	YLR243w	strong similarity to hypothetical protein YOR262w
YOR013w	strong similarity to hypothetical protein YDR391c	YLR413w	strong similarity to hypothetical protein YKL187c	YMR233w	strong similarity to hypothetical protein YOR295w
YJR133w	strong similarity to hypothetical protein YDR399w	YJL082w	strong similarity to hypothetical protein YKR018c	YGL258w	strong similarity to hypothetical protein YOR387c
YOL002c	strong similarity to hypothetical protein YDR492w	YJL084c	strong similarity to hypothetical protein YKR021w	YPL279c	strong similarity to hypothetical protein YOR390w
YOR383c	strong similarity to hypothetical protein YDR534c and similarity to <i>L. mexicana</i> secreted acid phosphatase 2	YJL134w	strong similarity to hypothetical protein YKR053c	YGR086c	strong similarity to hypothetical protein YPL004c
YPR193c	strong similarity to hypothetical protein YEL066w	YOR081c	strong similarity to hypothetical protein YKR089c	YPR004w	strong similarity to hypothetical protein YPL019c
YGL224c	strong similarity to hypothetical protein YER037w	YIR013c	strong similarity to hypothetical protein YLR013w	YBR183w	strong similarity to hypothetical protein YPL087w
YIL057c	strong similarity to hypothetical protein YER067w	YLL010c	strong similarity to hypothetical protein YLR019w	YBR177c	strong similarity to hypothetical protein YPL095c
YPL019c	strong similarity to hypothetical protein YFL004w	YDR125c	strong similarity to hypothetical protein YLR099c	YOR227w	strong similarity to hypothetical protein YPL137c and to microtubule-interacting protein MHP1
YMR096w	strong similarity to hypothetical protein YFL059w, YNL333w, and Para rubber tree ethylene-responsing protein 1	YDR132c	strong similarity to hypothetical protein YLR108c	YGL084c	strong similarity to hypothetical protein YPL189w
YHR016c	strong similarity to hypothetical protein YFR024c-a	YDR185c	strong similarity to hypothetical protein YLR168c	YGL082w	strong similarity to hypothetical protein YPL191c
<i>YSC84</i>		YDL161w	strong similarity to hypothetical protein YLR206w and to human KIAA0171 protein	YGL139w	strong similarity to hypothetical protein YPL221w
YBR214w	strong similarity to hypothetical protein YGL056c	YDR222w	strong similarity to hypothetical protein YLR225c	YMR177w	strong similarity to hypothetical protein YPL224c
YBR216c	strong similarity to hypothetical protein YGL060w	YDR213w	strong similarity to hypothetical protein YLR228c	YDR190c	strong similarity to hypothetical protein YPL235w
YPL191c	strong similarity to hypothetical protein YGL082w	YOR171c	strong similarity to hypothetical protein YLR260w	YMR253c	strong similarity to hypothetical protein YPL264c
YPL189w	strong similarity to hypothetical protein YGL084c	YOR173w	strong similarity to hypothetical protein YLR270w		
YBR242w	strong similarity to hypothetical protein YGL101w	YOR180c	strong similarity to hypothetical protein YLR284c		

YOR390w	strong similarity to hypothetical protein YPL279c	YHL017w	strong similarity to putative transmembrane protein PTM1	YLR466w	strong similarity to subtelomeric encoded proteins
YIL029c	strong similarity to hypothetical protein YPR071w	YHR017w	strong similarity to <i>S. douglasii</i> YSD83	YLR467w	strong similarity to subtelomeric encoded proteins
YDL242w	strong similarity to hypothetical protein YPR079w	YDL219w	strong similarity to <i>S. equisimilis</i> hypothetical protein	YML132w	strong similarity to subtelomeric encoded proteins
YGR141w	strong similarity to hypothetical protein YPR157w	YPL118w	strong similarity to <i>S. kluveri</i> hypothetical protein	YNL336w	strong similarity to subtelomeric encoded proteins
YLR456w	strong similarity to hypothetical protein YPR172w	YNL072w	strong similarity to <i>S. pombe</i> hypothetical protein SPAC31A2.02	YNL337w	strong similarity to subtelomeric encoded proteins
YEL066w	strong similarity to hypothetical protein YPR193c	YDR032c	strong similarity to <i>S. pombe</i> obr1	YNL338w	strong similarity to subtelomeric encoded proteins
YGL053w	strong similarity to hypothetical proteins YAR031, YGL051w, YAR028w, Fun55p and YCR007c	YOL010w	strong similarity to <i>S. pombe</i> SPAC4G9.02	YNL339c	strong similarity to subtelomeric encoded proteins
YMR324c	strong similarity to hypothetical proteins YBL108w, YCR103c and YKL223w	YOR163w	strong similarity to <i>S. pombe</i> SPAC13G6.14	YNR077c	strong similarity to subtelomeric encoded proteins
YNR048w	strong similarity to hypothetical proteins YCR094w and YNL323w	YOR256c	strong similarity to secretory protein SSP134	YOL158c	strong similarity to subtelomeric encoded proteins
YNL323w	strong similarity to hypothetical proteins YCR094w and YNR048w	YCL024w	strong similarity to ser/thr protein kinase GNP1	YPL282c	strong similarity to subtelomeric encoded proteins
YBR016w	strong similarity to hypothetical proteins YDL012c and YDR210w	YOR310c	strong similarity to SIK1 protein	YPL283c	strong similarity to subtelomeric encoded proteins
YNL334c	strong similarity to hypothetical proteins YFL060c and YMR095c	YDR247w	strong similarity to Sks1p	YPR202w	strong similarity to subtelomeric encoded proteins
YPL221w	strong similarity to hypothetical proteins YGL139w and YAL053w	O7535	strong similarity to subtelomeric encoded proteins	YNR075w	<i>EDL1</i>
YDR326c	strong similarity to hypothetical proteins YHR080c, YFL042c and YLR072w	YAL068c	strong similarity to subtelomeric encoded proteins	YER042w	strong similarity to transcription factors and peptide methionine sulphoxide reductases
YMR251w	strong similarity to hypothetical proteins YKR076w and YGR154c	YBL108w	strong similarity to subtelomeric encoded proteins	YPR203w	strong similarity to subtelomeric encoded proteins
YGR154c	strong similarity to hypothetical proteins YKR076w and YMR251w	YBL111c	strong similarity to subtelomeric encoded proteins	YPR204w	strong similarity to subtelomeric encoded proteins
YKR076w	strong similarity to hypothetical proteins YMR251w and YGR154c	YBL112c	strong similarity to subtelomeric encoded proteins	YPR205w	strong similarity to subtelomeric encoded proteins
YFL060c	strong similarity to hypothetical proteins YNL334c and YMR095c	YBL113c	strong similarity to subtelomeric encoded proteins	YJL186w	strong similarity to Ttp1p
YCR094w	strong similarity to hypothetical proteins YNR048w and YNL323w	YBR302c	strong similarity to subtelomeric encoded proteins	YEL041w	strong similarity to Utr1p
YOR230w	strong similarity to hypothetical proteins YOR229w and YPL139c	YCL073c	strong similarity to subtelomeric encoded proteins	YCR063w	strong similarity to <i>Xenopus</i> G10 and human edg-2 protein
YPL139c	strong similarity to hypothetical proteins YOR230w and YOR229w	YCR103c	strong similarity to subtelomeric encoded proteins	YAR027w	<i>FUN55</i>
YOR229w	strong similarity to hypothetical proteins YOR230w and YPL139c	YDL248w	strong similarity to subtelomeric encoded proteins	YAR029w	<i>FUN57</i>
YAL053w	strong similarity to hypothetical proteins YOR365c, YGL139w, YPL221w	YDR542w	strong similarity to subtelomeric encoded proteins	YAR033w	<i>FUN59</i>
YPL280w	strong similarity to hypothetical proteins YOR391c, YMR322c and YDR533c	YDR543c	strong similarity to subtelomeric encoded proteins	YAR031w	strong similarity to YGL053w, Fun59p, YGL051w, Fun55p and YGL051w
YMR321c	strong similarity to hypothetical proteins YPL273w and YLL062c	YDR544c	strong similarity to subtelomeric encoded proteins	YIL102c	strong similarity to YIL014c-a
YLL062c	strong similarity to hypothetical proteins YPL273w, weak similarity to <i>M. leprae</i> metH2 protein	YDR545w	strong similarity to subtelomeric encoded proteins	YBR025c	strong similarity to YIL014c-a
YOR391c	strong similarity to hypothetical proteins YPL280w, YMR322c and YDR533c	YEL075c	strong similarity to subtelomeric encoded proteins	YKL065c	strong similarity to YMR040w
YDR533c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c	YEL076c-b	strong similarity to subtelomeric encoded proteins	YOL112w	strong similarity to YNL293w, similarity to M1c1p and human transforming protein tre-2
YMR322c	strong similarity to hypothetical proteins YPL280w, YOR391c and YMR322c	YER188c-a	strong similarity to subtelomeric encoded proteins	YBL106c	strong similarity to YPR032w
YHR069c	strong similarity to hypothetical <i>S. pombe</i> and human proteins	YER189w	strong similarity to subtelomeric encoded proteins	YLR045c	suppressor of a cs tubulin mutation
YMR288w	strong similarity to hypothetical <i>S. pombe</i> protein	YER190w	strong similarity to subtelomeric encoded proteins	YER120w	suppressor of an inositol auxotrophic and a choline sensitive mutant
YER049w	strong similarity to hypothetical <i>S. pombe</i> protein YER049W	YFL062w	strong similarity to subtelomeric encoded proteins	YCR044c	suppressor of <i>cdc1-1</i> ts growth defect
YNL240c	strong similarity to <i>K. marxianus</i> LET1 protein	YFL063w	strong similarity to subtelomeric encoded proteins	YGL083w	suppressor of GTPase mutant
YBR301w	strong similarity to members of the Srp1p/Tip1p family	YFL064c	strong similarity to subtelomeric encoded proteins	YDR510w	suppressor of <i>mi2f</i> temperature-sensitive mutation
YGL261c	strong similarity to members of the Srp1p/Tip1p family	YFL065c	strong similarity to subtelomeric encoded proteins	YOL102c	suppressor of <i>shr3</i>
YGR294w	strong similarity to members of the Srp1p/Tip1p family	YFL066c	strong similarity to subtelomeric encoded proteins	YOL102c	suppressor of toxicity of Gal4-IKB tRNA 2'-phosphotransferase
YIL176c	strong similarity to members of the Srp1p/Tip1p family	YGL260w	strong similarity to subtelomeric encoded proteins	YOL102c	TPT1
YKL224c	strong similarity to members of the Srp1p/Tip1p family	YGR295c	strong similarity to subtelomeric encoded proteins	YOL102c	strong similarity to <i>C. fragment</i>
YLL025w	strong similarity to members of the Srp1p/Tip1p family	YGR296w	strong similarity to subtelomeric encoded proteins	YOL102w	Ty3-2 or C fragment
YLL064c	strong similarity to members of the Srp1p/Tip1p family	YHL045w	strong similarity to subtelomeric encoded proteins	YOL102c	type II membrane protein
YLR037c	strong similarity to members of the Srp1p/Tip1p family	YHL048w	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to <i>A. niger</i> carbon catabolite repressor protein
YMR325w	strong similarity to members of the Srp1p/Tip1p family	YHR217c	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to <i>A. parasiticus</i> nor-1 protein
YOR394w	strong similarity to members of the Srp1p/Tip1p family	YHL218w-a	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to <i>A. thaliana</i> nitrilase 3
YEL047c	strong similarity to Osm1p	YIR040c	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to <i>A. thaliana</i> protein phosphatase 2C
YFL059w	strong similarity to Para rubber tree ethylene-responsive protein1	YJL225c	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to a-agglutinin core protein AGA1
YNL333w	strong similarity to Para rubber tree ethylene-responsive protein 1 and identical to hypothetical protein YFL059w	YJR161c	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to adenylate cyclases
YNR065c	strong similarity to Pep1p	YJR162c	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to Afr1p
YNR066c	strong similarity to Pep1p	YKL223w	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to aminopeptidase Y
YER089c	strong similarity to phosphoprotein phosphatases	YKL225w	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to ankyrins
P7C2	strong similarity to protein kinase Kin4p	YKR106w	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to <i>Anopheles</i> mitochondrial NADH dehydrogenase subunit 2
YPL141c	strong similarity to protein kinase Mck1p	YLL066c	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to AST1 and AST2 protein
YOL128c	strong similarity to protein kinase Pak1p	YLL067c	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to ATPase Drs2p
YNL020c	strong similarity to protein kinase PAK1	YLR462w	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to ATP-dependent RNA helicases
YJR150c	strong similarity to proteins of the Srp1p/Tip1p family	YLR463c	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to <i>B. tubulin</i>
YDL214c	strong similarity to putative protein kinase NPr1	YLR464w	strong similarity to subtelomeric encoded proteins	YOL102c	weak similarity to <i>B. subtilis</i> 1,3-1,4-glucanase
YEL077c	strong similarity to putative purine nucleotide-binding protein YIL177c			YNL203c	weak similarity to <i>B. subtilis</i> CDP-diacylglycerol-serine O-phosphatidyltransferase
				YOL203c	weak similarity to <i>B. subtilis</i> hypothetical protein X
				YOL203c	weak similarity to <i>B. subtilis</i> maf protein
				YOL203c	weak similarity to <i>B. subtilis</i> nitrite reductase (nirB)
				YOL203c	weak similarity to bovine interferon γ
				YOL203c	weak similarity to <i>C. burnetii</i> FMU protein
				YOL203c	weak similarity to <i>C. elegans</i> dom-3 protein
				YOL203c	weak similarity to <i>C. elegans</i> hypothetical protein
				YOL203c	weak similarity to <i>C. elegans</i> ZK63.2
				YOL203c	weak similarity to <i>C. elegans</i> R05H5.5 protein and <i>T. borreli</i> apocytochrome b

YKL037w	weak similarity to <i>C. elegans</i> ubc-2 protein	YNR061c	weak similarity to hypothetical protein YDL218w	YNR022c	weak similarity to protein phosphatases
YHR012w	<i>PEP11</i> weak similarity to <i>C. elegans</i> Z47357_A	YOR004w	weak similarity to hypothetical protein YDR339c	YBR276c	weak similarity to protein-tyrosine-phosphatase
YJR024c	weak similarity to <i>C. elegans</i> Z49131_E	YMR010w	weak similarity to hypothetical protein YDR352w	YMR241w	weak similarity to putative carrier protein RIM2
YBR086c	weak similarity to calcium and sodium channel proteins	YGR223c	weak similarity to hypothetical protein YFR021w	YJR044c	weak similarity to putative transport protein YKR103w
YGR225w	weak similarity to Cdc20p	YGR095c	weak similarity to hypothetical protein YGR195w	YBR103w	weak similarity to Pwp2p
YNR061c	weak similarity to chicken nucleolin	YHR160c	weak similarity to hypothetical protein YGR239c	YMR093w	weak similarity to Pwp2p
YMR272c	weak similarity to cytochrome b5	YGR239c	weak similarity to hypothetical protein YHR160c	YNR064c	weak similarity to <i>R. capsulatus</i> bchO protein
YEL045c	weak similarity to cytochrome c oxidase III of <i>T. brucei</i> kinetoplast	YMR299c	weak similarity to hypothetical protein YLR351c	YEL018w	weak similarity to Rad50p
YHR142w	weak similarity to cytochrome c oxidases	YKL041w	weak similarity to hypothetical protein YCR082w	YGL244w	weak similarity to Rad50p
YDL035c	weak similarity to <i>D. discoideum</i> protein tyrosine phosphatase	YMR124w	weak similarity to hypothetical protein YOR246c	YHR022c	weak similarity to RAS-related protein
YGL242c	weak similarity to <i>D. melanogaster</i> ANK protein	YPL109c	weak similarity to hypothetical protein YJL062w	YLR351c	weak similarity to rat β -alanine synthase
YPR200c	weak similarity to <i>D. melanogaster</i> cdc25 protein, and similarity to hypothetical protein YGR203w	YBR168w	weak similarity to hypothetical protein YCR082w	YCR082w	weak similarity to Rbk1p
YHL041w	weak similarity to <i>D. melanogaster</i> hypothetical protein 6	YNR014w	weak similarity to hypothetical protein YKL002w	YJL012c	weak similarity to reductases
YOR022c	weak similarity to <i>D. melanogaster</i> probable Ca^{2+} transporter rdgB	YER186c	weak similarity to hypothetical protein YMR206w	YEL012w	weak similarity to regulatory protein PHOB1
YPL229w	weak similarity to <i>D. melanogaster</i> transcription factor shn	YER129c	weak similarity to hypothetical protein YMR206w	YDL114w	weak similarity to <i>Rhizobium</i> nodulation protein nodG
YGL185c	weak similarity to dehydrogenases	YJL016w	weak similarity to hypothetical protein YLR031w	YGR068c	weak similarity to <i>S. pombe</i> Rod1p
YLR222c	weak similarity to Dip2p	YMR206w	weak similarity to hypothetical protein YLR253w	YKL107w	weak similarity to <i>S. antibioticus</i> probable oxidoreductase
YER041w	weak similarity to DNA repair protein Rad2p	YDL218w	weak similarity to hypothetical protein YLR324w	YER093c	weak similarity to <i>S. epidermidis</i> PepB protein
YOR032c	weak similarity to DNA-binding proteins	YDR339c	weak similarity to hypothetical protein YMR206w	YMR065w	weak similarity to <i>S. pombe</i> hypothetical protein SPAC13C6.03
YJL162c	weak similarity to dnaJ proteins	YLR253w	weak similarity to hypothetical protein YLR187w	YGR212w	weak similarity to <i>S. pombe</i> hypothetical protein SPAC18B11.03c
YBR220c	weak similarity to <i>E. coli</i> ampG protein	YPR151c	weak similarity to hypothetical protein YMR206w	YER127w	weak similarity to <i>S. pombe</i> hypothetical protein SPAC18B11.06
YNL217w	weak similarity to <i>E. coli</i> bis(5'-nucleosyl)-tetraphosphatase	YPL159c	weak similarity to hypothetical protein YMR206w	YBR271w	weak similarity to <i>S. pombe</i> uvi22 protein and hypothetical protein YNL024c
YER126c	weak similarity to <i>E. coli</i> colicin N	YER159c	weak similarity to hypothetical protein YMR206w	YLR311c	weak similarity to <i>S. tarentiae</i> cryptogene protein G4
YGL136c	weak similarity to <i>E. coli</i> ftsI protein	YPR151c	weak similarity to hypothetical protein YMR206w	YLR380w	weak similarity to Sec14p
YKL094w	<i>YJU3</i> weak similarity to <i>E. coli</i> hypothetical protein	YLR253w	weak similarity to hypothetical protein YMR206w	YNL231c	weak similarity to Sec14p
YMR155w	weak similarity to <i>E. coli</i> hypothetical protein f402	YPR156c	weak similarity to hypothetical protein YMR206w	YJL123c	weak similarity to Sec7p
YER152c	weak similarity to <i>E. coli</i> hypothetical protein f470	YGR126w	weak similarity to hypothetical protein YMR206w	YKL056c	weak similarity to short-chain alcohol dehydrogenases
YJR019c	weak similarity to <i>E. coli</i> thioesterase II	YLR391w	weak similarity to hypothetical proteins YMR206w and YHR214w-a	YNR030w	weak similarity to Smp3p
YPR067w	weak similarity to <i>F. alni</i> nitrogen fixation protein	YNL024c	weak similarity to hypothetical proteins YBR271w and YJR129c	YDR486c	weak similarity to Snf7p
YDR063w	weak similarity to glia maturation factor β	YAL018c	weak similarity to hypothetical proteins YOL047c and YOL048c	YEL015w	weak similarity to Spa2p
YCL028w	weak similarity to glutaminines, high molecular weight subunit	YDR352w	weak similarity to hypothetical proteins YOL092w, YBR147w and YMR010w	YHR177w	weak similarity to Spombe pac2 protein
YPL206c	weak similarity to glycerophosphoryl ester phosphodiesterases	YDR517w	weak similarity to hypothetical proteins YOL092w, YBR147w and YMR010w	YJR101w	weak similarity to stress-induced St1p
YOR272w	weak similarity to GTP-binding protein β subunits	YCR013c	weak similarity to hypothetical proteins YOL092w, YBR147w and YMR010w	YBR099c	weak similarity to superoxide dismutases
YAL048c	weak similarity to GTP-binding proteins	YPL273w	weak similarity to hypothetical proteins YOL092w, YBR147w and YMR010w	YJL145w	weak similarity to <i>T. brucei</i> mitochondrial hypothetical protein 6
YBR175w	weak similarity to GTP-binding proteins	YDR517w	weak similarity to hypothetical proteins YOL092w, YBR147w and YMR010w	YJL204c	weak similarity to <i>T. pacificus</i> retinal-binding protein
YPL093w	weak similarity to GTP-binding proteins	YDR517w	weak similarity to hypothetical proteins YOL092w, YBR147w and YMR010w	YER045c	weak similarity to Tor2p
YGL067w	weak similarity to <i>H. influenzae</i> hypothetical protein	YCR013c	weak similarity to <i>M. leprae</i> B1496_F1_41 protein	YDR520c	weak similarity to transcription factors
YLR165c	weak similarity to <i>H. influenzae</i> hypothetical protein HI0176	YPL273w	weak similarity to <i>M. leprae</i> meth2 protein, and strong similarity to hypothetical protein YLL062c	YHR063c	weak similarity to translational activator CBS2
YLR239c	weak similarity to <i>H. influenzae</i> lipote biosynthesis protein B	YEL043w	weak similarity to Mad1p	YGL004c	weak similarity to Tup1p
YNR062c	weak similarity to <i>H. influenzae</i> L-lactate permease (lctP) homologue	YBR186w	weak similarity to members of CDC48/PAS1/SEC18 family of ATPases	YJR046w	weak similarity to <i>Xenopus</i> vimentin 4
YNL176c	weak similarity to Hkr1p	YFL046w	weak similarity to middle part of <i>C. elegans</i> myosin heavy chain A	YOL031c	weak similarity to <i>Y. lipolytica</i> Sl1 protein
YBL032w	weak similarity to hnRNP complex protein homologue YBR233w	YOR350c	weak similarity to mitochondrial <i>L. illistris</i> cytochrome oxidase I	YLL056c	weak similarity to <i>Y. pseudotuberculosis</i> CDP-3,6-dideoxy-L-glycero-4-hexulose-5-epimerase
YER033c	weak similarity to human BRCA2 early onset breast cancer gene	MNE1	weak similarity to MSN1 protein	YCL063w	weak similarity to yeast translation regulator Gcd6p
YIL036w	weak similarity to human cAMP response element-binding protein	YMR111c	weak similarity to MSN1 protein	YGR110w	weak similarity to YLR099c and YDR125c
YJL148w	weak similarity to human chromatin assembly factor I	YMR172w	weak similarity to mucin	YDR090c	weak similarity to Yro2p
YDR030c	weak similarity to human CSA protein	YDL223c	weak similarity to Mvp1p	YIL044c	weak similarity to zinc-finger protein GCS1
YGL243w	weak similarity to human double-stranded RNA adenosine deaminase	YJL036w	weak similarity to <i>Mycoplasma</i> protoporphyrinogen oxidase	YLR040c	weak similarity to hypothetical protein YIL011w
YJL091c	weak similarity to human G protein-coupled receptor	YNR022c	weak similarity to myosin heavy chains	YNL212w	weak similarity to <i>C. cardunculus</i> cypro4 protein
YER063w	weak similarity to human heterogeneous ribonuclear particle protein U	YLR309c	weak similarity to myosins		
YJR002w	weak similarity to human kinesin-related protein CENP-E	IMH1	weak similarity to Na $^+$ /H $^+$ antiporter		
YMR029c	weak similarity to human nuclear autoantigen	YBR156c	weak similarity to NADH dehydrogenase		
YCL045c	weak similarity to human ORF	YAL022c	weak similarity to NADH dehydrogenases		
YJL057c	weak similarity to human P1/eIF-2a protein kinase	YDR413c	weak similarity to Nbp1p		
YNR008w	weak similarity to human phosphatidylcholine-sterol O-acyltransferase	YKR030w	weak similarity to negative regulator Srn1p/Hex2p		
YJL132w	weak similarity to human phospholipase D	YPR174c	weak similarity to N-methyltransferases		
YLL037w	weak similarity to human platelet-activating factor receptor	YKR075c	weak similarity to non-epidermal <i>Xenopus</i> keratin, type I		
YHR090c	weak similarity to human retinoblastoma binding protein 2	YCR047c	weak similarity to nuclear protein NOP4		
YOR064c	weak similarity to human retinoblastoma binding protein 2	YJL131c	weak similarity to <i>P. aeruginosa</i> anthranilate synthase component II		
YMR131c	weak similarity to human retinoblastoma-binding protein	YHL024w	weak similarity to <i>P. aeruginosa</i> regulatory protein mmsR		
YLR272c	weak similarity to hypothetical human ORF	YLR126c	weak similarity to <i>P. aeruginosa</i> regulatory protein mmsR		
YDL111c	weak similarity to hypothetical human protein	YMR009w	weak similarity to <i>P. aeruginosa</i> regulatory protein mmsR		
YCR059c	weak similarity to hypothetical protein YDL177c	YGR276c	weak similarity to <i>P. aeruginosa</i> regulatory protein mmsR		
		YER059w	weak similarity to <i>P. aeruginosa</i> regulatory protein mmsR		
		YOR281c	weak similarity to <i>P. aeruginosa</i> regulatory protein mmsR		
		YMR221c	weak similarity to <i>P. aeruginosa</i> regulatory protein mmsR		
		YBR094w	weak similarity to <i>P. aeruginosa</i> regulatory protein mmsR		
		YOR287c	weak similarity to <i>PITSLRE</i> protein kinase isoforms		
		YBR151w	weak similarity to potato sucrose cleavage protein		
		YML050w	weak similarity to potato sucrose cleavage protein		
		YGR262c	weak similarity to protein kinases		
		YPR106w	weak similarity to protein kinases		