

**Supplementary Table 3. List of identified proteins according to their biological function** <sup>a,b</sup>

**CARBON METABOLISM**

	<b>Glycolysis/gluconeogenesis</b>				
YGR254W	<b>ENO1</b>	enolase 1	YDR234W	<b>LYS4</b>	homoaconitase
YHR174W	<b>ENO2</b>	enolase 2	YNR050C	<b>LYS9</b>	saccharopine DHase
YKL060C	<b>FBA1</b>	fructose-biphosphate aldolase	YOR323C	<b>PRO2</b>	phosphoglutarate DHase
YLR377C	<b>FBP1</b>	fructose-1,6-bisphosphatase	YER023W	<b>PRO3</b>	pyrroline-5-carboxylate reductase
YCL040W	<b>GLK1</b>	glucokinase		<b>Aspartate family</b>	
YFR053C	<b>HXK1</b>	hexokinase PI	YPR145W	<b>ASN1</b>	asparagine Sase 1
YGL253W	<b>HXK2</b>	hexokinase PII	YGR124W	<b>ASN2</b>	asparagine Sase 2
YKR097W	<b>PCK1</b>	phosphoenol pyruvate carboxykinase	YJR137C	<b>ECM17</b>	sulfite reductase beta sub
YGR240C	<b>PFK1</b>	phosphofructokinase alpha-sub	YDR158W	<b>HOM2</b>	aspartate-semialdehyde DHase
YMR205C	<b>PFK2</b>	phosphofructokinase beta-sub	YER052C	<b>HOM3</b>	aspartate kinase
YBR196C	<b>PGI1</b>	phosphoglucoisomerase	YJR139C	<b>HOM6</b>	homoserine DHase
YJR009C	<b>TDH2</b>	glyceraldehyde-3-P-DHase	YFR030W	<b>MET10</b>	sulfite reductase alpha sub
YGR192C	<b>TDH3</b>	glyceraldehyde-3-P-DHase	YGL125W	<b>MET13</b>	methylene tetrahydrofolate reductase
YDR050C	<b>TPI1</b>	triose-P isomerase	YPR167C	<b>MET16</b>	3'-phosphoadenylsulfate reductase
	<b>Fermentation</b>		YLR303W	<b>MET17</b>	O-acetylhomoserine-O-acetylserine sulfhydrylase
YOL086C	<b>ADH1</b>	alcohol DHase I	YJR010W	<b>MET3</b>	ATP-sulfurylase
YGL256W	<b>ADH4</b>	alcohol DHase IV	YER091C	<b>MET6</b>	homocysteine methyltransferase
YLR044C	<b>PDC1</b>	pyruvate decarboxylase	YLR180W	<b>SAM1</b>	S-adenosylmethionine Sase 1
YLR134W	<b>PDC5</b>	pyruvate decarboxylase	YDR502C	<b>SAM2</b>	S-adenosylmethionine Sase 2
	<b>Pentose-phosphate shunt</b>		YPL273W	<b>SAM4</b>	S-adenosylmethionine homocysteine methyltransferase
YHR183W	<b>GND1</b>	6-phosphogluconate DHase	YHR025W	<b>THR1</b>	homoserine kinase
YLR354C	<b>TAL1</b>	transaldolase	YCR053W	<b>THR4</b>	threonine Sase
YPR074C	<b>TKL1</b>	transketolase 1		<b>Pyruvate family</b>	
YBR117C	<b>TKL2</b>	transketolase 2	YMR108W	<b>ILV2</b>	acetolactate Sase
YNL241C	<b>ZWF1</b>	glucose-6-P DHase	YLR355C	<b>ILV5</b>	acetoxyhydroxyacid reductoisomerase
	<b>Tricarboxylic acid cycle</b>		YCL009C	<b>ILV6</b>	acetolactate Sase regulatory sub
YLR304C	<b>ACO1</b>	aconitase	YGL009C	<b>LEU1</b>	isopropylmalate isomerase
YJL200C	<b>ACO2</b>	aconitase	YCL018W	<b>LEU2</b>	beta-isopropylmalate DHase
YNR001C	<b>CIT1</b>	mitochondrial citrate Sase	YNL104C	<b>LEU4</b>	2-isopropylmalate Sase2
YIL125W	<b>KGD1</b>	2-oxoglutarate DHase complex (E1)		<b>Glycine-serine family/ sulfur metabolism</b>	
YDR148C	<b>KGD2</b>	2-oxoglutarate DHase complex (E2)	YAL012W	<b>CYS3</b>	cystathionine gamma-lyase
YGR244C	<b>LSC2</b>	succinate-CoA ligase, beta-sub	YGR155W	<b>CYS4</b>	cystathionine beta-Sase
YKL085W	<b>MDH1</b>	mitochondrial malate DHase	YEL046C	<b>GLY1</b>	threonine aldolase
YKL148C	<b>SDH1</b>	succinate DHase	YOR184W	<b>SER1</b>	phosphoserine transaminase
	<b>Routes towards Krebs cycle</b>		YGR208W	<b>SER2</b>	phosphoserine phosphatase
YAL054C	<b>ACS1</b>	acetyl-CoA Sase	YER081W	<b>SER3</b>	3-phosphoglycerate DHase
YLR153C	<b>ACS2</b>	acetyl-CoA Sase	YIL074C	<b>SER33</b>	3-phosphoglycerate DHase
YMR303C	<b>ADH2</b>	alcohol DHase II		<b>Aromatic amino acid family</b>	
YMR169C	<b>ALD3</b>	aldehyde DHase	YDR127W	<b>ARO1</b>	Arom pentafunctional enzyme
YOR374W	<b>ALD4</b>	aldehyde DHase mito	YBR249C	<b>ARO4</b>	2-dehydro-3-deoxy-phosphoheptone aldolase
YPL061W	<b>ALD6</b>	aldehyde DHase	YDR007W	<b>TRP1</b>	phosphoribosylanthranilate isomerase
YDL174C	<b>DLA1</b>	D-lactate DHase	YER090W	<b>TRP2</b>	anthranilate Sase (component 1)
YLR174W	<b>IDP2</b>	isocitrate DHase, cytosolic	YKL211C	<b>TRP3</b>	anthranilate Sase (component 2)
YNL071W	<b>LAT1</b>	dihydroliipoamide acetyltransferase	YDR354W	<b>TRP4</b>	anthranilate Pr transferase
YFL018C	<b>LPD1</b>	dihydroliipoamide DHase	YGL026C	<b>TRP5</b>	tryptophan Sase
YOL126C	<b>MDH2</b>	cytosolic malate DHase		<b>Histidine</b>	
YER178W	<b>PDA1</b>	pyruvate DHase complex E1-alpha sub	YER055C	<b>HIS1</b>	ATP Pr transferase
YBR221C	<b>PDB1</b>	pyruvate DHase complex E1-beta sub	YOR202W	<b>HIS3</b>	imidazoleglycerol-P dehydratase
YGL062W	<b>PYC1</b>	pyruvate carboxylase 1	YCL030C	<b>HIS4</b>	trifunctional enzyme
YBR218C	<b>PYC2</b>	pyruvate carboxylase 2	YIL116W	<b>HIS5</b>	histidinol-P aminotransferase
	<b>Glyoxylate cycle</b>		YBR248C	<b>HIS7</b>	glutamine amidotransferase
YCR005C	<b>CIT2</b>	citrate Sase		<b>Polyamines</b>	
YIR031C	<b>DAL7</b>	malate Sase 2	YKL184W	<b>SPE1</b>	ornithine decarboxylase
YER065C	<b>ICL1</b>	isocitrate lyase	YOL052C	<b>SPE2a</b>	S-adenosylmethionine decarboxylase alpha chain
YNL117W	<b>MLS1</b>	malate Sase 1	YPR069C	<b>SPE3</b>	spermidine Sase
	<b>Cellular respiration</b>		YLR146C	<b>SPE4</b>	spermine Sase
YJR121W	<b>ATP2</b>	F1-ATP Sase beta-sub		<b>Nucleotides</b>	
YBL045C	<b>COR1</b>	ubiquinol cyt-c reductase core prt		<b>Purine nucleotides</b>	
YPR191W	<b>QCR2</b>	ubiquinol cytochrome c reductase core prt 2	YAR015W	<b>ADE1</b>	SAICAR Sase
YEL024W	<b>RIP1</b>	ubiquinol cytochrome c reductase iron-sulfur prt	YLR359W	<b>ADE13</b>	adenylosuccinate lyase
	<b>Others</b>		YLR028C	<b>ADE16</b>	AICAR transformylase
YBR149W	<b>ARA1</b>	D-arabinose DHase	YMR120C	<b>ADE17</b>	bifunctional enzyme
YDL178W	<b>DLA2</b>	D-lactate DHase, mitochondrial	YOR128C	<b>ADE2</b>	Pr-amino-imidazole carboxylase
YEL071W	<b>DLA3</b>	D-lactate DHase	YMR300C	<b>ADE4</b>	amido-Pr transferase
YEL047C	<b>FRD51</b>	fumarate reductase	YGL234W	<b>ADE5,7</b>	GAR Sase + AIR Sase.
YKL029C	<b>MAE1</b>	mitochondrial malate DHase	YGR061C	<b>ADE6</b>	5'-Pr-formyl glycinamide Sase
YER003C	<b>PMI40</b>	mannose-6-P isomerase	YDR226W	<b>ADK1</b>	adenylate kinase
YCR036W	<b>RBK1</b>	ribokinase	YJR105W	<b>ADO1</b>	Adenosine kinase
			YML022W	<b>APT1</b>	adenine Pr transferase
			YMR217W	<b>GUA1</b>	GMP Sase
			YDR454C	<b>GUK1</b>	guanylate kinase
			YHR216W	<b>IMD2</b>	inosine-5'-monoP DHase
			YDR399W	<b>HPT1</b>	hypoxanthine-guanine phosphoribosyl transferase
			YJR133W	<b>XPT1</b>	xanthine phosphoribosyl transferase
				<b>Pyrimidine nucleotides</b>	
			YHR128W	<b>FUR1</b>	uracil phosphoribosyltransferase
			YKL216W	<b>URA1</b>	dihydroorotate DHase
			YJL130C	<b>URA2</b>	multifunctional prt of pyrimidine biosynthesis pathway
			YEL021W	<b>URA3</b>	OMP decarboxylase
			YLR420W	<b>URA4</b>	dihydroorotate
			YML106W	<b>URA5</b>	orotate phosphoribosyltransferase
			YBL039C	<b>URA7</b>	CTP Sase
				<b>Others</b>	
			YER070W	<b>RNR1</b>	ribonucleotide reductase large sub
			YGR180C	<b>RNR4</b>	ribonucleotide reductase small sub
				<b>Sugars and sugar nucleotides</b>	
			YMR105C	<b>PGM2</b>	phosphoglycerate mutase
			YBR126C	<b>TPS1</b>	trehalose-6-P Sase sub
			YKL035W	<b>UGP1</b>	UDP-glucose pyrophosphorylase

**BIOSYNTHESIS OF SMALL MOLECULES**

	<b>Amino acids</b>				
	<b>Glutamate family/nitrogen assimilation</b>				
YOL058W	<b>ARG1</b>	argininosuccinate Sase			
YJL088W	<b>ARG3</b>	ornithin carbamoyl transferase			
YHR018C	<b>ARG4</b>	arginosuccinate lyase	YHR128W		
YER069W	<b>ARG5</b>	acetylglutamate kinase	YKL216W		
YER069W	<b>ARG6</b>	acetylglutamyl-P reductase	YJL130C		
YMR062C	<b>ARG7</b>	ornithine acetyltransferase	YEL021W		
YOL140W	<b>ARG8</b>	acetylornithine aminotransferase	YLR420W		
YOR303W	<b>CPA1</b>	carbamoyl-P Sase, small sub	YML106W		
YJR109C	<b>CPA2</b>	carbamoyl-P Sase, large sub	YBL039C		
YOR375C	<b>GDH1</b>	NADP-dependent glutamate DHase			
YAL062W	<b>GDH3</b>	NADP-dependent glutamate DHase 2	YER070W		
YPR035W	<b>GLN1</b>	glutamine Sase	YGR180C		
YIL094C	<b>LYS12</b>	homocitrate DHase			
YBR115C	<b>LYS2</b>	alpha-aminoadipate reductase	YMR105C		
YDL182W	<b>LYS20</b>	homocitrate Sase	YBR126C		
YDL131W	<b>LYS21</b>	homocitrate Sase	YKL035W		

**Cofactors and prosthetic groups**

YGR204W	<b>ADE3</b>	C1-tetrahydrofolate Sase
YJR025C	<b>BNA1</b>	3-hydroxyanthranilate 3,4-dioxygenase
YML110C	<b>COQ5</b>	coenzyme Q biosynthesis 5
YOR209C	<b>NPT1</b>	nicotinate phosphoribosyltransferase
YDR487C	<b>RIB3</b>	3,4-dihydroxy-2-butanone 4-phosphate Sase
YOL143C	<b>RIB4</b>	6,7-dimethyl-8-ribityllumazine Sase
YBR256C	<b>RIB5</b>	riboflavin Sase
YOL055C	<b>THI20</b>	hydroxymethylpyrimidine phosphate kinase
YPR121W	<b>THI22</b>	hydroxymethylpyrimidine phosphate kinase
YGR144W	<b>THI4</b>	thiamine repressed prt
YPL214C	<b>THI6</b>	thiamine-P pyrophosphorylase and 4-methyl-5-beta-hydroxyethylthiazole kinase activities

**Fatty acids and lipids**

YBL015W	<b>ACH1</b>	acetyl-CoA hydrolase
YNR043W	<b>ERG19</b>	mevalonate diP decarboxylase
YML008C	<b>ERG6</b>	SAM-24-sterol-C-methyltransferase
YPL231W	<b>FAS2</b>	fatty-acyl-CoA Sase, sub
YPL117C	<b>IDI1</b>	IPP isomerase
YJL153C	<b>INO1</b>	myo-inositol-1-P Sase
YPL145C	<b>KES1</b>	prt involved in ergosterol biosynthesis

## MACROMOLECULE METABOLISM

**Protein synthesis and modification**

**Ribosomal proteins**

YMR116C	<b>ASC1</b>	ribosomal prt of the 40S sub
YKL142W	<b>MRP8</b>	mitochondrial ribosomal prt of the 40S sub
YPL131W	<b>RLP1</b>	ribosomal prt
YLR340W	<b>RPP0</b>	ribosomal prt
YOL039W	<b>RPP2A</b>	ribosomal prt
YDR382W	<b>RPP2B</b>	ribosomal prt
YGR214W	<b>RPS0A</b>	ribosomal prt of the 40S sub
YLR048W	<b>RPS0B</b>	ribosomal prt of the 40S sub
YOR369C	<b>RPS12</b>	ribosomal prt
YJR123W	<b>RPS5</b>	ribosomal prt

**Aminoacyl-tRNA synthetases**

YOR335C	<b>ALA1</b>	alanyl-tRNA Sase
YPL160W	<b>CDC60</b>	leucyl-tRNA Sase
YHR019C	<b>DED81</b>	asparaginyl-tRNA Sase
YLL018C	<b>DPS1</b>	apartyl-tRNA Sase
YLR060W	<b>FRS1</b>	phenylalanyl-tRNA Sase, alpha-sub
YFL022C	<b>FRS2</b>	phenylalanyl-tRNA Sase, beta -sub
YBR121C	<b>GRS1</b>	glycyl-tRNA Sase
YPR033C	<b>HTS1</b>	histidyl-tRNA Sase
YDR037W	<b>KRS1</b>	lysyl-tRNA Sase
YGR264C	<b>MES1</b>	methionyl-tRNA Sase
YDR023W	<b>SES1</b>	seryl-tRNA Sase
YIL078W	<b>THS1</b>	threonyl-tRNA Sase
YOL097C	<b>WRS1</b>	tryptophanyl-tRNA Sase
YDR341C	<b>YDR341C</b>	arganyl-tRNA Sase
YHR020W	<b>YHR020W</b>	putative prolyl-tRNA Sase

**Protein translation**

YAL003W	<b>EFB1</b>	translation elongation factor EF-1beta
YOR133W	<b>EFT1</b>	translation elongation factor EF-2
YLR192C	<b>HCR1</b>	putative component of translation initiation factor eIF3
YLR069C	<b>MEF1</b>	mitochondrial elongation factor G
YOR361C	<b>PRT1</b>	translation initiation factor eIF3 (sub)
YBR143C	<b>SUP45</b>	translational release factor ERF1
YKR059W	<b>TIF1</b>	translation initiation factor eIF4A
YMR260C	<b>TIF11</b>	translation initiation factor eIF1A
YPR163C	<b>TIF3</b>	translation initiation factor eIF4B
YMR146C	<b>TIF34</b>	translation initiation factor eIF3 (sub)
YDR429C	<b>TIF35</b>	translation initiation factor eIF3 (sub)
YOL139C	<b>TIF45</b>	translation initiation factor eIF4E
YPR041W	<b>TIF5</b>	translation initiation factor eIF5
YEL034W	<b>TIF51A</b>	translation initiation factor eIF5A
YPR016C	<b>TIF6</b>	translation initiation factor eIF6
YOR187W	<b>TUF1</b>	mitochondrial elongation factor
YLR249W	<b>YEF3</b>	translation elongation factor EF-3

**Protein folding**

YMR038C	<b>CCS1</b>	copper chaperone for Sod1p
YDR212W	<b>CCT1</b>	chaperonin-containing T-complex (sub)
YIL142W	<b>CCT2</b>	chaperonin-containing T-complex (sub)
YJL014W	<b>CCT3</b>	chaperonin-containing T-complex (sub)
YJR064W	<b>CCT5</b>	chaperonin-containing T-complex (sub)
YDR188W	<b>CCT6</b>	chaperonin-containing T-complex (sub)
YJL111W	<b>CCT7</b>	chaperonin-containing T-complex (sub)
YJL008C	<b>CCT8</b>	chaperonin-containing T-complex (sub)
YMR186W	<b>HSC82</b>	chaperonin
YLL026W	<b>HSP104</b>	heat shock prt
YBR072W	<b>HSP26</b>	heat shock prt
YLR259C	<b>HSP60</b>	heat shock prt
YDR258C	<b>HSP78</b>	heat shock prt, mitochondrial
YPL240C	<b>HSP82</b>	heat shock prt
YJL034W	<b>KAR2</b>	heat shock prt
YOR232W	<b>MGE1</b>	prt folding, mitochondrial
YKL117W	<b>SBA1</b>	Ste5p-associated prt
YAL005C	<b>SSA1</b>	heat shock prt (HSP70 family)
YLL024C	<b>SSA2</b>	heat shock prt (HSP70 family)
YBL075C	<b>SSA3</b>	heat shock prt (HSP70 family)
YER103W	<b>SSA4</b>	heat shock prt (HSP70 family)
YDL229W	<b>SSB1</b>	heat shock prt (HSP70 family)

YNL209W	<b>SSB2</b>	heat shock prt (HSP70 family)
YJR045C	<b>SSC1</b>	heat shock prt (HSP70 family)
YPL106C	<b>SSE1</b>	heat shock prt (HSP70 family)
YOR027W	<b>STI1</b>	stress induced prt
YNL064C	<b>YDJ1</b>	prt import into mito. and ER

**Protein modification**

YHR013C	<b>ARD1</b>	N-acetyltransferase sub
YDR155C	<b>CPR1</b>	peptidyl-prolyl cis-trans isomerase
YDR304C	<b>CPR5</b>	peptidyl-prolyl cis-trans isomerase
YLR172C	<b>DPH5</b>	diphthamide methyltransferase
YHR068W	<b>DYS1</b>	deoxyhypusine Sase
YEL056W	<b>HAT2</b>	histone acetyltransferase sub
YBR034C	<b>HMT1</b>	HnRNP methyltransferase 1
YJR070C	<b>LIA1</b>	deoxyhypusine hydroxylase
YCL043C	<b>PD11</b>	prt disulfide isomerase
YDL236W	<b>PHO13</b>	4-Nitrophenylphosphatase
YDL055C	<b>PSA1</b>	mannose-1-phosphate guanyltransferase

**RNA synthesis, modification and DNA transcription**

YPL037C	<b>EGD1</b>	Gal4 enhancer prt
YHR193C	<b>EGD2</b>	Gal4 enhancer prt
YDR432W	<b>NPL3</b>	prt involved in pre-rRNA processing
YER165W	<b>PAB1</b>	poly(A)-binding prt
YBR088C	<b>POL30</b>	polymerase 30
YNL016W	<b>PUB1</b>	polyadenylated RNA-binding prt
YHL034C	<b>SBP1</b>	single-stranded nucleic acid-binding prt
YDL084W	<b>SUB2</b>	essential pre-mRNA splicing factor
YOR230W	<b>WTM1</b>	transcriptional modulator

**Macromolecule catabolism**

**Proteins**

YJL172W	<b>CPS1</b>	Gly-X carboxypeptidase yscS
YBL091C	<b>MAP2</b>	methionine aminopeptidase isoform 2
YPL154C	<b>PEP4</b>	protease A
YBL022C	<b>PIM1</b>	ATP-dependent protease
YEL060C	<b>PRB1</b>	protease B
YCL057W	<b>PRD1</b>	proteinase yscD (saccharolysin)
YER012W	<b>PRE1</b>	proteasome sub
YPR103W	<b>PRE2</b>	proteasome sub
YJL001W	<b>PRE3</b>	proteasome sub
YFR050C	<b>PRE4</b>	proteasome sub
YMR314W	<b>PRE5</b>	proteasome sub
YOL038W	<b>PRE6</b>	proteasome sub
YBL041W	<b>PRE7</b>	proteasome sub
YML092C	<b>PRE8</b>	proteasome sub
YGR135W	<b>PRE9</b>	proteasome sub
YOR157C	<b>PUP1</b>	proteasome sub
YGR253C	<b>PUP2</b>	proteasome sub
YER094C	<b>PUP3</b>	proteasome sub
YHR200W	<b>RPN10</b>	proteasome sub
YFR052W	<b>RPN12</b>	proteasome sub
YDL097C	<b>RPN6</b>	proteasome sub
YKL145W	<b>RPT1</b>	proteasome sub
YDR394W	<b>RPT3</b>	proteasome sub
YOR259C	<b>RPT4</b>	proteasome sub
YOR117W	<b>RPT5</b>	proteasome sub
YGL011C	<b>SCL1</b>	proteasome sub
YKL210W	<b>UBA1</b>	ubiquitin-activating enzyme
YBR082C	<b>UBC4</b>	ubiquitin-conjugating enzyme

**Amino acids**

YDR380W	<b>ARO10</b>	phenylpyruvate decarboxylase
YGL202W	<b>ARO8</b>	aromatic amino acid aminotransferase I
YHR137W	<b>ARO9</b>	aromatic amino acid aminotransferase II
YPL111W	<b>CAR1</b>	arginase
YLR438W	<b>CAR2</b>	ornithine aminotransferase
YHR037W	<b>PUT2</b>	delta-1-pyrroline-5-carboxylate dehydrogenase
YER043C	<b>SAH1</b>	adenosylhomocysteinase

**Purine**

YNL141W	<b>AAH1</b>	adenine deaminase
---------	-------------	-------------------

## CYTOSKELETON ORGANIZATION

YCR088W	<b>ABP1</b>	actin binding prt
YFL039C	<b>ACT1</b>	actin
YDL029W	<b>ARP2</b>	actin-related prt
YJR065C	<b>ARP3</b>	actin-related prt
YNL059C	<b>ARP5</b>	actin-related prt
YIL034C	<b>CAP2</b>	actin-capping prt 2
YLL050C	<b>COF1</b>	cofilin
YDR388W	<b>RVS167</b>	prt involved in actin distribution
YNL189W	<b>SRP1</b>	karyopherin-alpha
YNL138W	<b>SRV2</b>	adenylate cyclase-associated prt
YNL079C	<b>TPM1</b>	tropomyosine
YML085C	<b>TUB1</b>	tubulin alpha 1-chain
YFL037W	<b>TUB2</b>	tubulin beta chain
YML124C	<b>TUB3</b>	tubulin alpha 3-chain

## CELLULAR PROCESSES

**Response to stress**

YGR088W	<b>CTT1</b>	catalase T1
YML070W	<b>DAK1</b>	dihydroxyacetone kinase
YOL151W	<b>GRE2</b>	alpha-acetoxy ketone reductase
YHR104W	<b>GRE3</b>	aldo/keto reductase with NADPH specificity

	<b>Response to heat</b>		YDR190C	<b>RVB1</b>	sub of the Swr1p-containing (SWR-C) complex
YER133W	<b>GLC7</b>	prt serine/threonine phosphatase	YPL235W	<b>RVB2</b>	sub of the Swr1p-containing (SWR-C) complex
YPL004C	<b>LSP1</b>	negative regulator of Pkh1p and downstream effectors		<b>Others</b>	
YGR086C	<b>PIL1</b>	regulator of Pkh1p activity	YCL050C	<b>APA1</b>	AP4A phosphorylase
	<b>Response to oxidative stress</b>		YAL060W	<b>BDH1</b>	stereospecific (2R, 3R)-2,3-butanediol DHase
YKR066C	<b>CCP1</b>	cytochrome-c peroxidase	YGR282C	<b>BGL2</b>	endo-beta-1,3-glucanase
YDR098C	<b>GRX3</b>	glutaredoxin	YER177W	<b>BMH1</b>	brain modulosignalin homolog 1
YJR104C	<b>SOD1</b>	copper-zinc superoxide dismutase	YDR099W	<b>BMH2</b>	brain modulosignalin homolog 2
YHR008C	<b>SOD2</b>	manganese superoxide dismutase		<b>CAPSID</b>	capside prt of virus L-A
	<b>Response to osmotic stress</b>		YDR168W	<b>CDC37</b>	cell cycle prt
YDL022W	<b>GPD1</b>	glycerol-3-P DHase	YMR276W	<b>DSK2</b>	prt required for duplication of spindle pole body
YER062C	<b>HOR2</b>	DL-glycerol phosphatase		<b>GAG</b>	major coat prt of virus L-A
YIL053W	<b>RHR2</b>	DL-glycerol-3-phosphatase	YFR009W	<b>GCN20</b>	required for activation of Gcn2 prt kinase
	<b>Cell redox homeostasis</b>		YDL125C	<b>HNT1</b>	adenosine monophosphoramidase
YLR109W	<b>AHP1</b>	alkyl hydroperoxide reductase	YBR011C	<b>IPP1</b>	inorganic pyrophosphatase
YDR353W	<b>TRR1</b>	thioredoxin reductase	YDL044C	<b>MTF2</b>	mitochondrial prt/mRNA splicing and prt synthesis
YML028W	<b> TSA1</b>	thiol specific antioxidant	YHR179W	<b>OYE2</b>	NADPH DHase (old yellow enzyme)
	<b>Glutathione metabolism</b>		YHR064C	<b>PDR13</b>	pleiotropic drug resistance prt
YML004C	<b>GLO1</b>	glyoxalase I	YEL037C	<b>RAD23</b>	nucleotide excision repair prt
YIR038C	<b>GTT1</b>	glutathione transferase	YMR131C	<b>RRB1</b>	prt involved in ribosome assembly
	<b>Vacuolar acidification</b>		YJL080C	<b>SCP160</b>	mitotic chromosomal transmission
YDL126C	<b>CDC48</b>	putative ATPase	YDL168W	<b>SFA1</b>	long chain alcohol DHase
YDL185W	<b>VMA1</b>	vacuolar H-ATPase catalytic sub	YHL058W	<b>SHP1</b>	adaptor for Cdc48p-mediated prt degradation
YBR127C	<b>VMA2</b>	vacuolar H-ATPase regulatory sub	YLR178C	<b>TFS1</b>	cell cycle regulator
YOR332W	<b>VMA4</b>	vacuolar H-ATPase hydrophilic sub	YLR222C	<b>UTP13</b>	component of the 80S U3 snoRNA complex
YLR447C	<b>VMA6</b>	vacuolar H-ATPase catalytic sub	YGR234W	<b>YHB1</b>	flavo-hemoglobin
YEL051W	<b>VMA8</b>	vacuolar H-ATPase catalytic sub			
	<b>Transport</b>				
	<b>Nucleocytoplasmic transport</b>		YDR516C	<b>EMI2</b>	early meiotic induction 2
YER036C	<b>ARB1</b>	ABC prt involved in ribosome biogenesis	YHR049W	<b>FSH1</b>	dihydrofolate reductase activity
YLR293C	<b>GSP1</b>	GTP-binding prt of the ras superfamily	YIL041W	<b>GVP36</b>	golgi vesicle prt of 36 kDa
YOR185C	<b>GSP2</b>	GTP-binding prt of the ras superfamily	YJR069C	<b>HAM1</b>	prt controlling 6-N-hydroxylaminopurine sensitivity
YER009W	<b>NTF2</b>	nuclear transport factor	YNL123W	<b>NMA111</b>	putative serine protease
YLL034C	<b>RIX7</b>	putative ATPase involved in rib. large subunit export	YDR032C	<b>PST2</b>	similarity to YCP4P and S. pombe prt
YNL229C	<b>URE2</b>	regulator of nitrogen catabolite repression	YCL028W	<b>RNQ1</b>	prt required for resistance to certain drugs
YDR002W	<b>YRB1</b>	nuclear prt transport and RNA export	YOR007C	<b>SGT2</b>	prt containing six tetratricopeptide repeats
	<b>Golgi vesicle transport</b>		YGR229C	<b>SMI1</b>	molecular function unknown
YDL226C	<b>GCS1</b>	GTPase-activating prt	YMR096W	<b>SNZ1</b>	putative pyridoxine (vitamin B6) biosynthetic enzyme
YDL100C	<b>GET3</b>	ATPase, subunit of the GET complex	YNL333W	<b>SNZ2</b>	putative pyridoxine (vitamin B6) biosynthetic enzyme
YPL218W	<b>SAR1</b>	GTP-binding prt of ras superfamily	YKL056C	<b>TMA19</b>	translationally-controlled tumor prt homolog
YMR079W	<b>SEC14</b>	(PI/PC) transfer prt	YER049W	<b>TPA1</b>	prt associated with the mRNA cap-binding/eIF4F complex
YBL050W	<b>SEC17</b>	prt involved in secretory pathway	YPL239W	<b>YAR1</b>	involved in resistance to environmental stress
YPR181C	<b>SEC23</b>	involved in endoplasmic reticulum to Golgi transport	YBL036C	<b>YBL036C</b>	similarity to Pseudomonas aeruginosa twitching motility prt
	<b>Protein import</b>		YDL124W	<b>YDL124W</b>	NAD(P)H-dependent reductase
YKR095W	<b>MLP1</b>	myosin-like prt	YER067W	<b>YER067W</b>	prt of unknown function
YMR203W	<b>TOM40</b>	prt of the mitochondrial import channel	YFR044C	<b>YFR044C</b>	prt with high similarity to cytosolic nonspecific dipeptidase 2
YNL121C	<b>TOM70</b>	prt-mitochondrial targeting	YGR043C	<b>YGR043C</b>	putative transaldolase
	<b>Other transport</b>		YIR035C	<b>YIR035C</b>	putative oxidoreductase
YGR167W	<b>CLC1</b>	clathrin light chain	YKL033W-A	<b>YKL033W-A</b>	similarity to halacid-halidohydrolase
YER136W	<b>GDI1</b>	GDP dissociation inhibitor	YKR043C	<b>YKR043C</b>	similarity to phosphoglycerate mutase
YCR002C	<b>CDC10</b>	septin	YLR179C	<b>YLR179C</b>	prt of unknown function
YFL045C	<b>SEC53</b>	phosphomannomutase	YLR301W	<b>YLR301W</b>	prt of unknown function
YDR328C	<b>SKP1</b>	component of Cbf3 kinetochore complex	YNL010W	<b>YNL010W</b>	prt of unknown function
YLR025W	<b>SNF7</b>	prt involved in glucose derepression	YNL134C	<b>YNL134C</b>	member of the zinc-binding dehydrogenase family
	<b>Chromatin architecture</b>		YOR021C	<b>YOR021C</b>	hypothetical prt
YLR285W	<b>NNT1</b>	methyltransferase involved in rDNA silencing	YPR127W	<b>YPR127W</b>	prt with similarity to S. pombe pyridoxal reductase
YDR071C	<b>PAA1</b>	polyamine acetyl-transferase	YGR211W	<b>ZPR1</b>	unknown function
YGL037C	<b>PNC1</b>	Pyrazinamidase and NiCotinamidase	YOL154W	<b>ZPS1</b>	zinc- and pH-regulated surface prt

<sup>a</sup>. Sorting of proteins was based on their Gene Ontology annotation in YPD<sup>TM</sup>(45). Only "experimentally determined" biological processes were considered.

<sup>b</sup>. Abbreviations: Dhase, dehydrogenase; Pr, phosphoribosyl; prt, protein; Sase, synthase; sub, subunit