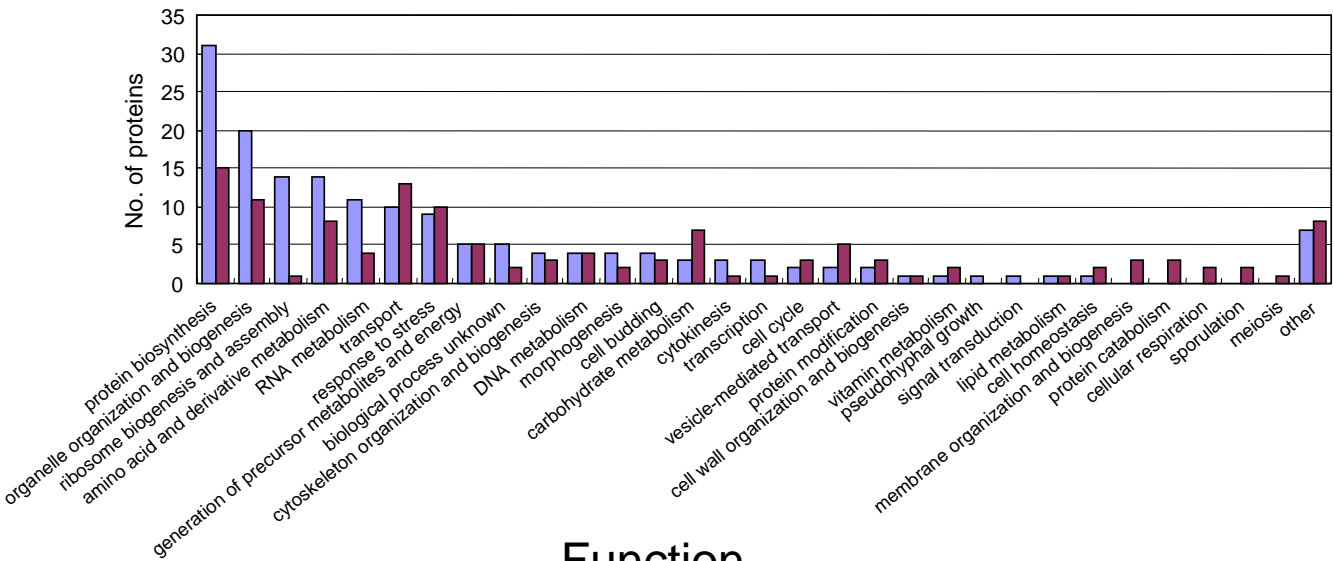
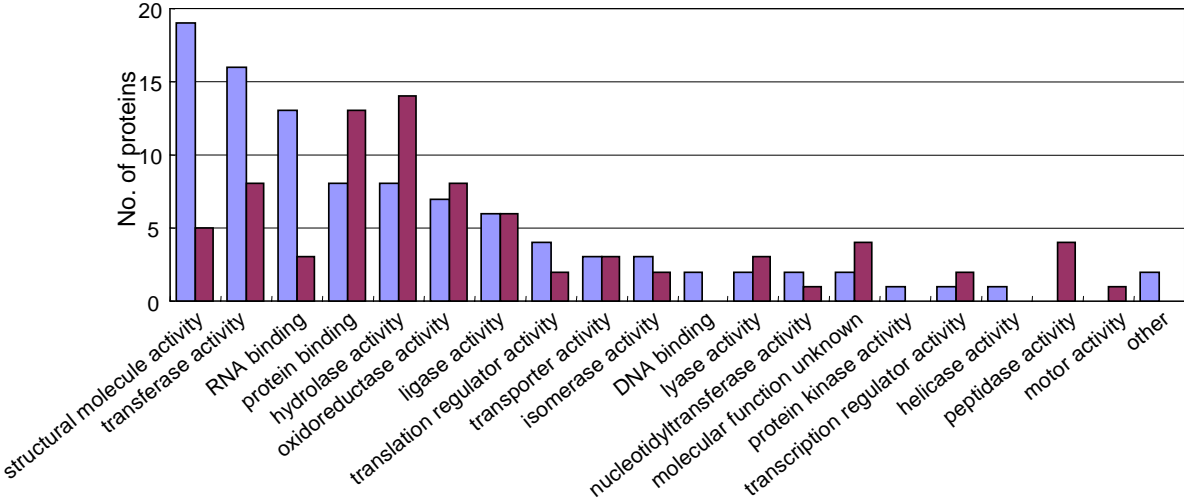


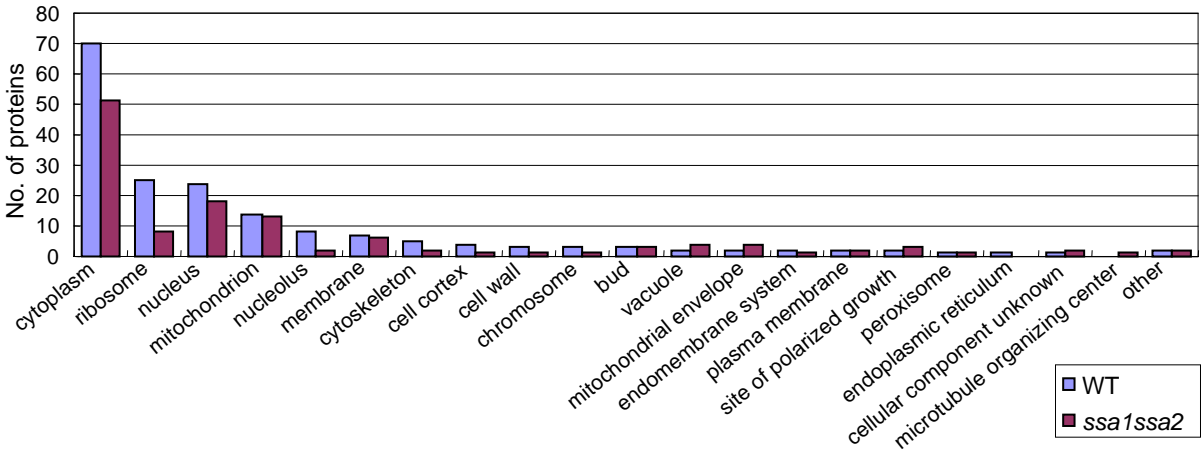
Biological Process



Function



Component



Supplementary Figure 1
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Supplementary Table 1. Identified proteins by nESI-LC-MS/MS.

acc Num	Protein Name	ORF cod
UCR7_YEAS	(P00128) Ubiquinol-cytochrome c reductase complex 14 kDa protein (EC 1.10.2.2) (Comple	YDR529C
ADH1_YEAS	(P00330) Alcohol dehydrogenase I (EC 1.1.1.1) (YADH-1)	YOL086C
G3P2_YEAS	(P00358) Glyceraldehyde-3-phosphate dehydrogenase 2 (EC 1.2.1.12) (GAPDH 2)	YJR009C
G3P3_YEAS	(P00359) Glyceraldehyde-3-phosphate dehydrogenase 3 (EC 1.2.1.12) (GAPDH 3)	YGR192C
SODM_YEAS	(P00447) Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1)	YHR008C
KPYK1_YEA	(P00549) Pyruvate kinase 1 (EC 2.7.1.40) (PK 1)	YAL038W
PGK_YEAST	(P00560) Phosphoglycerate kinase (EC 2.7.2.3)	YCR012W
IPYR_YEAS	(P00817) Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPa	YBR011C
ATPB_YEAS	(P00830) ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	YJR121W
ENO1_YEAS	(P00924) Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerat	YGR254W
ENO2_YEAS	(P00925) Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerat	YHR174W
TPIS_YEAST	(P00942) Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase)	YDR050C
PMG1_YEAS	(P00950) Phosphoglycerate mutase 1 (EC 5.4.2.1) (Phosphoglyceromutase 1) (PGAM 1) (M	YKL152C
H2B1_YEAS	(P02293) Histone H2B.1	YDR224C
RS28_YEAS	(P02380) 40S ribosomal protein S28 (S33) (YS27)	YOR167C
RLA4_YEAS	(P02400) 60S acidic ribosomal protein P2-beta (L45) (YL44C) (YPA1) (L12EIA)	YBR167C
RL28_YEAS	(P02406) 60S ribosomal protein L28 (L27A) (L29) (YL24) (RP62)	YGL103W
RS17A_YEA	(P02407) 40S ribosomal protein S17-A (RP51A)	YML024W
TBB_YEAST	(P02557) Tubulin beta chain (Beta tubulin)	YFL037W
HSP82_YEAS	(P02829) ATP-dependent molecular chaperone HSP82 (Heat shock protein Hsp90 heat indu	YPL240C
EF1A_YEAS	(P02994) Elongation factor 1-alpha (EF-1-alpha)	YPR080W
RL23_YEAS	(P04451) 60S ribosomal protein L23 (L17)	YBL087C
RL25_YEAS	(P04456) 60S ribosomal protein L25 (YL25) (RP61L)	YOL127W
RS22_YEAS	(P04648) 40S ribosomal protein S22 (S24) (YS22) (RP50) (YP58)	YJL190C
RL31_YEAS	(P04649) 60S ribosomal protein L31 (L34) (YL28)	YDL075W
HXKB_YEAS	(P04807) Hexokinase B (EC 2.7.1.1) (Hexokinase PII)	YGL253W
VDAC1_YEA	(P04840) Outer mitochondrial membrane protein porin 1 (Voltage-dependent anion-selectiv	YNL055C
H2A1_YEAS	(P04911) Histone H2A.1	YDR225W
PMA1_YEAS	(P05030) Plasma membrane ATPase 1 (EC 3.6.3.6) (Proton pump 1)	YGL008C
RLA0_YEAS	(P05317) 60S acidic ribosomal protein P0 (L10E)	YLR340W
RLA2_YEAS	(P05319) 60S acidic ribosomal protein P2-alpha (A2) (L44) (L12EIB)	YOL039W
METE_YEAS	(P05694) 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1	YER091C
RL19_YEAS	(P05735) 60S ribosomal protein L19 (L23) (YL14) (RP33) (RP15L)	YBR084C
RL2_YEAST	(P05736) 60S ribosomal protein L2 (YL6) (L5) (RP8)	YFR031C
RL7A_YEAS	(P05737) 60S ribosomal protein L7-A (L6A) (YL8A) (RP11)	YGL076C
RL9A_YEAS	(P05738) 60S ribosomal protein L9-A (L8) (YL11) (RP25)	YGL147C
RL6B_YEAS	(P05739) 60S ribosomal protein L6-B (L17) (YL16) (RP18)	YLR448W
RL17A_YEA	(P05740) 60S ribosomal protein L17-A (YL17-A)	YKL180W
RS3_YEAST	(P05750) 40S ribosomal protein S3 (YS3) (RP13)	YNL178W
RS4_YEAST	(P05753) 40S ribosomal protein S4 (S7) (YS6) (RP5)	YJR145C
RS8_YEAST	(P05754) 40S ribosomal protein S8 (S14) (YS9) (RP19)	YBL072C
RS9B_YEAS	(P05755) 40S ribosomal protein S9-B (S13) (YS11) (RP21) (YP28)	YBR189W
RS13_YEAS	(P05756) 40S ribosomal protein S13 (S27A) (YS15)	YDR064W
RS21_YEAS	(P05760) 40S ribosomal protein S21 (S26) (YS25)	YJL136C
SCP160_YEAS	(P06105) SCP160 protein (Protein HX)	YJL080C
ILV5_YEAST	(P06168) Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86) (Acetohydrox	YLR355C
PDC1_YEAS	(P06169) Pyruvate decarboxylase isozyme 1 (EC 4.1.1.1) (EC 4.1.1.-)	YLR044C
RL11_YEAS	(P06380) 60S ribosomal protein L11 (L16) (YL16) (39A) (RP39)	YPR102C
DED1_YEAS	(P06634) Probable ATP-dependent RNA helicase DED1	YOR204W
FAS1_YEAS	(P07149) Fatty acid synthase subunit beta (EC 2.3.1.86) [Includes: 3-hydroxypalmitoyl-[acy	YKL182W
KAD1_YEAS	(P07170) Adenylate kinase cytosolic (EC 2.7.4.3) (ATP-AMP transphosphorylase)	YDR226W
PYR1_YEAS	(P07259) URA1 protein [Includes: Glutamine-dependent carbamoyl-phosphate synthase (EC	YJL130C
IF4E_YEAST	(P07260) Eukaryotic translation initiation factor 4E (eIF4E) (eIF-4E) (mRNA cap-binding p	YOL139C
PROF_YEAS	(P07274) Profilin	YOR122C

RS19A_YEAS	(P07280) 40S ribosomal protein S19-A (S16A) (YS16) (RP55) (YP45)	YOL121C
ILVB_YEAS	(P07342) Acetolactate synthase, mitochondrial precursor (EC 2.2.1.6) (Acetohydroxy-acid synthase)	YMR108W
SYV_YEAST	(P07806) Valyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.9) (Valine--tRNA ligase)	YGR094W
FPPS_YEAS	(P08524) Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthase)	YJL167W
ARO1_YEAS	(P08566) Pentafunctional AROM polypeptide [Includes: 3-dehydroquinate synthase (EC 4.2.1.11) (3-dehydroquinate synthase)]	YDR127W
SYIC_YEAS	(P09436) Isoleucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.5) (Isoleucine--tRNA ligase) (IleRS)	YBL076C
IF4A_YEAST	(P10081) Eukaryotic initiation factor 4A (eIF4A) (eIF-4A) (Stimulator factor I 37 kDa component)	YKR059W
RL4A_YEAS	(P10664) 60S ribosomal protein L4-A (L2A) (RP2)	YBR031W
ARF1_YEAS	(P11076) ADP-ribosylation factor 1	YDL192W
PYC1_YEAS	(P11154) Pyruvate carboxylase 1 (EC 6.4.1.1) (Pyruvic carboxylase 1) (PCB 1)	YGL062W
HSP75_YEAS	(P11484) Heat shock protein SSB1 (Cold-inducible protein YG101)	YDL229W
HSP77_YEAS	(P12398) Heat shock protein SSC1, mitochondrial precursor (Endonuclease SCEI 75 kDa subunit)	YJR045C
G6PI_YEAST	(P12709) Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (GPI)	YBR196C
RL30_YEAS	(P14120) 60S ribosomal protein L30 (YL32) (RP73)	YGL030W
ALF_YEAST	(P14540) Fructose-bisphosphate aldolase (EC 4.1.2.13)	YKL060C
GFA1_YEAS	(P14742) Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)	YKL104C
CYPH_YEAS	(P14832) Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin)	YDR155C
HSC82_YEAS	(P15108) ATP-dependent molecular chaperone HSC82 (Heat shock protein Hsp90 constituent)	YMR186W
SYKC_YEAS	(P15180) Lysyl-tRNA synthetase, cytoplasmic (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)	YDR037W
SEC23_YEAS	(P15303) Protein transport protein SEC23	YPR181C
SYFA_YEAS	(P15625) Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase)	YFL022C
STI1_YEAST	(P15705) Heat shock protein STI1	YOR027W
THRC_YEAS	(P16120) Threonine synthase (EC 4.2.3.1) (TS)	YCR053W
VATB_YEAS	(P16140) Vacuolar ATP synthase subunit B (EC 3.6.3.14) (V-ATPase B subunit) (Vacuolar ATP synthase)	YBR127C
GRP78_YEAS	(P16474) 78 kDa glucose-regulated protein homolog precursor (GRP 78) (Immunoglobulin heavy chain binding protein)	YJL034W
EF3A_YEAS	(P16521) Elongation factor 3A (EF-3A) (EF-3)	YLR249W
K6PF1_YEAS	(P16861) 6-phosphofructokinase alpha subunit (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphofructokinase)	YGR240C
K6PF2_YEAS	(P16862) 6-phosphofructokinase beta subunit (EC 2.7.1.11) (Phosphofructokinase 2) (Phosphofructokinase)	YMR205C
RL8A_YEAS	(P17076) 60S ribosomal protein L8-A (L7A-2) (L4-2) (YL5) (RP6)	YHL033C
RL12_YEAS	(P17079) 60S ribosomal protein L12 (L15) (YL23)	YEL054C
VATA_YEAS	(P17255) Vacuolar ATP synthase catalytic subunit A (EC 3.6.3.14) (V-ATPase A subunit) (Vacuolar ATP synthase)	YDL185W
CAP_YEAST	(P17555) Adenylyl cyclase-associated protein (CAP)	YNL138W
GLRX_YEAS	(P17695) Glutaredoxin (Thioltransferase)	YDR513W
PDI_YEAST	(P17967) Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI) (Thioredoxin-related glycoprotein)	YCL043C
FAS2_YEAS	(P19097) Fatty acid synthase subunit alpha (EC 2.3.1.86) [Includes: Acyl carrier; 3-oxoacyl synthase]	YPL231W
HSP60_YEAS	(P19882) Heat shock protein 60, mitochondrial precursor (Stimulator factor I 66 kDa component)	YLR259C
SAR1_YEAS	(P20606) GTP-binding protein SAR1	YPL218W
VPS1_YEAS	(P21576) Vacuolar sorting protein 1	YKR001C
CLH_YEAST	(P22137) Clathrin heavy chain	YGL206C
VATE_YEAS	(P22203) Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase E subunit) (Vacuolar ATP synthase)	YOR332W
UBA1_YEAS	(P22515) Ubiquitin-activating enzyme E1 1	YKL210W
RS3B_YEAS	(P23248) 40S ribosomal protein S1-B (RP10B)	YML063W
TKT1_YEAS	(P23254) Transketolase 1 (EC 2.2.1.1) (TK 1)	YPR074C
IF5A2_YEAS	(P23301) Eukaryotic translation initiation factor 5A-2 (eIF-5A-2) (eIF-4D) (Hypusine containing protein)	YEL034W
MPCP_YEAS	(P23641) Mitochondrial phosphate carrier protein (Phosphate transport protein) (PTP) (mPDC)	YJR077C
ERG6_YEAS	(P25087) Sterol 24-C-methyltransferase (EC 2.1.1.41) (Delta(24)-sterol C-methyltransferase)	YML008C
GLRX1_YEAS	(P25373) Glutaredoxin 1	YCL035C
RS2_YEAST	(P25443) 40S ribosomal protein S2 (S4) (YS5) (RP12) (Omnipotent suppressor protein SUP1)	YGL123W
MAS5_YEAS	(P25491) Mitochondrial protein import protein MAS5 (Protein YDJ1)	YNL064C
CDC48_YEAS	(P25694) Cell division control protein 48	YDL126C
RL5_YEAST	(P26321) 60S ribosomal protein L5 (L1) (YL3) (Ribosomal 5S RNA-binding protein)	YPL131W
SYLC_YEAS	(P26637) Leucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS)	YPL160W
RS24_YEAST	(P26782) 40S ribosomal protein S24 (RP50)	YER074W
RS5_YEAST	(P26783) 40S ribosomal protein S5 (S2) (YS8) (RP14)	YJR123W
RL16B_YEAS	(P26785) 60S ribosomal protein L16-B (YL15) (RP23)	YNL069C
RS7A_YEAS	(P26786) 40S ribosomal protein S7-A (RP30)	YOR096W
BMH1_YEAS	(P29311) BMH1 protein	YER177W

RL8B_YEAS	(P29453) 60S ribosomal protein L8-B (L7A-1) (L4-1) (YL5) (RP6)	YLL045C
MANA_YEA	(P29952) Mannose-6-phosphate isomerase (EC 5.3.1.8) (Phosphomannose isomerase) (PMI)	YER003C
PSB4_YEAS	(P30657) Proteasome component PRE4 (EC 3.4.25.1) (Macropain subunit PRE4) (Proteinase	YFR050C
DHOM_YEA	(P31116) Homoserine dehydrogenase (EC 1.1.1.3) (HDH)	YJR139C
CYS3_YEAS	(P31373) Cystathionine gamma-lyase (EC 4.4.1.1) (Gamma-cystathionase)	YAL012W
HS104_YEAS	(P31539) Heat shock protein 104	YLL026W
ACBP_YEAS	(P31787) Acyl-CoA-binding protein (ACBP)	YGR037C
EF2_YEAST	(P32324) Elongation factor 2 (EF-2)	YDR385W
EF1B_YEAS	(P32471) Elongation factor 1-beta (EF-1-beta)	YAL003W
CBS_YEAST	(P32582) Cystathionine beta-synthase (EC 4.2.1.22) (Serine sulfhydrase) (Beta-thionase)	YGR155W
HSP7F_YEA	(P32589) Heat shock protein homolog SSE1 (Chaperone protein MSI3)	YPL106C
RS23_YEAS	(P32827) 40S ribosomal protein S23 (S28) (YS14) (RP37)	YGR118W
RS0A_YEAS	(P32905) 40S ribosomal protein S0-A (Nucleic acid-binding protein NAB1A)	YGR214W
RS3A_YEAS	(P33442) 40S ribosomal protein S1-A (RP10A)	YLR441C
GCN1_YEAS	(P33892) Translational activator GCN1	YGL195W
TSA1_YEAS	(P34760) Peroxiredoxin TSA1 (EC 1.11.1.15) (Thioredoxin peroxidase) (Cytoplasmic thiol	YML028W
RS18_YEAS	(P35271) 40S ribosomal protein S18	YDR450W
TCTP_YEAS	(P35691) Translationally controlled tumor protein homolog (TCTP)	YKL056C
EF1G2_YEA	(P36008) Elongation factor 1-gamma 2 (EF-1-gamma 2)	YKL081W
RL14A_YEA	(P36105) 60S ribosomal protein L14-A	YKL006W
GLYC_YEAS	(P37291) Serine hydroxymethyltransferase, cytosolic (EC 2.1.2.1) (Serine methylase) (Glyc	YLR058C
GBLP_YEAS	(P38011) Guanine nucleotide-binding protein beta subunit-like protein	YMR116C
AHP1_YEAS	(P38013) Peroxiredoxin type II (EC 1.11.1.15) (Peroxisomal alkyl hydroperoxide reductase)	YLR109W
RL32_YEAS	(P38061) 60S ribosomal protein L32	YBL092W
SYG_YEAST	(P38088) Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS)	YBR121C
YBN5_YEAS	(P38219) Hypothetical GTP-binding protein YBR025C	YBR025C
YBV1_YEAS	(P38260) Hypothetical 32.6 kDa protein in VPS15-YMC2 intergenic region	YBR101C
RS20_YEAS	(P38701) 40S ribosomal protein S20	YHL015W
RL27_YEAS	(P38706) 60S ribosomal protein L27	YHR010W
YHI0_YEAS	(P38708) Putative prolyl-tRNA synthetase YHR020W (EC 6.1.1.15) (Proline--tRNA ligase)	YHR020W
6PGD1_YEA	(P38720) 6-phosphogluconate dehydrogenase, decarboxylating 1 (EC 1.1.1.44)	YHR183W
YHM4_YEAS	(P38788) Heat shock protein 70 homolog YHR064C	YHR064C
EGD2_YEAS	(P38879) EGD2 protein (GAL4 DNA-binding enhancer protein 2)	YHR193C
CH10_YEAS	(P38910) 10 kDa heat shock protein, mitochondrial (HSP10) (10 kDa chaperonin)	YOR020C
STM1_YEAS	(P39015) Suppressor protein STM1 (MPT4 protein) (GU4 nucleic-binding protein 2) (G4p2	YLR150W
FHP_YEAST	(P39676) Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin) (Nitric oxide dic	YGR234W
SAHH_YEAS	(P39954) Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (A	YER043C
YNU8_YEAS	(P40159) Hypothetical 22.0 kDa protein in SSB2-SPX18 intergenic region	YNL208W
MMF1_YEAS	(P40185) MMF1 protein, mitochondrial precursor (Maintenance of mitochondrial function 1	YIL051C
RL13B_YEA	(P40212) 60S ribosomal protein L13-B	YMR142C
RS16_YEAS	(P40213) 40S ribosomal protein S16 (RP61R)	YMR143W
THIL_YEAS	(P41338) Acetyl-CoA acetyltransferase (EC 2.3.1.9) (Acetoacetyl-CoA thiolase)	YPL028W
RL10_YEAS	(P41805) 60S ribosomal protein L10 (L9) (Ubiquinol-cytochrome C reductase complex sub	YLR075W
MPG1_YEAS	(P41940) Mannose-1-phosphate guanyltransferase (EC 2.7.7.13) (ATP-mannose-1-phosphat	YDL055C
SYEC_YEAS	(P46655) Glutamyl-tRNA synthetase, cytoplasmic (EC 6.1.1.17) (Glutamate--tRNA ligase)	YGL245W
YJZ9_YEAS	(P47100) Transposon Ty1 protein B	YJR029W
ADK_YEAST	(P47143) Adenosine kinase (EC 2.7.1.20)	YJR105W
RL20_YEAS	(P47913) 60S ribosomal protein L20 (L18A)	YMR242C
RS7B_YEAS	(P48164) 40S ribosomal protein S7-B	YNL096C
RS12_YEAS	(P48589) 40S ribosomal protein S12	YOR369C
VATG_YEAS	(P48836) Vacuolar ATP synthase subunit G (EC 3.6.3.14) (V-ATPase G subunit) (Vacuolar	YHR039C
ASNS2_YEA	(P49090) Asparagine synthetase [glutamine-hydrolyzing] 2 (EC 6.3.5.4) (Glutamine-depend	YGR124W
RL38_YEAS	(P49167) 60S ribosomal protein L38	YLR325C
RL1_YEAST	(P53030) 60S ribosomal protein L1 (L10a)	YPL220W
YNN4_YEAS	(P53912) Hypothetical 41.2 kDa protein in FPR1-TOM22 intergenic region	YNL134C
ALDH6_YEA	(P54115) Magnesium-activated aldehyde dehydrogenase, cytosolic (EC 1.2.1.3) (Mg(2+)-ac	YPL061W
ACT_YEAST	(P60010) Actin	YFL039C

UBIQ_YEAS	(P61864) Ubiquitin	YIL148W
COAC_YEAS	(Q00955) Acetyl-CoA carboxylase (EC 6.4.1.2) (ACC) [Includes: Biotin carboxylase (EC 6	YNR016C
RS15_YEAS	(Q01855) 40S ribosomal protein S15 (S21) (YS21) (RP52) (RIG protein)	YOL040C
RL21A_YEA	(Q02753) 60S ribosomal protein L21-A	YBR191W
COFI_YEAS	(Q03048) Cofilin	YLL050C
OYE2_YEAS	(Q03558) NADPH dehydrogenase 2 (EC 1.6.99.1) (Old yellow enzyme 2)	YHR179W
HNT1_YEAS	(Q04344) Hit family protein 1 (Adenosine 5'-monophosphoramidase)	YDL125C
YM71_YEAS	(Q05016) Hypothetical oxidoreductase in MRPL44-MTF1 intergenic region (EC 1.-.-.-)	YMR226C
IMB1_YEAS	(Q06142) Importin beta-1 subunit (Karyopherin beta-1 subunit) (Importin 95)	YLR347C
RIB3_YEAS	(Q99258) 3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase)	YDR487C

Gene na Description

QCR7	Subunit 7 of the ubiquinol cytochrome-c reductase complex, which is a component of the mitochondrial
ADH1	Alcohol dehydrogenase, fermentative isozyme active as homo- or heterotetramers; required for the redu
TDH2	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 2, involved in glycolysis and gluconeogenesis; te
TDH3	Glyceraldehyde-3-phosphate dehydrogenase, isozyme 3, involved in glycolysis and gluconeogenesis; te
SOD2	Manganese-containing superoxide dismutase; protects cells against oxygen toxicity
CDC19/PY	Pyruvate kinase, functions as a homotetramer in glycolysis to convert phosphoenolpyruvate to pyruvate
PGK1	3-phosphoglycerate kinase, catalyzes transfer of high-energy phosphoryl groups from the acyl phosphat
IPP1	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with
ATP2	Beta subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily cons
ENO1	Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosph
ENO2	Enolase II, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosph
TPI1	Triose phosphate isomerase, abundant glycolytic enzyme; mRNA half-life is regulated by iron availabil
GPM1	Tetrameric phosphoglycerate mutase, mediates the conversion of 3-phosphoglycerate to 2-phosphoglyc
HTB1	One of two nearly identical (see HTB2) histone H2B subtypes required for chromatin assembly and chr
RPS28A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps28Ap and has similarity
POP7/RPP	Subunit of both RNase MRP, which cleaves pre-rRNA, and nuclear RNase P, which cleaves tRNA prec
RPL28	Ribosomal protein L29 of the large (60S) ribosomal subunit, has similarity to E. coli L15 and rat L27a r
RPS17A	Ribosomal protein 51 (rp51) of the small (40s) subunit; nearly identical to Rps17Bp and has similarity t
TUB2	Beta-tubulin; associates with alpha-tubulin (Tub1p and Tub3p) to form tubulin dimer, which polymeriz
HSP82	Cytoplasmic chaperone (Hsp90 family) required for pheromone signaling and negative regulation of Hs
TEF1	Translational elongation factor EF-1 alpha; also encoded by TEF2; functions in the binding reaction of :
RPL23A	Protein component of the large (60S) ribosomal subunit, identical to Rpl23Bp and has similarity to E. co
RPL25	Primary rRNA-binding ribosomal protein component of the large (60S) ribosomal subunit, has similarit
RPS22A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Bp and has similarity
RPL31A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl31Bp and has similarity
HXK2	Hexokinase isoenzyme 2 that catalyzes phosphorylation of glucose in the cytosol; predominant hexokin
POR1	Mitochondrial porin (voltage-dependent anion channel), outer membrane protein required for the maint
HTA1	One of two nearly identical (see also HTA2) histone H2A subtypes; core histone required for chromatin
PMA1	Plasma membrane H ⁺ -ATPase, pumps protons out of the cell; major regulator of cytoplasmic pH and p
RPP0	Conserved ribosomal protein P0 similar to rat P0, human P0, and E. coli L10e; shown to be phosphoryl
RPP2A	Ribosomal protein P2 alpha, a component of the ribosomal stalk, which is involved in the interaction be
MET6	Cobalamin-independent methionine synthase, involved in amino acid biosynthesis; requires a minimum
RPL19A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl19Bp and has similarity
RPL2A	Protein component of the large (60S) ribosomal subunit, identical to Rpl2Bp and has similarity to E. col
RPL7A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl7Bp and has similarity to
RPL9A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl9Bp and has similarity to
RPL6A	Protein component of the large (60S) ribosomal subunit, has similarity to Rpl6Bp and to rat L6 ribosom
RPL17A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl17Bp and has similarity
RPS3	Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic (AP) endonuclease :
RPS4A	Protein component of the small (40S) ribosomal subunit; mutation affects 20S pre-rRNA processing; id
RPS8A	Protein component of the small (40S) ribosomal subunit; identical to Rps8Ap and has similarity to rat S
RPS9B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps9Bp and has similarity t
RPS13	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 ribosc
RPS21B	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps21Bp and has similarity
SCP160	Essential RNA-binding G protein effector of mating response pathway, predominantly associated with i
ILV5	Acetohydroxyacid reductoisomerase, mitochondrial protein involved in branched-chain amino acid bios
PDC1	Major of three pyruvate decarboxylase isozymes, key enzyme in alcoholic fermentation, decarboxylates
RPL11A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl11Bp; involved in ribosc
DED1	ATP-dependent DEAD (Asp-Glu-Ala-Asp)-box RNA helicase, required for translation initiation of all y
FAS1	Beta subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; c
ADK1	Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; lac
URA2	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes
CDC33/TI	Cytoplasmic mRNA cap binding protein; the eIF4E-cap complex is responsible for mediating cap-depe
PFY1	Profilin, actin- and phosphatidylinositol 4,5-bisphosphate-binding protein, plays a role in cytoskeleton c

RPS19A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps19Bp and has similarity to Rps19Ap
ILV2	Acetolactate synthase, catalyses the first common step in isoleucine and valine biosynthesis and is the first of three genes in the <i>ilv</i> operon
VAS1	Mitochondrial and cytoplasmic valyl-tRNA synthetase
ERG20/FP	Farnesyl pyrophosphate synthetase, has both dimethylallyltranstransferase and geranyltranstransferase activities
ARO1	Pentafunctional arom protein, catalyzes steps 2 through 6 in the biosynthesis of chorismate, which is a precursor of aromatic amino acids
ILS1	Cytoplasmic isoleucine-tRNA synthetase, target of the G1-specific inhibitor reveromycin A
TIF1	Translation initiation factor eIF4A, identical to Tif2p; DEA(D/H)-box RNA helicase that couples ATP hydrolysis to RNA unwinding
RPL4A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl4Bp
ARF1	ADP-ribosylation factor, GTPase of the Ras superfamily involved in regulation of coated formation vesicle trafficking
PYC1	Pyruvate carboxylase isoform, cytoplasmic enzyme that converts pyruvate to oxaloacetate; highly similar to mitochondrial isoform
SSB1	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone; may be involved in the folding of nascent polypeptides
SSC1	Mitochondrial matrix ATPase that is a subunit of the presequence translocase-associated protein import complex
PGI1	Glycolytic enzyme phosphoglucose isomerase, catalyzes the interconversion of glucose-6-phosphate and fructose-6-phosphate
RPL30	Protein component of the large (60S) ribosomal subunit, has similarity to rat L30 ribosomal protein; involved in protein synthesis
FBA1	Fructose 1,6-bisphosphate aldolase, a cytosolic enzyme required for glycolysis and gluconeogenesis; catalyzes the reversible cleavage of fructose-1,6-bisphosphate into dihydroxyacetone phosphate and glyceraldehyde-3-phosphate
GFA1	Glutamine-fructose-6-phosphate amidotransferase, catalyzes the formation of glucosamine-6-P and glutamate from fructose-6-phosphate and glutamine
CPR1	Cytoplasmic peptidyl-prolyl cis-trans isomerase (cyclophilin), catalyzes the cis-trans isomerization of proline residues in peptides
HSC82	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and Hsp90p
KRS1	Lysyl-tRNA synthetase; also identified as a negative regulator of general control of amino acid biosynthesis
SEC23	GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat
FRS2	Alpha subunit of cytoplasmic phenylalanyl-tRNA synthetase, forms a tetramer with Frs1p to form active enzyme
STI1	Hsp90 cochaperone, interacts with the Ssa group of the cytosolic Hsp70 chaperones; activates the ATPase activity of Hsp90
THR4	Threonine synthase, conserved protein that catalyzes formation of threonine from O-phosphohomoserine
VMA2	Subunit B of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase)
KAR2	ATPase involved in protein import into the ER, also acts as a chaperone to mediate protein folding in the ER
YEF3	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by promoting translocation
PFK1	Alpha subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth
PFK2	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth
RPL8A	Ribosomal protein L4 of the large (60S) ribosomal subunit, nearly identical to Rpl8Bp and has similarity to Rpl8Ap
RPL12A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl12Bp; rpl12a rpl12b double mutant is lethal
TFP1/VM1	Vacuolar ATPase V1 domain subunit A containing the catalytic nucleotide binding sites; protein precursor of VMA1
SRV2	CAP (cyclase-associated protein) subunit of adenylyl cyclase complex; N-terminus binds adenylyl cyclase
GRX2/TTI1	Cytoplasmic glutaredoxin, thioltransferase, glutathione-dependent disulfide oxidoreductase involved in protein folding
PDI1	Protein disulfide isomerase, multifunctional protein resident in the endoplasmic reticulum lumen, essential for protein folding
FAS2	Alpha subunit of fatty acid synthetase, which catalyzes the synthesis of long-chain saturated fatty acids; involved in lipid metabolism
HSP60	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptide chains
SAR1	GTPase, GTP-binding protein of the ARF family, component of COPII coat of vesicles; required for transport of proteins into the ER
VPS1	GTPase required for vacuolar protein sorting, functions in actin cytoskeleton organization via its interaction with Arp23 complex
CHC1	Clathrin heavy chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis
VMA4	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase)
UBA1	Ubiquitin activating enzyme, involved in ubiquitin-mediated protein degradation and essential for viability
RPS1B	Ribosomal protein 10 (rp10) of the small (40S) subunit; nearly identical to Rps1Ap and has similarity to Rps1Bp
TKL1	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to glyceraldehyde-3-phosphate and fructose-6-phosphate
HYP2	Translation initiation factor eIF-5A, promotes formation of the first peptide bond; similar to and functions with eIF4G
MIR1	Mitochondrial phosphate carrier, imports inorganic phosphate into mitochondria; functionally redundant with MIR2
ERG6	Delta(24)-sterol C-methyltransferase, converts zymosterol to fecosterol in the ergosterol biosynthetic pathway
GRX1	Hydroperoxide and superoxide-radical responsive heat-stable glutathione-dependent disulfide oxidoreductase
RPS2	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to Rps2Bp
YDJ1	Protein chaperone involved in regulation of the HSP90 and HSP70 functions; involved in protein translocation
CDC48	ATPase in ER, nuclear membrane and cytosol with homology to mammalian p97; in a complex with Nup133p
RPL5	Protein component of the large (60S) ribosomal subunit with similarity to E. coli L18 and rat L5 ribosomal protein
CDC60	Cytosolic leucyl tRNA synthetase, ligates leucine to the appropriate tRNA. Also known as: LeuRS
RPS24A	Protein component of the small (40S) ribosomal subunit; identical to Rps24Bp and has similarity to rat Rps24Ap
RPS5	Protein component of the small (40S) ribosomal subunit, the least basic of the non-acidic ribosomal proteins
RPL16B	N-terminally acetylated protein component of the large (60S) ribosomal subunit, binds to 5.8 S rRNA; involved in protein synthesis
RPS7A	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps7Bp; interacts with Kti11
BMH1	14-3-3 protein, major isoform; binds proteins and DNA, involved in regulation of many processes including cell cycle

RPL8B	Ribosomal protein L4 of the large (60S) ribosomal subunit, nearly identical to Rpl8Ap and has similarit
PMI40	Mannose-6-phosphate isomerase, catalyzes the interconversion of fructose-6-P and mannose-6-P; requi
PRE4	20S proteasome beta-type subunit
HOM6	Homoserine dehydrogenase (L-homoserine:NADP oxidoreductase), dimeric enzyme that catalyzes the t
CYS3	Cystathionine gamma-lyase, catalyzes one of the two reactions involved in the transsulfuration pathway
HSP104	Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate prev
ACB1	Acyl-CoA-binding protein, transports newly synthesized acyl-CoA esters from fatty acid synthetase (Fa
EFT2	Elongation factor 2 (EF-2), also encoded by EFT1; catalyzes ribosomal translocation during protein syn
EFB1	Translation elongation factor 1 beta; stimulates nucleotide exchange to regenerate EF-1 alpha-GTP for t
CYS4	Cystathionine beta-synthase, catalyzes the synthesis of cystathionine from serine and homocysteine, the
SSE1	ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded protei
RPS23A	Ribosomal protein 28 (rp28) of the small (40S) ribosomal subunit, required for translational accuracy; n
RPS0A	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Bp; required for matur
RPS1A	Ribosomal protein 10 (rp10) of the small (40S) subunit; nearly identical to Rps1Bp and has similarity to
GCN1	Positive regulator of the Gcn2p kinase activity, forms a complex with Gcn20p; proposed to stimulate G
TSA1	Ubiquitous housekeeping thioredoxin peroxidase, reduces reactive oxygen, nitrogen and sulfur species i
RPS18A	Protein component of the small (40S) ribosomal subunit; nearly identical to Rps18Bp and has similarity
TMA19	Protein of unknown function; putative ribosomal protein; homolog of translationally controlled tumor p
TEF4	Translation elongation factor EF-1 gamma
RPL14A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl
SHM2	Cytosolic serine hydroxymethyltransferase, involved in one-carbon metabolism
ASC1	WD repeat protein (G-beta like protein) involved in translation regulation; required for repression of Gc
AHP1	Thiol-specific peroxiredoxin, reduces hydroperoxides to protect against oxidative damage; function in v
RPL32	Protein component of the large (60S) ribosomal subunit, has similarity to rat L32 ribosomal protein; ove
GRS1	Cytoplasmic and mitochondrial glycyl-tRNA synthase that ligates glycine to the cognate anticodon bear
YBR025C	Hypothetical protein
FES1	Hsp70 (Ssa1p) nucleotide exchange factor, cytosolic homolog of Sil1p, which is the nucleotide exchang
RPS20	Protein component of the small (40S) ribosomal subunit; overproduction suppresses mutations affecting
RPL27A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl27Bp and has similarity
YHR020W	Putative protein of unknown function, has similarity to proline-tRNA ligase; YHR020W is an essential
GND1	6-phosphogluconate dehydrogenase (decarboxylating), catalyzes an NADPH regenerating reaction in th
SSZ1	Hsp70 protein that interacts with Zuo1p (a DnaJ homolog) to form a ribosome-associated complex that
EGD2	Alpha subunit of the heteromeric nascent polypeptide-associated complex (NAC) involved in protein sc
HSP10	Mitochondrial matrix co-chaperonin that inhibits the ATPase activity of Hsp60p, a mitochondrial chape
STM1	Protein that binds G4 quadruplex and purine motif triplex nucleic acid; acts with Cdc13p to maintain tel
YHB1	Nitric oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the
SAH1	S-adenosyl-L-homocysteine hydrolase, catabolizes S-adenosyl-L-homocysteine which is formed after d
YNL208W	Hypothetical protein
MMF1	Mitochondrial protein involved in maintenance of the mitochondrial genome
RPL13B	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl13Ap; not essential for v
RPS16A	Protein component of the small (40S) ribosomal subunit; identical to Rps16Bp and has similarity to E. c
ERG10	Acetyl-CoA C-acetyltransferase (acetoacetyl-CoA thiolase), cytosolic enzyme that transfers an acetyl g
RPL10	Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subuni
PSA1/MPC	GDP-mannose pyrophosphorylase (mannose-1-phosphate guanyltransferase), synthesizes GDP-mannos
GUS1	Glutamyl-tRNA synthetase (GluRS), forms a complex with methionyl-tRNA synthetase (Mes1p) and A
TY1B	TyB Gag-Pol protein; proteolytically processed to make the Gag, RT, PR, and IN proteins that are requi
ADO1	Adenosine kinase, required for the utilization of S-adenosylmethionine (AdoMet); may be involved in r
RPL20A	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl20Bp and has similarity
RPS7B	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps7Ap; interacts with Kti1
RPS12	Protein component of the small (40S) ribosomal subunit; has similarity to rat ribosomal protein S12
VMA10	Vacuolar H+ ATPase subunit G of the catalytic (V1) sector, involved in vacuolar acidification. Also kno
ASN2	Asparagine synthetase, isozyme of Asn1p; catalyzes the synthesis of L-asparagine from L-aspartate in t
RPL38	Protein component of the large (60S) ribosomal subunit, has similarity to rat L38 ribosomal protein
RPL1A	N-terminally acetylated protein component of the large (60S) ribosomal subunit, nearly identical to Rpl
YNL134C	no comments
ALD6	Cytosolic aldehyde dehydrogenase that is activated by Mg2+ and utilizes NADP+ as the preferred coen
ACT1	Actin, structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions

RPL40A/U Fusion protein, identical to Rpl40Bp, that is cleaved to yield ubiquitin and a ribosomal protein of the large ribosomal subunit

ACC1/FAA Acetyl-CoA carboxylase, biotin containing enzyme that catalyzes the carboxylation of acetyl-CoA to form malonyl-CoA

RPS15 Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S19 and rat S15 ribosomal proteins

RPL21A Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl21Bp and has similarity to Rpl21Ap

COF1 Cofilin, promotes actin filament depolarization in a pH-dependent manner; binds both actin monomers and actin filaments

OYE2 Widely conserved NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to OYE1 and OYE3

HNT1 Adenosine 5'-monophosphoramidase; interacts physically and genetically with Kin28p, a CDK and TFIIB

YMR226C NADP(+)-dependent dehydrogenase; acts on serine, L-allo-threonine, and other 3-hydroxy acids

KAP95 Karyopherin beta, forms a dimeric complex with Srp1p (Kap60p) that mediates nuclear import of cargo

RIB3 3,4-dihydroxy-2-butanone-4-phosphate synthase (DHBP synthase), required for riboflavin biosynthesis

inner membrane electron transport chain; oriented facing the mitochondrial matrix; N-terminus appears to play a role in the oxidation of acetaldehyde to ethanol, the last step in the glycolytic pathway

trimer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm

trimer that catalyzes the reaction of glyceraldehyde-3-phosphate to 1,3 bis-phosphoglycerate; detected in the cytoplasm

the input for aerobic (TCA cycle) or anaerobic (glucose fermentation) respiration

conversion of 1,3-bisphosphoglycerate to ADP to produce ATP; key enzyme in glycolysis and gluconeogenesis

water, highly expressed and essential for viability, active-site residues show identity to those from E. coli PPase

conserved enzyme complex required for ATP synthesis

enolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose

enolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is induced in response to glucose

ity; transcription is controlled by activators Reb1p, Gcr1p, and Rap1p through binding sites in the 5' non-coding region

erate during glycolysis and the reverse reaction during gluconeogenesis

mitochondrion function; Rad6p-Bre1p-Lge1p mediated ubiquitination regulates transcriptional activation, meiotic DSB formation

7 to rat S28 ribosomal protein

enzymes to generate mature 5' ends

ribosomal proteins; may have peptidyl transferase activity; can mutate to cycloheximide resistance

60 to rat S17 ribosomal protein

assembles to form microtubules

EF1p; docks with the mitochondrial import receptor Tom70p for preprotein delivery; interacts with co-chaperones Ccr1p and aminoacyl-tRNA (AA-tRNA) to ribosomes. Also known as: EF-1 alpha, eEF1A

oligo L14 and rat L23 ribosomal proteins

homologous to E. coli L23 and rat L23a ribosomal proteins; binds to 26S rRNA via a conserved C-terminal motif

7 to E. coli S8 and rat S15a ribosomal proteins

homologous to rat L31 ribosomal protein; associates with the karyopherin Sxm1p

ase during growth on glucose; functions in the nucleus to repress expression of HXK1 and GLK1 and to induce expression of mitochondrial osmotic stability and mitochondrial membrane permeability

in DNA assembly and chromosome function; DNA damage-dependent phosphorylation by Mec1p facilitates DNA repair; also involved in plasma membrane potential; part of the P2 subgroup of cation-transporting ATPases

located on serine 302

interacts between translational elongation factors and the ribosome; regulates the accumulation of P1 (Rpp1Ap and Rpp1Bp) in the nucleus

1 of two glutamates on the methyltetrahydrofolate substrate, similar to bacterial metE homologs

homologous to rat L19 ribosomal protein; rpl19a and rpl19b single null mutations result in slow growth, while the double null mutation is lethal

oligo L2 and rat L8 ribosomal proteins

60 to E. coli L30 and rat L7 ribosomal proteins; contains a conserved C-terminal Nucleic acid Binding Domain (NDB2)

60 to E. coli L6 and rat L9 ribosomal proteins

ribosomal protein; binds to 5.8S rRNA

homologous to E. coli L22 and rat L17 ribosomal proteins; copurifies with the components of the outer kinetochore DASH complex

activity; essential for viability; has similarity to E. coli S3 and rat S3 ribosomal proteins

homologous to Rps4Bp and has similarity to rat S4 ribosomal protein

5.8S ribosomal protein

homologous to E. coli S4 and rat S9 ribosomal proteins

ribosomal proteins

7 to rat S21 ribosomal protein

outer nuclear envelope and ER, interacts in mRNA-dependent manner with translating ribosomes via multiple KH domain

in mitochondrial DNA synthesis, also required for maintenance of wild-type mitochondrial DNA

conversion of pyruvate to acetaldehyde; subject to glucose-, ethanol-, and autoregulation; involved in amino acid catabolism

ribosomal assembly; depletion causes degradation of proteins and RNA of the 60S subunit; has similarity to E. coli L5 and yeast mRNAs; mutations in human DEAD-box DBY are a frequent cause of male infertility

contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities

contains a cleavable signal sequence

the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition

independent mRNA translation via interactions with the translation initiation factor eIF4G (Tif4631p or Tif4632p). Also known as: eIF4G

organization, required for normal timing of actin polymerization in response to thermal stress; localizes to plasma membrane

to rat S19 ribosomal protein

target of several classes of inhibitors, localizes to the mitochondria; expression of the gene is under general amino acid

activities; catalyzes the formation of C15 farnesyl pyrophosphate units for isoprenoid and sterol biosynthesis
precursor to aromatic amino acids

use activity to RNA binding and unwinding; forms a dumbbell structure of two compact domains connected by a linker
4Bp and has similarity to E. coli L4 and rat L4 ribosomal proteins

roles in intracellular trafficking within the Golgi; functionally interchangeable with Arf2p

similar to isoform Pyc2p but differentially regulated; mutations in the human homolog are associated with lactic acidosis

regulation of newly-synthesized polypeptide chains; member of the heat shock protein 70 (HSP70) family; interacts with the

motor (PAM); involved in protein translocation into the matrix and protein folding; member of the heat shock protein

and fructose-6-phosphate; required for cell cycle progression and completion of the gluconeogenic events of sporulation

involved in pre-rRNA processing in the nucleolus; autoregulates splicing of its transcript

catalyzes the conversion of fructose 1,6 biphosphate into two 3-carbon products: glyceraldehyde-3-phosphate and dihydroxyacetone

derivate from fructose-6-P and glutamine in the first step of chitin biosynthesis

peptide bonds N-terminal to proline residues; binds the drug cyclosporin A

and together they are essential; expressed constitutively at 10-fold higher basal levels than HSP82 and induced 2-3 fold
in stress

coat, involved in ER to Golgi transport and autophagy; stimulates the GDP-bound form of Sar1p

the enzyme; evolutionarily distant from mitochondrial phenylalanyl-tRNA synthetase based on protein sequence, but

use activity of Ssa1p; homolog of mammalian Hop protein

role; expression is regulated by the GCN4-mediated general amino acid control pathway

role), an electrogenic proton pump found throughout the endomembrane system; contains nucleotide binding sites; also

role in the ER and may play a role in ER export of soluble proteins; regulates the unfolded protein response via interaction with

by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP. Also known

for slow growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related

slow growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related

similar to rat L7a ribosomal protein; mutation results in decreased amounts of free 60S subunits

slow growing mutant exhibits slow growth and slow translation; has similarity to E. coli L11 and rat L12 ribosomal proteins

precursor undergoes self-catalyzed splicing to yield the extein Tfp1p and the intein Vde (PI-SceI), which is a site-specific

enzyme and facilitates activation by RAS; C-terminus binds ADP-actin monomers, facilitating regulation of actin dynamics

in maintaining redox state of target proteins, also exhibits glutathione peroxidase activity, expression induced in response

critical for the formation of disulfide bonds in secretory and cell-surface proteins, unscrambles non-native disulfide bonds

role; contains beta-ketoacyl reductase and beta-ketoacyl synthase activities

roles in protein and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA trans-

port vesicle formation during ER to Golgi protein transport

interaction with Sla1p; required for late Golgi-retention of some proteins including Kex2p; involved in regulating peroxisome

endocytosis; two heavy chains form the clathrin triskelion structural component; the light chain (CLC1) is thought to

role), an electrogenic proton pump found throughout the endomembrane system; required for the V1 domain to assemble

activity

to rat S3a ribosomal protein

converts sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis

functionally redundant with Anb1p; undergoes an essential hypusination modification; expressed under aerobic conditions

similar to Pic2p but more abundant than Pic2p under normal conditions

regulated by methylating position C-24

oxidoreductase with active site cysteine pair; protects cells from oxidative damage

similarity to E. coli S5 and rat S2 ribosomal proteins

localization across membranes; member of the DnaJ family

Rpl4p and Ufd1p participate in retrotranslocation of ubiquitinated proteins from the ER into the cytosol for degradation

of nuclear proteins; binds 5S rRNA and is required for 60S subunit assembly

S24 ribosomal protein

proteins; phosphorylated in vivo; essential for viability; has similarity to E. coli S7 and rat S5 ribosomal proteins

has similarity to Rpl16Ap, E. coli L13 and rat L13a ribosomal proteins; transcriptionally regulated by Rap1p

Rpl1p; deletion causes hypersensitivity to zymocin; has similarity to rat S7 and Xenopus S8 ribosomal proteins

regulating exocytosis and vesicle transport, Ras/MAPK signaling during pseudohyphal development, rapamycin-sensitive

y to rat L7a ribosomal protein; mutation results in decreased amounts of free 60S subunits
red for early steps in protein mannosylation. Also known as: PMI

third step in the common pathway for methionine and threonine biosynthesis; enzyme has nucleotide-binding, dimeric
that yields cysteine from homocysteine with the intermediary formation of cystathionine
iously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved
s1p-Fas2p) to acyl-CoA-consuming processes
thesis; contains diphthamide, the unique posttranslationally modified histidine residue specifically ADP-ribosylated
the next elongation cycle; part of the EF-1 complex, which facilitates binding of aminoacyl-tRNA to the ribosomal
first committed step in cysteine biosynthesis
ns; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm
early identical to Rps23Bp and similar to E. coli S12 and rat S23 ribosomal proteins; deletion of both RPS23A and
ration of 18S rRNA along with Rps0Bp; deletion of either RPS0 gene reduces growth rate, deletion of both genes is
rat S3a ribosomal protein
n2p activation by an uncharged tRNA
using thioredoxin as hydrogen donor; mediates redox regulation of the nuclear localization of Yap1p; deletion result
to E. coli S13 and rat S18 ribosomal proteins
rotein; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YKL056C is not an essential gene

14Bp and has similarity to rat L14 ribosomal protein; rpl14a csh5 double null mutant exhibits synthetic slow growth

n4p activity in the absence of amino-acid starvation; core component of the ribosome; ortholog of mammalian RAC
vivo requires covalent conjugation to Urm1p. Also known as: cTPxIII
erepression disrupts telomeric silencing
ring tRNA; transcription termination factor that may interact with the 3'-end of pre-mRNA to promote 3'-end format

ge factor for BiP (Kar2p) in the endoplasmic reticulum
; RNA polymerase III-dependent transcription; has similarity to E. coli S10 and rat S20 ribosomal proteins
to rat L27 ribosomal protein
gene
ie pentose phosphate pathway; required for growth on D-glucono-delta-lactone and adaptation to oxidative stress
is bound to the ribosome via the Zuo1p subunit; also involved in pleiotropic drug resistance via sequential activation
orting and translocation, associated with cytoplasmic ribosomes
ronin; involved in protein folding and sorting in the mitochondria; 10 kD heat shock protein with similarity to E. cc
lomere structure; interacts with ribosomes and subtelomeric Y' DNA; multicopy suppressor of tom1 and pop2 muta
oxidative and nitrosative stress responses
location of the activated methyl group of S-adenosyl-L-methionine (AdoMet) to an acceptor

viability; has similarity to rat L13 ribosomal protein
coli S9 and rat S16 ribosomal proteins
roup from one acetyl-CoA molecule to another, forming acetoacetyl-CoA; involved in the first step in mevalonate b
its; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene famil
ie from GTP and mannose-1-phosphate in cell wall biosynthesis; required for normal cell wall structure
rc1p; complex formation increases the catalytic efficiency of both tRNA synthetases and ensures their correct local
ired for retrotransposition
ecycling adenosine produced through the methyl cycle
to rat L18a ribosomal protein
l1p; deletion causes hypersensitivity to zymocin; has similarity to rat S7 and Xenopus S8 ribosomal proteins

own as: YHR039BC
he asparagine biosynthetic pathway

1Bp and has similarity to E. coli L1 and rat L10a ribosomal proteins; rpl1a rpl1b double null mutation is lethal

zyme; required for the conversion of acetaldehyde to acetate; constitutively expressed

large (60S) ribosomal subunit with similarity to rat L40; ubiquitin may facilitate assembly of the ribosomal protein into
form malonyl-CoA; required for de novo biosynthesis of long-chain fatty acids

ribosomal proteins

to rat L21 ribosomal protein

and filaments and severs filaments, thought to be regulated by phosphorylation at SER4, ubiquitous and essential in
yeast with slight differences in ligand binding and catalytic properties; may be involved in sterol metabolism. Also
IK subunit, and genetically with CAK1; member of the histidine triad (HIT) superfamily of nucleotide-binding prot

proteins via a nuclear localization signal (NLS), interacts with nucleoporins to guide transport across the nuclear pore
from ribulose-5-phosphate, also has an unrelated function in mitochondrial respiration

ole in complex assembly

lasm and cell-wall
lasm and cell-wall

e to glucose
; to glucose
gion

formation and H3 methylation

is1p, Cpr6p, Cpr7p, and Sti1p

pression of its own gene

acetylated by Nat4p

n the cytoplasm

utation is lethal

)

plex

is, similar to vertebrate vigilins

id rat L11

s

ibition by UTP
nown as: eIF-4E
embrane and cytosol

id control

ker; interacts with eIF4G

s
phosphatase subunit Reg1p
ein 70 (HSP70) family
on

hydroxyacetone phosphate

ld by heat shock

substrate binding is similar

o detected in the cytoplasm
with Ire1p. Also known as: BIP
nown as: EF-3
ed genes
d genes

endonuclease
ics and cell morphogenesis
onse to stress
ids

ssmission; similarity to groEL

ome biogenesis
regulate function
ole onto the vacuolar membrane

sis of aromatic amino acids
s. Also known as: TIF51A

ion by the proteasome

e signaling, and others

rization and catalytic regions

l in [PSI+] propagation

l by diphtheria toxin
A site. Also known as: EF-1 beta

RPS23B is lethal
lethal. Also known as: NAB1As

ts in mutator phenotype. Also known as: cTPxI

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known as: Old Yellow Enzyme

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core complex

Supplementary Table 2. Quantification of proteins.

	score	acc	Num	Protein Name	relative wild	ratio mutnat	
overlap detection	547	gi 6319279 re	Pyruvate kinase; Cdc19p		1	0.85	internal standard
	298	gi 6319279 re	Pyruvate kinase; Cdc19p		1	0.86	
	104	gi 6319673 re	Glucose-6-phosphate isomerase; Pgi1p		1	0.72	
	652	gi 6319857 re	3-phosphoglycerate kinase; Pgi1p		1	1.00	
	70	gi 6320145 re	Integrin analogue gene; Uso1p		1	1.00	
	152	gi 6320255 re	triosephosphate isomerase; Tpi1p		1	0.60	
	74	gi 6321131 re	type II PI(4)P5-kinase (PIP4,5 kinase) similar to human PIP5K-II; Fab1p		1	0.74	
	104	gi 6321243 re	translational activator of GCN4 through activation of GCN2 in response to starvation; Gcn1p				
	42	gi 6321757 re	involved in cell wall biogenesis; Ecm29p				
	529	gi 6321968 re	enolase; Eno2p		1	1.67	
	76	gi 6322042 re	colied-coil protein (putative), similar to myosin and TPR; Mlp2p				
	68	gi 6322988 re	component of peripheral vacuolar membrane protein complex; Vps13p				
	44	gi 6323002 re	104 kDa heat shock protein; Hsp104p		1	37.07	
	335	gi 6323073 re	pyruvate decarboxylase; Pdc1p		1	0.66	
	97	gi 6323462 re	component of a nuclear-localized tRNA splicing complex; Sen1p		1	1.18	
	52	gi 6323483 re	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme; Hmg2p				
	311	gi 6324120 re	Heat shock protein of HSP70 family, homolog of SSB1; Ssb2p		1	0.56	
	55	gi 6324358 re	A MAP kinase kinase; activator of Pbs2p; Ssk2p				
	108	gi 6325151 re	HSP70 family member, highly homologous to Ssa1p and Sse2p; Sse1p		1	2.68	
wild dominant detection	62	gi 6319262 re	Yal056wp				
	355	gi 6319314 re	Heat shock protein of HSP70 family, cytoplasmic; Ssa1p		1	0.00	
	48	gi 6319339 re	Shows homology to the human oxysterol binding protein (OSBP); Osh1p				
	93	gi 6319383 re	putative phosphatidylinositol kinase; Tel1p				
	65	gi 6319399 re	Ribosomal protein S8A (S14A) (rp19) (YS9); Rps8ap		1	0.35	
	43	gi 6319408 re	kinesin related protein; Kip1p				
	69	gi 6319444 re	Ribosomal protein L19B (YL14) (L23B) (rpl5L); Rpl19bp		1	0.45	
	52	gi 6319483 re	Inorganic pyrophosphatase; Ipp1p				
	102	gi 6319499 re	probable purine nucleotide-binding protein; Ybr025cp		1	1.26	
	148	gi 6319505 re	Ribosomal protein L4A (L2A) (rp2) (YL2); Rpl4ap		1	0.53	
	391	gi 6319594 re	translational elongation factor EF-1 alpha; Tef2p		1	2.78	
	42	gi 6319602 re	56 kD synthase subunit of trehalose-6-phosphate synthase/phosphatase complex; Tps1p				
	43	gi 6319616 re	GTPase activating protein; Ira1p				
	55	gi 6319666 re	Ribosomal protein S9B (S13) (rp21) (YS11); Rps9bp		1	1.13	
	45	gi 6319900 re	subunit of chromatin remodeling complex; Rsc6p				
	58	gi 6319918 re	shows similarity to glucose-6-phosphate dehydrogenase homologous to Sol1p				
	580	gi 6319972 re	cytoplasmic member of the HSP70 family; Ssb1p		1	0.22	
	52	gi 6320030 re	Glutamate synthase (NADPH); Glt1p				
	64	gi 6320100 re	UDP-N-acetylglucosamine pyrophosphorylase; Qri1p				
	73	gi 6320121 re	Ribosomal protein L13A; Rpl13ap				
	44	gi 6320223 re	Ydr020cp				
	77	gi 6320226 re	seryl-tRNA synthetase; Ses1p				
	41	gi 6320381 re	transcription factor; genetic and mutant analyses suggest that Ngg1p (Ada3p)		1	0.09	
	50	gi 6320386 re	Scc2p				
	91	gi 6320432 re	adenylate kinase; Adk1p		1	0.44	
	77	gi 6320496 re	Rtt103p				
	125	gi 6320499 re	Ssd1p		1	0.00	
	343	gi 6320593 re	translation elongation factor 2 (EF-2); Eft2p		1	0.83	
	87	gi 6320598 re	similar to ubiquitin activating enzyme (E1); Uba2p		1	0.11	
	57	gi 6320805 re	similar to Hsp70, involved in cell wall biogenesis; Ecm10p		1	0.24	
	109	gi 6320882 re	putative S-adenosyl-L-homocysteine hydrolase; Sah1p		1	1.16	
	92	gi 6320933 re	nuclear protein with Myb domain involved in telomeric silencing; Dot6p				
	56	gi 6320936 re	vitamin B12-(cobalamin)-independent isozyme of methionine synthase		1	0.42	
	72	gi 6320992 re	Putative Ubiquitin-specific protease; Ubp5p				
	43	gi 6321075 re	Yfi034wp				
	117	gi 37362646 re	Blm10p		1	0.00	
	133	gi 6321145 re	Ribosomal protein L2A (L5A) (rp8) (YL6); Rpl2ap		1	0.83	
	41	gi 6321184 re	Hexokinase II (PII) (also called Hexokinase B); Hxk2p		1	0.89	
	129	gi 6321192 re	Ygl245wp		1	0.93	
	54	gi 6321305 re	A subunit of Isw2 chromatin remodeling complex; Itc1p				
	45	gi 6321315 re	Ribosomal protein S2 (S4) (rp12) (YS5); Rps2p		1	0.42	
	154	gi 6321362 re	Ribosomal protein L7A (L6A) (rp11) (YL8); Rpl7ap		1	0.53	
	54	gi 6321522 re	60S ribosomal protein L11B (L16B) (rp39B) (YL22); Rpl11bp		1	1.39	
	57	gi 6321523 re	Ygr086cp		1	2.09	
	324	gi 6321631 re	Glyceraldehyde-3-phosphate dehydrogenase 3; Tdh3p		1	1.67	
	49	gi 6321673 re	Yhb1p		1	0.52	
	251	gi 6321693 re	enolase I; Eno1p		1	3.48	
	124	gi 6321786 re	Ribosomal protein L14B; Rpl14bp		1	0.39	
	76	gi 6321809 re	40S Ribosomal protein S27B (rp61) (YS20); Rps27bp		1	1.81	
	66	gi 6321812 re	Class II Myosin; Myo1p		1	0.21	
	70	gi 6321817 re	Dipeptidyl aminopeptidase B (DPAP B); Dap2p				
	81	gi 6321891 re	ATM/Mec1/TOR1+2-related; Tra1p				

	87 gi 6321948 re involved in silencing; Esc4p		
	60 gi 6322022 re serine-, threonine-rich protein; Yil169cp		
	59 gi 6322112 re Threonyl-tRNA synthetase, cytoplasmic; Ths1p	1	0.97
	71 gi 6322136 re DL-glycerol-3-phosphatase; Rhr2p	1	0.44
	63 gi 6322271 re Ribosomal protein S22A (S24A) (rp50) (YS22); Rps22ap	1	2.78
	54 gi 6322294 re Farnesyl diphosphate synthetase (FPP synthetase); Erg20p	1	1.76
	93 gi 6322323 re translation initiation factor eIF4A; Tif2p	1	1.04
	76 gi 6322331 re carbamoyl-phosphate synthetase, Ura2p	1	0.00
	43 gi 6322366 re MEKK serine/threonine kinase; Bck1p	1	0.00
	55 gi 6322426 re Homologue of mammalian BiP (GPR78) protein; member of the HSP70 gene family; Ka	1	1.85
	75 gi 6322505 re Mitochondrial matrix protein involved in protein import; subunit of Scl endonuclease; S	1	0.00
	74 gi 6322564 re Cu, Zn superoxide dismutase; Sod1p	1	1.39
	61 gi 6322565 re Yjr105wp	1	0.98
	48 gi 6322581 re F(1)F(0)-ATPase complex beta subunit, mitochondrial; Atp2p		
	173 gi 6322583 re Ribosomal protein S5 (S2) (rp14) (YS8); Rps5p	1	0.70
	147 gi 6322668 re Ribosomal protein L17A (L20A) (YL17); Rpl17ap	1	0.59
	392 gi 6322697 re Phosphoglycerate mutase; Gpm1p	1	1.39
	49 gi 6322714 re Beta-adaptin, large subunit of the clathrin-associated protein (AP-1) complex; Apl2p	1	0.82
	81 gi 6322790 re aldolase; Fba1p	1	0.70
	49 gi 6322813 re transcriptional repressor and activator; Rgt1p		
	54 gi 6322840 re U1 snRNP protein; Prp40p		
	61 gi 6322842 re involved in ubiquitin-mediated protein degradation; Ufd4p		
	122 gi 6322907 re heavy chain of cytoplasmic dynein; Dyn1p		
	85 gi 6322937 re Hbs1p		
	165 gi 6322984 re Ribosomal protein L8B (L4B) (rp6) (YL5); Rpl8bp	1	0.70
	399 gi 6323004 re member of 70 kDa heat shock protein family; Ssa2p	1	0.00
	246 gi 6323004 re member of 70 kDa heat shock protein family; Ssa2p	1	0.00
	98 gi 6323087 re serine hydroxymethyltransferase; Shm2p	1	1.11
	80 gi 6323104 re Ribosomal protein L10; Ubiquinol-cytochrome C reductase complex subunit VI requiring	1	0.46
	98 gi 6323135 re Ylr106cp		
	233 gi 6323278 re EF-3 (translational elongation factor 3); Yef3p	1	0.37
	289 gi 6323288 re mitochondrial chaperonin, homolog of E. coli groEL protein; Hsp60p	1	3.82
	48 gi 6323340 re Imh1p		
	113 gi 6323371 re 60S ribosomal protein P0 (A0) (L10E); Rpp0p	1	0.86
	49 gi 6323459 re Ylr427wp		
	69 gi 6323464 re Ylr432wp		
	60 gi 6323474 re Ribosomal protein S1A (rp10A); Rps1ap		
	49 gi 6323539 re zinc-finger transcription factor of the Zn(2)-Cys(6) binuclear cluster domain type; Arg81p		
	162 gi 6323577 re Ribosomal protein S1B (rp10B); Rps1bp	1	0.83
	54 gi 6323613 re thioredoxin-peroxidase (TPx); reduces H2O2 and alkyl hydroperoxides with the use of hy	1	0.95
	430 gi 6323840 re constitutively expressed heat shock protein; Hsc82p	1	4.46
	95 gi 6323861 re phosphofructokinase beta subunit; Pfk2p	1	0.28
	93 gi 6324151 re Ribosomal protein S3 (rp13) (YS3); Rps3p	1	0.11
	54 gi 6324162 re CREB like repressor, bZIP protein that binds to CRE motifs, interacts with Mig1p; Sko1p	1	0.00
	64 gi 6324314 re Ynl014wp		
	58 gi 6324434 re Yol138cp		
	200 gi 6324486 re Alcohol dehydrogenase; Adh1p	1	1.11
	43 gi 6324660 re Yor086cp	1	0.00
	180 gi 6324670 re Ribosomal protein S7A (rp30); Rps7ap	1	1.33
	83 gi 6324791 re Subunit 1 of Replication Factor C; homologous to human RFC 140 kDa subunit; Rfc1p		
	62 gi 6324801 re Yor227wp		
	60 gi 6324870 re Yor296wp		
	53 gi 6324897 re dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase; Pmt3p		
	64 gi 6324911 re Cytoplasmic alanyl-tRNA synthetase gene; Ala1p	1	0.81
	59 gi 6325126 re Ribosomal protein L5 (L1a)(YL3); Rpl5p	1	1.04
	116 gi 6325176 re Ribosomal protein S9A (S13) (rp21) (YS11); Rps9ap	1	0.98
	222 gi 6325196 re Cytosolic Aldehyde Dehydrogenase; Ald6p	1	0.49
	57 gi 6325241 re Zinc-finger transcription factor; Swi1p		
	69 gi 6325372 re Ypr115wp		
	59 gi 6325432 re Ypr174cp		
mutant dominant detection	44 gi 6226520 re maturase aI1; intron-specific reverse transcriptase activity; Ailp	1	0.52
	58 gi 6319300 re SNF2 protein family; Fun30p	0	1.00
	42 gi 6319329 re similar to Pau3, member of Pau1 family; Pau7p		
	52 gi 6319336 re membrane protein; Yar033wp	1	8.34
	75 gi 6319344 re Yar061wp		
	45 gi 6319396 re heat-inducible cytosolic member of the 70 kDa heat shock protein family; Ssa3p	1	13.90
	46 gi 6319413 re putative regulatory subunit for Glc7p, a phosphatase required for glucose repression;	1	1.85
	49 gi 6319497 re chitin synthase 3; Chs3p	0	1.00
	58 gi 6319616 re GTPase activating protein; Ira1p	1	6.95
	84 gi 6319718 re Probable sugar transport protein; Ybr241cp	1	1.85
	65 gi 6319724 re Putative 57 kDa protein with an apparent MW of 70 kDa by SDS-PAGE; Enp1p	0	1.00
	60 gi 6319737 re (putative) GTPase-activating protein; Rgd1p		
	81 gi 6319772 re Putative P-type Cu(2+)-transporting ATPase; Pca1p	1	8.34
	54 gi 6319941 re permease involved in the uptake of glycerophosphoinositol (GroPIns); Git1p	1	1.95
	66 gi 6320047 re MutS homolog involved in chromosome exchange; Msh5p		

70 gi 6320091 re tRNA (Gm18) ribose methylase; Trm3p	1	20.85
46 gi 6320245 re Plasma membrane Na+ pump; P-type ATPase; Ena1p	1	1.39
49 gi 6320318 re 42-kDa nuclear protein; Pds1p		
50 gi 6320347 re (putative) transcriptional regulator; San1p		
67 gi 6320419 re Ydr213wp	1	3.48
51 gi 6320433 re regulator of silencing at HML, HMR, and telomeres; Sir4p	1	11.12
51 gi 6320517 re Component of transcription initiation factor IIb, 75 kDa subunit; Tfb1p	1	0.46
41 gi 6320614 re probable multidrug resistance transporter; Pdr15p		
72 gi 6320813 re ARF GTP/GDP exchange factor; Gea2p		
44 gi 6320914 re ribonucleotide reductase; Rnr1p		
54 gi 6320919 re Protein tyrosine phosphatase; Ptp3p		
52 gi 6320931 re Yer087wp		
43 gi 6321005 re Sec34p is a 92.5 kD protein that is primarily cytosolic but a small pool associates with the	1	6.95
70 gi 6321076 re Trehalose-associated protein kinase related to S. pombe cek1+; Rim15p		
42 gi 6321079 re Yfl030wp		
54 gi 6321104 re SMC chromosomal ATPase family member; Smc1p		
43 gi 6321110 re TyB Gag-Pol protein.; Yfl002w-ap		
49 gi 6321196 re Kap114p		
50 gi 6321298 re Ygl140cp		
103 gi 6321552 re transcriptional regulator, interacts with histones, primarily histone H3, possesses nucleosome asse		
45 gi 6321613 re ubiquinol--cytochrome-c reductase assembly factor; Cbp4p	1	2.57
90 gi 6321653 re Ribosomal protein S0A; Rps0ap	0	1.00
70 gi 6321662 re Ygr223cp		
44 gi 6321813 re 53 kDa subunit of the mitochondrial processing protease; Mas2p		
47 gi 6321891 re ATM/Mec1/TOR1+2-related; Tra1p	1	2.32
59 gi 6321895 re involved in bud growth; Sbe22p	1	45.87
53 gi 6321995 re Cytosolic exopolyphosphatase; Ppx1p		
46 gi 6322010 re TyB Gag-Pol protein.; Yhr214c-bp	1	2.76
70 gi 6322020 re potential membrane glycoprotein with strong similarity to Vth2 and Pep1/Vps10; Vth1p		
112 gi 6322062 re Tao3p		
53 gi 6322254 re Yjl207cp		
72 gi 6322254 re Yjl207cp		
48 gi 6322390 re Acetylglutamate Synthase; Arg2p		
45 gi 6322631 re Pyridoxal-5'phosphate-dependent enzyme homologous to mouse glial serine racemase; S	1	8.34
82 gi 6322634 re Ykl215cp		
93 gi 6322636 re phospholipase A2-activating protein; Doa1p		
45 gi 6322830 re putative metal-binding nucleic acid-binding protein, interacts with Cdc23p and Cdc27p to catalyze t		
50 gi 6322835 re DNA helicase A; Hcs1p		
43 gi 6322883 re Phospholipase D; Spo14p		
58 gi 6322932 re Ykr079cp		
48 gi 6323076 re Ylr047cp		
65 gi 6323115 re SMC chromosomal ATPase family member; Smc4p	1	6.95
76 gi 6323135 re Ylr106cp		
53 gi 6323487 re Ylr454wp		
75 gi 6323568 re Yml072cp		
48 gi 6323647 re involved in protein synthesis; Mpt1p		
112 gi 6323753 re Yku80p		
41 gi 6323961 re alcohol dehydrogenase II; Adh2p		
45 gi 6324058 re contains formin homology domains; homologous to BNRI (BNI1 related protein); Bni1p		
62 gi 6324109 re adenylosuccinate synthetase; Ade12p		
44 gi 6324456 re 43 kDa protein, transcriptional activator; Msn1p		
67 gi 6324497 re involved in mitochondrial inheritance and actin assembly; Mdm20p		
126 gi 6324585 re Yor011wp		
53 gi 6324829 re Yor255wp		
68 gi 6324917 re RNA polymerase I subunit 190 (alpha); Rpa190p		
75 gi 6324925 re involved in chromosome segregation; Cin1p		
52 gi 6325016 re 82 kDa heat shock protein; homolog of mammalian Hsp90; Hsp82p		
51 gi 6325078 re protein phosphatase Q; Ppq1p		
60 gi 6325089 re Ypl168wp		
97 gi 6325153 re Aspartyl-tRNA synthetase, mitochondrial; Msd1p	1	9.27
45 gi 6325238 re polyphosphate synthetase (putative); Phm2p		
44 gi 6325282 re novel cyclin gene; encodes subunits of TFIIF, a subcomplex of transcription factor TFIIF; Ccl1p		
53 gi 6325302 re Ypr045cp		
47 gi 6325331 re Transketolase 1; Tk1p	1	13.90
44 gi 6325361 re Protein with a domain similar to the fork head DNA-binding domain found in the developmental fork h		
47 gi 6381999 re intron of mitochondrial COX1, aI5-beta; Ai5_betap		

Supplementary Table 3. Description of the up-regulated proteins in the *ssa1/2* mutant (over 2-fold).

GI Acc. Num.	ORF Code	Common Name	Relative Ratio	Description (SGD)	Biological Process (GO)	mRNA*
6319497	YBR023C	Chs3p	ss	Chitin synthase III, catalyzes the transfer of N-acetylglucosamine (GlcNAc) to chitin; required for synthesis of the majority of cell wall chitin, the chitin ring during bud emergence, and spore wall chitosan	cell wall chitin biosynthesis cytokinesis spore wall assembly	0.6
6319724	YBR247C	Enp1p	ss	Protein associated with U3 and U14 snoRNAs, required for pre-rRNA processing and 40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the nucleolus	35S primary transcript processing rRNA processing ribosome biogenesis and assembly	1.6
6321653	YGR214W	Rps0ap	ss	Protein component of the small (40S) ribosomal subunit, nearly identical to Rps0Bp; required for maturation of 18S rRNA along with Rps0Bp; deletion of either RPS0 gene reduces growth rate, deletion of both genes is lethal. Also known as: NAB1A	translation ribosomal small subunit assembly and maintenance	1.3
6319300	YAL019W	Fun30p	ss	Protein whose overexpression affects chromosome stability, potential Cdc28p substrate; homolog of Snf2p	chromosome organization and biogenesis	1
6321895	YHR103W	Sbe22p	45.9	Protein involved in the transport of cell wall components from the Golgi to the cell surface; similar in structure and functionally redundant with Sbe2p; involved in bud growth	cell wall organization and biogenesis	1.5
6323002	YLL026W	Hsp104p	37.1	Heat shock protein that cooperates with Ydj1p (Hsp40) and Ssa1p (Hsp70) to refold and reactivate previously denatured, aggregated proteins; responsive to stresses including: heat, ethanol, and sodium arsenite; involved in [PSI ⁺] propagation	chaperone cofactor dependent protein folding response to stress telomere maintenance	5.5
6320091	YDL112W	Trm3p	20.9	2'-O-ribose methyltransferase, catalyzes the ribose methylation of the guanosine nucleotide at position 18 of tRNAs	tRNA methylation	0.6
6325331	YPR074C	Tkl1p	13.9	Transketolase, similar to Tkl2p; catalyzes conversion of xylulose-5-phosphate and ribose-5-phosphate to sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate in the pentose phosphate pathway; needed for synthesis of aromatic amino acids	pentose-phosphate shunt	nd
6319396	YBL075C	Ssa3p	13.9	ATPase involved in protein folding and the response to stress; plays a role in SRP-dependent cotranslational protein-membrane targeting and translocation; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm	SRP-dependent cotranslational protein targeting to membrane, translocation protein folding response to stress	3
6320433	YDR227W	Sir4p	11.1	Silent information regulator that, together with SIR2 and SIR3, is involved in assembly of silent chromatin domains at telomeres and the silent mating-type loci; potentially phosphorylated by Cdc28p; some alleles of SIR4 prolong lifespan	chromatin silencing double-strand break repair via nonhomologous end-joining loss of chromatin silencing during replicative cell aging telomere maintenance	1.2**
6325153	YPL104W	Msd1p	9.3	Mitochondrial aspartyl-tRNA synthetase, required for acylation of aspartyl-tRNA; yeast and bacterial aspartyl-, asparaginyl-, and lysyl-tRNA synthetases contain regions with high sequence similarity, suggesting a common ancestral gene	translation	1.3
6319336	YAR033W	Mst28p	8.3	Putative integral membrane protein, involved in vesicle formation; forms complex with Mst27p; member of DUP240 gene family; binds COPI and COPII vesicles	vesicle organization and biogenesis	1
6319772	YBR295W	Pca1p	8.3	P-type metal-transporting ATPase with a role in copper and iron homeostasis; R970G-substitution in the C-terminal region confers cadmium resistance	cadmium ion transport iron homeostasis metal ion homeostasis	1
6322631	YKL218C	Sry1p	8.3	3-hydroxyaspartate dehydratase, deaminates L-threo-3-hydroxyaspartate to form oxaloacetate and ammonia; required for survival in the presence of hydroxyaspartate	amino acid derivative catabolic process	1
6321005	YER157W	Cog3p	7.0	Essential component of the conserved oligomeric Golgi complex (Cog1p through Cog8p), a cytosolic tethering complex that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments	ER to Golgi vesicle-mediated transport intra-Golgi vesicle-mediated transport retrograde transport, vesicle recycling within Golgi	0.6
6323115	YLR086W	Smc4p	7.0	Subunit of the condensin complex, which reorganizes chromosomes during cell division, forms a stable complex with Smc2p that has ATP-hydrolyzing and DNA-binding activity and promotes knotting of circular DNA; potential Cdc28p substrate	mitotic chromosome condensation mitotic sister chromatid segregation	0.8
6319616	YBR140C	Ira1p	7.0	GTPase-activating protein that negatively regulates RAS by converting it from the GTP- to the GDP-bound inactive form, required for reducing cAMP levels under nutrient limiting conditions, mediates membrane association of adenylate cyclase	negative regulation of Ras protein signal transduction negative regulation of cAMP biosynthetic process positive regulation of Ras GTPase activity regulation of adenylatecyclase activity	nd
6323840	YMR186W	Hsc82p	4.5	Cytoplasmic chaperone of the Hsp90 family, redundant in function and nearly identical with Hsp82p, and together they are essential; expressed constitutively at 10-fold higher basal levels than HSP82 and induced 2-3 fold by heat shock	proteasome assembly protein folding response to stress telomere maintenance	3.1
6323288	YLR259C	Hsp60p	3.8	Tetradecameric mitochondrial chaperonin required for ATP-dependent folding of precursor polypeptides and complex assembly; prevents aggregation and mediates protein refolding after heat shock; role in mtDNA transmission; similarity to groEL	protein folding protein import into mitochondrial matrix	2.5

6321693	YGR254W	Eno1p	3.5 Enolase I, a phosphopyruvate hydratase that catalyzes the conversion of 2-phosphoglycerate to phosphoenolpyruvate during glycolysis and the reverse reaction during gluconeogenesis; expression is repressed in response to glucose	gluconeogenesis glycolysis regulation of vacuole fusion, non-autophagic	1.6
6320419	YDR213W	Upc2p	3.5 Sterol regulatory element binding protein, induces transcription of sterol transport and biosynthetic genes; involved in the anaerobic induction of DAN/TIR mannoproteins and seripauperins; binucleate zinc cluster protein; Ecm22p homolog	steroid metabolism sterol biosynthesis	0.8
6319594	YBR118W	Tef2p	2.8 Translational elongation factor EF-1 alpha; also encoded by TEF1; functions in the binding reaction of aminoacyl-tRNA (AA-tRNA) to ribosomes. Also known as: EF-1 alpha, eEF1A	tRNA export from nucleus translational elongation	1.5
6322271	YLR367W	Rps22bp	2.8 Protein component of the small (40S) ribosomal subunit; nearly identical to Rps22Ap and has similarity to E. coli S8 and rat S15a ribosomal proteins	translation	0.8
6322010	YHR214C-B	Yhr214c-bp	2.8 Retrotransposon TYA Gag and TYB Pol genes; transcribed/translated as one unit; polyprotein is processed to make a nucleocapsid-like protein (Gag), reverse transcriptase (RT), protease (PR), and integrase (IN); similar to retroviral genes	transposition, RNA-mediated	nd
6325151	YPL106W	Sse1p	2.7 ATPase that is a component of the heat shock protein Hsp90 chaperone complex; binds unfolded proteins; member of the heat shock protein 70 (HSP70) family; localized to the cytoplasm	protein folding telomere maintenance	3.1
6321613	YGR174C	Cbp4p	2.6 Mitochondrial protein required for assembly of ubiquinol cytochrome-c reductase complex (cytochrome bc1 complex); interacts with Cbp3p and function is partially redundant with that of Cbp3p	protein complex assembly	0.9
6321891	YHR099W	Tra1p	2.3 Subunit of SAGA and NuA4 histone acetyltransferase complexes; interacts with acidic activators (e.g., Gal4p) which leads to transcription activation; similar to human TRRAP, which is a cofactor for c-Myc mediated oncogenic transformation	DNA repair histone acetylation regulation of transcription from RNA polymerase II promoter	nd
6321523	YGR086C	Pil1p	2.1 Integral membrane protein that along with Lsp1p is a primary component of eisosomes, large immobile patch structures at the cell cortex associated with endocytosis; null mutants show activation of Pkc1p/Ypk1p stress resistance pathways	endocytosis protein localization response to heat	1.4

*mRNA ratio is described in Matsumoto et al (2005)

**reference data which was determined by single experiment

ss. *ssa1/2* mutant specific

nd. not detected

Supplementary Table 4. Description of the down-regulated proteins in the *ssa1/2* mutant (less than 2-fold).

GI Acc. Num.	ORF Code	Common Name	Relative Ratio	Description (SGD)	Biological Process (GO)	mRNA*
6320499	YDR293C	Ssd1p	ws	Protein with a role in maintenance of cellular integrity; interacts with components of the TOR pathway; ssd1 mutant of a clinical <i>S. cerevisiae</i> strain displays elevated virulence	cell wall organization and biogenesis replicative cell aging response to drug	0.6
37362646	YFL007W	Blm10p	ws	Proteasome activator subunit; found in association with core particles, with and without the 19S regulatory particle; required for resistance to bleomycin, may be involved in protecting against oxidative damage; similar to mammalian PA200	proteasome assembly protein catabolic process	nd
6322331	YJL130C	Ura2p	ws	Bifunctional carbamoylphosphate synthetase (CPSase)-aspartate transcarbamylase (ATCase), catalyzes the first two enzymatic steps in the de novo biosynthesis of pyrimidines; both activities are subject to feedback inhibition by UTP	de novo' pyrimidine base biosynthetic process glutamine metabolic process pyrimidine base biosynthetic process	nd
6322366	YJL095W	Bck1p	ws	Mitogen-activated protein (MAP) kinase kinase kinase acting in the protein kinase C signaling pathway, which controls cell integrity; upon activation by Pkc1p phosphorylates downstream kinases Mkk1p and Mkk2p	establishment of cell polarity protein amino acid phosphorylation protein kinase cascade response to acid response to nutrient unfolded protein response	0.8
6322505	YJR045C	Ssc1p	ws	Mitochondrial matrix ATPase that is a subunit of the presequence translocase-associated protein import motor (PAM); involved in protein translocation into the matrix and protein folding; member of the heat shock protein 70 (HSP70) family. Also known as: mtHSP70	protein folding protein import into mitochondrial matrix	1.1
6323004	YLL024C	Ssa2p	ws	ATP binding protein involved in protein folding and vacuolar import of proteins; member of heat shock protein 70 (HSP70) family; associated with the chaperonin-containing T-complex; present in the cytoplasm, vacuolar membrane and cell wall	SRP-dependent cotranslational protein targeting membrane, translocation protein folding response to stress	nd
6324162	YNL167C	Sko1p	ws	Basic leucine zipper (bZIP) transcription factor of the ATF/CREB family that forms a complex with Tup1p and Ssn6p to both activate and repress transcription; cytosolic and nuclear protein involved in the osmotic and oxidative stress responses	negative regulation of transcription from RNA polymerase II promoter	0.8
6324660	YOR086C	Tcb1p	ws	Contains three calcium and lipid binding domains; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery; C-terminal portion of Tcb1p, Tcb2p and Tcb3p	biological process unknown	0.9
6320381	YDR176W	Ngg1p	-10.5	Transcriptional regulator involved in glucose repression of Gal4p-regulated genes; component of transcriptional adaptor and histone acetyltransferase complexes, the ADA complex, the SAGA complex, and the SLIK complex	chromatin modification histone acetylation response to drug	nd
6320598	YDR390C	Uba2p	-9.0	Nuclear protein that acts as a heterodimer with Aos1p to activate Smt3p (SUMO) before its conjugation to proteins (sumoylation), which may play a role in protein targeting; essential for viability	protein sumoylation	0.6
6324151	YNL178W	Rps3p	-8.8	Protein component of the small (40S) ribosomal subunit, has apurinic/apyrimidinic (AP) endonuclease activity; essential for viability; has similarity to E. coli S3 and rat S3 ribosomal	translation response to DNA damage stimulus	1.1
6321812	YHR023W	Myo1p	-4.8	Type II myosin heavy chain, required for wild-type cytokinesis and cell separation; localizes to the actomyosin ring; binds to myosin light chains contractile ring contraction and formation Mlc1p and Mlc2p through its IQ1 and IQ2 motifs respectively	cytokinesis, completion of separation; separation; localizes to the actomyosin ring; binds to myosin light chains contractile ring contraction and formation	0.6
6319972	YDL229W	Ssb1p	-4.5	Cytoplasmic ATPase that is a ribosome-associated molecular chaperone, functions with J-protein partner Zuo1p; may be involved in folding of newly-made polypeptide chains; member of the HSP70 family; interacts with phosphatase subunit Reg1p	cotranslational protein folding translation regulation of translational fidelity	0.7
6320805	YEL030W	Ecm10p	-4.2	Heat shock protein of the Hsp70 family, localized in mitochondrial nucleoids, plays a role in protein translocation, interacts with Mge1p in an ATP-dependent manner; overexpression induces extensive mitochondrial DNA aggregations	protein refolding protein targeting to mitochondrion	0.5
6323861	YMR205C	Pfk2p	-3.6	Beta subunit of heterooctameric phosphofructokinase involved in glycolysis, indispensable for anaerobic growth, activated by fructose-2,6-bisphosphate and AMP, mutation inhibits glucose induction of cell cycle-related genes	glycolysis	0.9
6319399	YBL072C	Rps8ap	-2.9	Protein component of the small (40S) ribosomal subunit; identical to Rps8Ap and has similarity to rat S8 ribosomal protein	translation	1.3
6323278	YLR249W	Yef3p	-2.7	Translational elongation factor, stimulates the binding of aminoacyl-tRNA (AA-tRNA) to ribosomes by releasing EF-1 alpha from the ribosomal complex; contains two ABC cassettes; binds and hydrolyses ATP. Also known as: EF-3	ribosome biogenesis and assembly translational elongation	0.9
6321786	YHL001W	Rpl14b	-2.6	Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl14Ap and has similarity to rat L14 ribosomal protein	translation	1.2
6320936	YER091C	Met6p	-2.4	Cobalamin-independent methionine synthase, involved in amino acid biosynthesis; requires a minimum of two glutamates on the methyltetrahydrofolate substrate, similar to bacterial metE homologs	methionine biosynthetic process	0.7
6321315	YGL123W	Rps2p	-2.4	Protein component of the small (40S) subunit, essential for control of translational accuracy; has similarity to E. coli S5 and rat S2 ribosomal proteins	translation regulation of translational fidelity	1.2

6320432	YDR226W	Adk1p	-2.3 Adenylate kinase, required for purine metabolism; localized to the cytoplasm and the mitochondria; lacks cleavable signal sequence	ADP biosynthetic process nucleotide metabolic process	1
6322136	YIL053W	Rhr2p	-2.3 Constitutively expressed isoform of DL-glycerol-3-phosphatase; involved in glycerol biosynthesis, induced in response to both anaerobic and, along with the Hor2p/Gpp2p isoform, osmotic stress	glycerol biosynthetic process response to osmotic stress	1.2
6319444	YBL027W	Rpl19b	-2.2 Protein component of the large (60S) ribosomal subunit, nearly identical to Rpl19Bp and has similarity to rat L19 ribosomal protein; rpl19a and rpl19b single null mutations result in slow growth, while the double null mutation is lethal	translation	1.4
6323104	YLR075W	Rpl10	-2.2 Protein component of the large (60S) ribosomal subunit, responsible for joining the 40S and 60S subunits; regulates translation initiation; has similarity to rat L10 ribosomal protein and to members of the QM gene family	translation ribosomal large subunit assembly and maintenance	0.9
6320517	YDR311W	Tfb1p	-2.2 Subunit of TFIIH and nucleotide excision repair factor 3 complexes, required for nucleotide excision repair, target for transcriptional activators	negative regulation of transcription from RNA polymerase II promoter, mitotic nucleotide-excision repair nucleotide-excision repair, DNA duplex unwinding transcription initiation from RNA polymerase II promoter	1.1
6325196	YPL061W	Ald6p	-2.0 Cytosolic aldehyde dehydrogenase that is activated by Mg ²⁺ and utilizes NADP ⁺ as the preferred coenzyme; required for the conversion of acetaldehyde to acetate; constitutively expressed	acetate biosynthetic process	1.8

*mRNA ratio is described in Matsumoto et al (2005)

ws. wild type specific

nd. not detected