

Table S3. Proteins present in three Brettanomyces strains

LAMAP LAMAP2480_0009	vacuolar protein sorting-associated protein 16 homolog
CBS2499v2 CBS2499_0032	vacuolar protein sorting-associated protein 16 homolog
AWRIv2 AWRI_0804	vacuolar protein sorting-associated protein 16 homolog
LAMAP LAMAP2480_0024	receptor cluster member 8 homolog
CBS2499v2 CBS2499_0048	receptor cluster member 8 homolog
AWRIv2 AWRI_0818	homolog C2A9.11c
LAMAP LAMAP2480_0028	binding protein with preference for single stranded tracts of U's involved in synthesis of both 18S and 5.8S rRNAs; component of both the ribosomal small subunit (SSU) processosome and the 90S preribosome
CBS2499v2 CBS2499_0052	binding protein involved in synthesis of both 18S and 5.8S rRNAs; component of both the ribosomal small subunit (SSU) processosome and the 90S preribosome; acts as part of a Mak21p-Noc2p-Rrp5p module that associates with nascent pre-rRNA during transcription and has a role in bigenesis of the large ribosomal subunit; has binding preference for single stranded tracts of U's; relocalizes from nucleolus to nucleus upon DNA replication stress
AWRIv2 AWRI_0822	nucleotidyltransferase
LAMAP LAMAP2480_0033	protein _1004
CBS2499v2 CBS2499_0057	protein _1004
AWRIv2 AWRI_0826	protein _1004
LAMAP LAMAP2480_0054	GIR2
CBS2499v2 CBS2499_0076	GIR2
AWRIv2 AWRI_0843	GIR2
LAMAP LAMAP2480_0070	protein _1041
CBS2499v2 CBS2499_0089	protein _1041
AWRIv2 AWRI_0854	protein _1041
LAMAP LAMAP2480_0098	fusion degradation protein 4
CBS2499v2 CBS2499_0111	fusion degradation protein 4
AWRIv2 AWRI_3815	fusion degradation protein 4
LAMAP LAMAP2480_0112	protein _3833
CBS2499v2 CBS2499_0125	protein _3833
AWRIv2 AWRI_3189	protein _3833
LAMAP LAMAP2480_0115	RPN4
CBS2499v2 CBS2499_0130	regulator RPN4
AWRIv2 AWRI_3194	regulator RPN4
LAMAP LAMAP2480_0117	nuclear membrane protein SRC1
CBS2499v2 CBS2499_0132	nuclear membrane protein SRC1
AWRIv2 AWRI_3196	chromatid separation protein
LAMAP LAMAP2480_0119	proton symporter of the plasma membrane, subject to glucose-induced inactivation, strongly but transiently induced when cells are subjected to osmotic shock
CBS2499v2 CBS2499_0134	proton symporter of the plasma membrane; subject to glucose-induced inactivation, strongly but transiently induced when cells are subjected to osmotic shock
AWRIv2 AWRI_3199	proton symporter of the plasma membrane; subject to glucose-induced inactivation, strongly but transiently induced when cells are subjected to osmotic shock

LAMAP LAMAP2480_0122	protein CUE5	
CBS2499v2 CBS2499_0137	protein CUE5	
AWRIv2 AWRI_3202	protein CUE5	
	of the Sec1p/Munc-18 family, essential for vacuolar protein sorting; required for the function of Pep12p and the early endosome/late Golgi SNARE Tlg2p; essential for fusion of Golgi-derived vesicles with the prevacuolar compartment	
LAMAP LAMAP2480_0131	of the Sec1p/Munc-18 family; essential for vacuolar protein sorting; required for the function of Pep12p and the early endosome/late Golgi SNARE Tlg2p; essential for fusion of Golgi-derived vesicles with the prevacuolar compartment	
	protein sorting-associated protein 45	
CBS2499v2 CBS2499_0144		2
AWRIv2 AWRI_3208		2
LAMAP LAMAP2480_0136		2
CBS2499v2 CBS2499_0148		
AWRIv2 AWRI_3214		
LAMAP LAMAP2480_0139	V, beta subunit	
CBS2499v2 CBS2499_0151	V, beta subunit	
AWRIv2 AWRI_3216	DNA helicase PcrA	
LAMAP LAMAP2480_0151	wos2	
CBS2499v2 CBS2499_0164	wos2	
AWRIv2 AWRI_2194	wos2	
LAMAP LAMAP2480_0152	oxidase, integral membrane protein with similarity to Fet3p; may have a role in iron transport	
CBS2499v2 CBS2499_0165	oxidase; integral membrane protein with similarity to Fet3p; may have a role in iron transport	
AWRIv2 AWRI_2195	oxidase; integral membrane protein with similarity to Fet3p; may have a role in iron transport	
LAMAP LAMAP2480_0155	transporter YNL095C	
CBS2499v2 CBS2499_0168	transporter YNL095C	
AWRIv2 AWRI_2198	transporter YNL095C	
	phosphatidylinositol transfer protein (PITP); exhibits PI- but not PC-transfer activity; localizes to the peripheral endoplasmic reticulum, cytosol and microsomes; similar to Sec14p	
LAMAP LAMAP2480_0177	protein	
CBS2499v2 CBS2499_0188	phosphatidylinositol transfer protein (PITP); exhibits PI- but not PC-transfer activity; localizes to the peripheral endoplasmic reticulum, cytosol and microsomes; similar to Sec14p; partially relocalizes to the plasma membrane upon DNA replication stress	
AWRIv2 AWRI_2216	OCA4	
LAMAP LAMAP2480_0180	OCA4	
CBS2499v2 CBS2499_0191	protein _2653	
AWRIv2 AWRI_2219	kinase PSK1	
LAMAP LAMAP2480_0184	kinase PSK1	
CBS2499v2 CBS2499_0196	kinase PSK2	
AWRIv2 AWRI_2224	chromatin-remodeling complex subunit snf5	
LAMAP LAMAP2480_0191	chromatin-remodeling complex subunit snf5	
CBS2499v2 CBS2499_0204	chromatin-remodeling complex subunit SNF5	
AWRIv2 AWRI_2231	factor 1-gamma 2	
LAMAP LAMAP2480_0192	S-transferase Y-2	
CBS2499v2 CBS2499_0205	S-transferase Y-2	
AWRIv2 AWRI_2232	S-transferase Y-2	

LAMAP|LAMAP2480_0196
CBS2499v2|CBS2499_0209
AWRIv2|AWRI_2235
LAMAP|LAMAP2480_0205
CBS2499v2|CBS2499_0218
AWRIv2|AWRI_2241
LAMAP|LAMAP2480_0214
CBS2499v2|CBS2499_0227
AWRIv2|AWRI_3284
LAMAP|LAMAP2480_0215
CBS2499v2|CBS2499_0228
AWRIv2|AWRI_3283
LAMAP|LAMAP2480_0239
CBS2499v2|CBS2499_0250
AWRIv2|AWRI_3263
LAMAP|LAMAP2480_0244
CBS2499v2|CBS2499_0255
AWRIv2|AWRI_3260
LAMAP|LAMAP2480_0256
CBS2499v2|CBS2499_0267
AWRIv2|AWRI_2007
LAMAP|LAMAP2480_0258
CBS2499v2|CBS2499_0269
AWRIv2|AWRI_2006

initiation factor IIE subunit alpha
initiation factor IIE subunit alpha
initiation factor IIE subunit alpha
fusion and transport protein UGO1
fusion and transport protein UGO1
fusion and transport protein UGO1
component SPP1
component SPP1
component SPP1
acetyltransferase type B subunit 2
acetyltransferase type B subunit 2
acetyltransferase type B subunit 2
family protein C10F6.14c
family protein C10F6.14c
family protein C10F6.14c
NRD1
NRD1
NRD1
protein _2405
protein _2405
protein _2405
protein YKL047W
protein ANR2
protein

LAMAP|LAMAP2480_0259

of unknown function that may interact with ribosomes, based on co-purification experiments; member of the ovarian tumor-like (OTU) superfamily of predicted cysteine proteases; shows cytoplasmic localization
of unknown function; may interact with ribosomes, based on co-purification experiments; member of the ovarian tumor-like (OTU) superfamily of predicted cysteine proteases; shows cytoplasmic localization; protein abundance increases in response to DNA replication stress
domain-containing protein 2

CBS2499v2|CBS2499_0271
AWRIv2|AWRI_2005
LAMAP|LAMAP2480_0267
CBS2499v2|CBS2499_0278
AWRIv2|AWRI_2002
LAMAP|LAMAP2480_0277
CBS2499v2|CBS2499_0288
AWRIv2|AWRI_1992
LAMAP|LAMAP2480_0286
CBS2499v2|CBS2499_0297
AWRIv2|AWRI_1987
LAMAP|LAMAP2480_0288
CBS2499v2|CBS2499_0299
AWRIv2|AWRI_1985
LAMAP|LAMAP2480_0295

repair protein RAD57
repair protein RAD57
repair protein RAD57
transcriptional regulatory protein C417.09c
transcriptional regulatory protein C417.09c
protein
protein _2375
protein _2375
protein _2375
kinase-like protein
kinase-like protein
kinase-like protein
dehydrogenase kinase 2, mitochondrial

CBS2499v2 CBS2499_0307 AWRIv2 AWRI_1980 LAMAP LAMAP2480_0312 CBS2499v2 CBS2499_0327 AWRIv2 AWRI_1965	dehydrogenase (acetyl-transferring)] kinase 2, mitochondrial dehydrogenase (acetyl-transferring)] kinase 2, mitochondrial light chain 5 light chain 5 light chain 5
LAMAP LAMAP2480_0350	of a Cdc48p-complex involved in protein quality control; exhibits cytosolic and ER-membrane localization, with Cdc48p, during normal growth, and contributes to ER-associated degradation (ERAD) of specific substrates at a step after their ubiquitination; forms a mitochondrially-associated complex with Cdc48p and Npl4p under oxidative stress that is required for ubiquitin-mediated mitochondria-associated protein degradation (MAD); conserved in <i>C. elegans</i> and humans
CBS2499v2 CBS2499_0366 AWRIv2 AWRI_3168 LAMAP LAMAP2480_0362 CBS2499v2 CBS2499_0378 AWRIv2 AWRI_3156 LAMAP LAMAP2480_0377 CBS2499v2 CBS2499_1423 AWRIv2 AWRI_3242 LAMAP LAMAP2480_0379 CBS2499v2 CBS2499_1425 AWRIv2 AWRI_3240	of a Cdc48p-complex involved in protein quality control; exhibits cytosolic and ER-membrane localization, with Cdc48p, during normal growth, and contributes to ER-associated degradation (ERAD) of specific substrates at a step after their ubiquitination; forms a mitochondrially-associated complex with Cdc48p and Npl4p under oxidative stress that is required for ubiquitin-mediated mitochondria-associated protein degradation (MAD); conserved in <i>C. elegans</i> and humans VMS1 ISD11 ISD11 ISD11 amidase C550.07 amidase C550.07 amidase C550.07 protein YOR352W protein YOR352W protein
LAMAP LAMAP2480_0403	subunit of the trehalose-6-phosphate synthase/phosphatase complex, which synthesizes the storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway subunit of the trehalose-6-P synthase/phosphatase complex; involved in synthesis of the storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway; protein abundance increases in response to DNA replication stress
CBS2499v2 CBS2499_1460 AWRIv2 AWRI_3768	of two isozymes of HMG-CoA reductase that catalyzes the conversion of HMG-CoA to mevalonate, which is a rate-limiting step in sterol biosynthesis; localizes to the nuclear envelope; overproduction induces the formation of karmellae
LAMAP LAMAP2480_0404	reductase; catalyzes the conversion of HMG-CoA to mevalonate, which is a rate-limiting step in sterol biosynthesis; one of two isozymes; localizes to the nuclear envelope; overproduction induces the formation of karmellae; forms foci at the nuclear periphery upon DNA replication stress; HMG1 has a paralog, HMG2, that arose from the whole genome duplication
CBS2499v2 CBS2499_1459 AWRIv2 AWRI_3769 LAMAP LAMAP2480_0416 CBS2499v2 CBS2499_1447	reductase, degradative type zinc finger protein asd-4 regulator GZF3

AWRlv2|AWRI_3224

regulator GZF3

component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); involved in protein import into mitochondrial matrix and inner membrane; with Tim17p, contributes to architecture and function of the import channel

LAMAP|LAMAP2480_0423

component of the TIM23 complex; involved in protein import into mitochondrial matrix and inner membrane; with Tim17p, contributes to architecture and function of the import channel; TIM23 complex is short for the translocase of the inner mitochondrial membrane

CBS2499v2|CBS2499_1440

component of the TIM23 complex; involved in protein import into mitochondrial matrix and inner membrane; with Tim17p, contributes to architecture and function of the import channel; TIM23 complex is short for the translocase of the inner mitochondrial membrane

AWRlv2|AWRI_3228

F-box protein ROY1

LAMAP|LAMAP2480_0430

F-box protein ROY1

CBS2499v2|CBS2499_1432

F-box protein ROY1

AWRlv2|AWRI_3232

starvation modulator protein 1

LAMAP|LAMAP2480_0441

starvation modulator protein 1

CBS2499v2|CBS2499_1422

starvation modulator protein 1

AWRlv2|AWRI_3243

finger protein YKR017C

LAMAP|LAMAP2480_0445

ubiquitin-protein ligase dbl4

CBS2499v2|CBS2499_1419

ubiquitin-protein ligase dbl4

AWRlv2|AWRI_3246

BCP1

LAMAP|LAMAP2480_0460

BCP1

CBS2499v2|CBS2499_1404

BCP1

AWRlv2|AWRI_2015

modification-related protein EAF1

LAMAP|LAMAP2480_0464

modification-related protein EAF1

CBS2499v2|CBS2499_1399

modification-related protein EAF1

AWRlv2|AWRI_2018

protein HPODL_02750

LAMAP|LAMAP2480_0479

protein HPODL_02750

CBS2499v2|CBS2499_1383

box protein I2

AWRlv2|AWRI_2035

kinase srk1

LAMAP|LAMAP2480_0512

kinase srk1

CBS2499v2|CBS2499_1351

kinase srk1

AWRlv2|AWRI_2062

polypeptide-associated complex subunit beta

LAMAP|LAMAP2480_0517

polypeptide-associated complex subunit beta

CBS2499v2|CBS2499_1345

polypeptide-associated complex subunit beta

AWRlv2|AWRI_2065

protein _2473

LAMAP|LAMAP2480_0522

protein _2473

CBS2499v2|CBS2499_1338

protein _2473

AWRlv2|AWRI_2071

peculiar membrane protein 1

LAMAP|LAMAP2480_0527

peculiar membrane protein 1

CBS2499v2|CBS2499_5081

peculiar membrane protein 1

AWRlv2|AWRI_2074

protein sorting-associated protein 52

LAMAP|LAMAP2480_0528

protein sorting-associated protein 52 A

CBS2499v2|CBS2499_1333

protein sorting-associated protein 52

AWRlv2|AWRI_2075

ATP-dependent helicase C144.05

LAMAP|LAMAP2480_0546

CBS2499v2 CBS2499_1319	ATP-dependent helicase C144.05
AWRiv2 AWRI_3590	ATP-dependent helicase IRC20
LAMAP LAMAP2480_0547	kinase srk1
CBS2499v2 CBS2499_1318	kinase srk1
AWRiv2 AWRI_3589	kinase srk1
LAMAP LAMAP2480_0552	protein _4281
CBS2499v2 CBS2499_1312	protein _4281
AWRiv2 AWRI_3584	protein _4281
LAMAP LAMAP2480_0555	polymerase I subunit A49
CBS2499v2 CBS2499_1308	polymerase I subunit A49; essential for nucleolar assembly and for high polymerase loading rate; required for nucleolar localization of Rpa34p
AWRiv2 AWRI_3580	polymerase I subunit A49; essential for nucleolar assembly and for high polymerase loading rate; required for nucleolar localization of Rpa34p
LAMAP LAMAP2480_0556	of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; induced by treatment with 8-methoxypsoralen and UVA irradiation
CBS2499v2 CBS2499_1307	of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; induced by treatment with 8-methoxypsoralen and UVA irradiation
AWRiv2 AWRI_3579	of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; induced by treatment with 8-methoxypsoralen and UVA irradiation
LAMAP LAMAP2480_0558	protein YMR310C
CBS2499v2 CBS2499_1305	methyltransferase YMR310C
AWRiv2 AWRI_3577	methyltransferase YMR310C
LAMAP LAMAP2480_0616	cytoplasmic protein of unknown function
CBS2499v2 CBS2499_1893	glycoside hydrolase of the mitochondrial intermembrane space
AWRiv2 AWRI_3988	glycoside hydrolase of the mitochondrial intermembrane space
LAMAP LAMAP2480_0618	protein
CBS2499v2 CBS2499_1896	protein
AWRiv2 AWRI_3984	protein
LAMAP LAMAP2480_0621	GDP-GTP exchange protein 2
CBS2499v2 CBS2499_1900	GDP-GTP exchange protein 2
AWRiv2 AWRI_3979	GDP-GTP exchange protein 2
LAMAP LAMAP2480_0630	protein _2022
CBS2499v2 CBS2499_4670	protein _2022
AWRiv2 AWRI_1716	protein _2022
LAMAP LAMAP2480_0636	kinase PTK1/STK1
CBS2499v2 CBS2499_4664	kinase PTK1/STK1
AWRiv2 AWRI_1718	kinase PTK2
LAMAP LAMAP2480_0638	endonuclease subunit SEN54
CBS2499v2 CBS2499_4663	endonuclease subunit SEN54
AWRiv2 AWRI_1719	endonuclease subunit SEN54
LAMAP LAMAP2480_0639	factor 11
CBS2499v2 CBS2499_4662	factor 11
AWRiv2 AWRI_1720	factor 11
LAMAP LAMAP2480_0646	phosphatase MSG5

CBS2499v2|CBS2499_4655
AWRIv2|AWRI_1724
LAMAP|LAMAP2480_0647
CBS2499v2|CBS2499_4654
AWRIv2|AWRI_1725
LAMAP|LAMAP2480_0649
CBS2499v2|CBS2499_4652
AWRIv2|AWRI_1727
LAMAP|LAMAP2480_0650
CBS2499v2|CBS2499_4651

phosphatase MSG5
phosphatase MSG5
repeat domain-containing protein 12
HOS4
protein
alcohol dehydrogenase transcriptional effector
alcohol dehydrogenase transcriptional effector
alcohol dehydrogenase transcriptional effector
III homolog
III homolog

AWRIv2|AWRI_1728
LAMAP|LAMAP2480_0651
CBS2499v2|CBS2499_4650
AWRIv2|AWRI_1729
LAMAP|LAMAP2480_0660
CBS2499v2|CBS2499_4639
AWRIv2|AWRI_1736
LAMAP|LAMAP2480_0679
CBS2499v2|CBS2499_4620
AWRIv2|AWRI_1750
LAMAP|LAMAP2480_0686
CBS2499v2|CBS2499_4613

N-glycosylase and apurinic/aprimidinic (AP) lyase; involved in base excision repair, localizes to the nucleus; sumoylated; NTG2 has a paralog, NTG1, that arose from the whole genome duplication
protein _2039
protein _2039
protein _2039
small nucleolar RNA-associated protein 5
small nucleolar RNA-associated protein 5
small nucleolar RNA-associated protein 5
phosphatase superfamily (branch 1)
phosphomutase ARB_03491
phosphomutase ARB_03491
SSO1
SSO1

AWRIv2|AWRI_1753
LAMAP|LAMAP2480_0690
CBS2499v2|CBS2499_5100
AWRIv2|AWRI_1755
LAMAP|LAMAP2480_0700
CBS2499v2|CBS2499_4067
AWRIv2|AWRI_1757
LAMAP|LAMAP2480_0715
CBS2499v2|CBS2499_4052
AWRIv2|AWRI_0322
LAMAP|LAMAP2480_0717
CBS2499v2|CBS2499_4050
AWRIv2|AWRI_0321
LAMAP|LAMAP2480_0721
CBS2499v2|CBS2499_4045
AWRIv2|AWRI_0318

membrane t-SNARE; involved in fusion of secretory vesicles at the plasma membrane and in vesicle fusion during sporulation; forms a complex with Sec9p that binds v-SNARE Snc2p; syntaxin homolog; functionally redundant with Sso2p; SSO1 has a paralog, SSO2, that arose from the whole genome duplication
protein STM1
protein STM1
protein STM1
protein _2086
protein _2086
protein _2086
c-terminal hydrolase family protein
c-terminal hydrolase family protein
c-terminal hydrolase family protein
hob3
hob3
hob3
protein rad52
protein rad52
protein rad52

LAMAP LAMAP2480_0745	oxide oxidoreductase, flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses
CBS2499v2 CBS2499_4023	oxide oxidoreductase; flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses; protein increases in abundance and relocalizes from nucleus to cytoplasmic foci upon DNA replication stress
AWRIv2 AWRI_0301	oxide oxidoreductase; flavohemoglobin involved in nitric oxide detoxification; plays a role in the oxidative and nitrosative stress responses; protein increases in abundance and relocalizes from nucleus to cytoplasmic foci upon DNA replication stress
LAMAP LAMAP2480_0753	factor for nuclear proteasome STS1
CBS2499v2 CBS2499_4014	factor for nuclear proteasome STS1
AWRIv2 AWRI_0295	factor for nuclear proteasome STS1
LAMAP LAMAP2480_0759	small nuclear ribonucleoprotein Prp3
CBS2499v2 CBS2499_4008	small nuclear ribonucleoprotein prp3
AWRIv2 AWRI_0292	small nuclear ribonucleoprotein Prp3
LAMAP LAMAP2480_0764	protein of unknown function; expression repressed by inosine and choline in an Opi1p-dependent manner; expression induced by mild heat-stress on a non-fermentable carbon source.
CBS2499v2 CBS2499_4004	of unknown function; inhibits haploid invasive growth when overexpressed; synthetically lethal with phospholipase C (PLC1); expression induced by mild heat-stress on a non-fermentable carbon source, upon entry into stationary phase and upon nitrogen deprivation; repressed by inosine and choline in an Opi1p-dependent manner; highly conserved from bacteria to human; Memo, the human homolog, is an ErbB2 interacting protein with an essential function in cell motility
AWRIv2 AWRI_0288	of unknown function; inhibits haploid invasive growth when overexpressed; synthetically lethal with phospholipase C (PLC1); expression induced by mild heat-stress on a non-fermentable carbon source, upon entry into stationary phase and upon nitrogen deprivation; repressed by inosine and choline in an Opi1p-dependent manner; highly conserved from bacteria to human; Memo, the human homolog, is an ErbB2 interacting protein with an essential function in cell motility
LAMAP LAMAP2480_0770	cluster assembly protein DRE2
CBS2499v2 CBS2499_3999	cluster assembly protein DRE2
AWRIv2 AWRI_0284	cluster assembly protein DRE2
LAMAP LAMAP2480_0773	D-site endonuclease NOB1
CBS2499v2 CBS2499_3996	D-site endonuclease NOB1
AWRIv2 AWRI_0281	D-site endonuclease nob1
LAMAP LAMAP2480_0792	protein ARP8
CBS2499v2 CBS2499_3977	protein ARP8
AWRIv2 AWRI_0267	protein ARP8
LAMAP LAMAP2480_0799	polymerase II transcription factor B subunit 1
CBS2499v2 CBS2499_3971	polymerase II transcription factor B subunit 1
AWRIv2 AWRI_0259	of TFIIH and nucleotide excision repair factor 3 complexes; required for nucleotide excision repair, target for transcriptional activators; relocalizes to the cytosol in response to hypoxia
LAMAP LAMAP2480_0806	protein kinase B
CBS2499v2 CBS2499_0475	protein kinase B
AWRIv2 AWRI_3035	protein kinase type 2
LAMAP LAMAP2480_0809	protein HPODL_02852

CBS2499v2 CBS2499_0478	protein HPODL_02852	
AWRIv2 AWRI_3037	domain protein	
LAMAP LAMAP2480_0829	signalosome complex subunit 5	
CBS2499v2 CBS2499_0500	signalosome complex subunit 5	
AWRIv2 AWRI_3855	signalosome complex subunit 5	
LAMAP LAMAP2480_0831	hydrolase involved in mRNA decapping, may function in a feedback mechanism to regulate deadenylation, contains pyrophosphatase activity and a HIT (histidine triad) motif; interacts with neutral trehalase Nth1p	
CBS2499v2 CBS2499_0502	hydrolase involved in mRNA decapping; activates Xrn1p; may function in a feedback mechanism to regulate deadenylation, contains pyrophosphatase activity and a HIT (histidine triad) motif; acts as inhibitor of neutral trehalase Nth1p; required for growth on glycerol medium; protein abundance increases in response to DNA replication stress; DCS1 has a paralog, DCS2, that arose from the whole genome duplication	
AWRIv2 AWRI_3857	hydrolase involved in mRNA decapping; activates Xrn1p; may function in a feedback mechanism to regulate deadenylation, contains pyrophosphatase activity and a HIT (histidine triad) motif; acts as inhibitor of neutral trehalase Nth1p; required for growth on glycerol medium; protein abundance increases in response to DNA replication stress; DCS1 has a paralog, DCS2, that arose from the whole genome duplication	
LAMAP LAMAP2480_0851	wry family protein 8	
CBS2499v2 CBS2499_0528		4
AWRIv2 AWRI_2389		4
LAMAP LAMAP2480_0887	specificity protein kinase KNS1	
CBS2499v2 CBS2499_5064	specificity protein kinase KNS1	
AWRIv2 AWRI_2376	specificity protein kinase KNS1	
LAMAP LAMAP2480_0893	protein _2846	
CBS2499v2 CBS2499_0564	protein _2846	
AWRIv2 AWRI_2373	protein _2846	
LAMAP LAMAP2480_0910	isoform of tropomyosin, binds to and stabilizes actin cables and filaments, which direct polarized cell growth and the distribution of several organelles; appears to have distinct and also overlapping functions with Tpm1p	
CBS2499v2 CBS2499_0587	isoform of tropomyosin; binds to and stabilizes actin cables and filaments, which direct polarized cell growth and the distribution of several organelles; appears to have distinct and also overlapping functions with Tpm1p; TPM2 has a paralog, TPM1, that arose from the whole genome duplication	
AWRIv2 AWRI_3449	isoform of tropomyosin; binds to and stabilizes actin cables and filaments, which direct polarized cell growth and the distribution of several organelles; appears to have distinct and also overlapping functions with Tpm1p; TPM2 has a paralog, TPM1, that arose from the whole genome duplication	
LAMAP LAMAP2480_0912	TMA108	
CBS2499v2 CBS2499_0589	TMA108	
AWRIv2 AWRI_3447	TMA108	
LAMAP LAMAP2480_0926	initiation factor 4F subunit p130	
CBS2499v2 CBS2499_0602	initiation factor 4F subunit p150	
AWRIv2 AWRI_3434	initiation factor 4F subunit p130	

LAMAP LAMAP2480_0928	protein product
CBS2499v2 CBS2499_0604	finger protein 251
AWRIv2 AWRI_3432	fusion degradation protein
LAMAP LAMAP2480_0931	dehydrogenase
CBS2499v2 CBS2499_0607	dehydrogenase
AWRIv2 AWRI_3430	dehydrogenase
LAMAP LAMAP2480_0958	and RSC complexes subunit <i>ssr2</i>
	of the RSC chromatin remodeling complex; essential for viability and mitotic growth; homolog of SWI/SNF
	subunit <i>Swi3p</i> , but unlike <i>Swi3p</i> , does not activate transcription of reporters
CBS2499v2 CBS2499_0632	and RSC complexes subunit <i>ssr2</i>
AWRIv2 AWRI_3632	coactivator HFI1/ADA1
LAMAP LAMAP2480_0971	coactivator HFI1/ADA1
CBS2499v2 CBS2499_0645	coactivator HFI1/ADA1
AWRIv2 AWRI_3642	coactivator HFI1/ADA1
LAMAP LAMAP2480_0977	ribosomal protein of the small subunit
CBS2499v2 CBS2499_0651	ribosomal protein of the small subunit
AWRIv2 AWRI_3647	ribosomal protein of the small subunit
LAMAP LAMAP2480_1007	transcription factor
CBS2499v2 CBS2499_0680	transcription factor CAP1
AWRIv2 AWRI_0159	transcription factor CAP1
LAMAP LAMAP2480_1010	35 NatC auxiliary subunit
CBS2499v2 CBS2499_0683	35 NatC auxiliary subunit
AWRIv2 AWRI_0156	subunit of n-terminal acetyltransferase of the type
	synthase, catalyzes only the formation of pseudouridine-55 (Psi55), a highly conserved tRNA modification, in
	mitochondrial and cytoplasmic tRNAs; PUS4 overexpression leads to translational derepression of GCN4
	(Gcd- phenotype)
LAMAP LAMAP2480_1020	
	synthase; catalyzes only the formation of pseudouridine-55 (Psi55), a highly conserved tRNA modification, in
	mitochondrial and cytoplasmic tRNAs; also responsible for pseudouracil modification of some mRNAs; PUS4
	overexpression leads to translational derepression of GCN4 (Gcd- phenotype)
CBS2499v2 CBS2499_2315	
	synthase; catalyzes only the formation of pseudouridine-55 (Psi55), a highly conserved tRNA modification, in
	mitochondrial and cytoplasmic tRNAs; also responsible for pseudouracil modification of some mRNAs; PUS4
	overexpression leads to translational derepression of GCN4 (Gcd- phenotype)
AWRIv2 AWRI_1372	protein YHR097C
LAMAP LAMAP2480_1033	protein YHR097C
CBS2499v2 CBS2499_2331	protein YHR097C
AWRIv2 AWRI_1365	protein YHR097C
LAMAP LAMAP2480_1037	division control protein 15
CBS2499v2 CBS2499_2336	division control protein 15
AWRIv2 AWRI_1361	division control protein 15
LAMAP LAMAP2480_1038	and cobalt transport protein CorA
CBS2499v2 CBS2499_2337	and cobalt transport protein CorA
AWRIv2 AWRI_1360	and cobalt transport protein CorA
LAMAP LAMAP2480_1045	tyrosine-protein phosphatase C
CBS2499v2 CBS2499_2345	tyrosine-protein phosphatase alpha

AWRiv2 AWRI_1351	tyrosine-protein phosphatase alpha
LAMAP LAMAP2480_1053	component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); acts as receptor for the TIM23 complex guiding incoming precursors from the TOM complex; may control the gating of the Tim23p-Tim17p channel
CBS2499v2 CBS2499_2352	component of the TIM23 complex; acts as receptor for the translocase of the inner mitochondrial membrane (TIM23) complex guiding incoming precursors from the TOM complex; may control the gating of the Tim23p-Tim17p channel
AWRiv2 AWRI_1343	import inner membrane translocase subunit TIM50
LAMAP LAMAP2480_1062	hypothetical protein
CBS2499v2 CBS2499_2362	protein MEO_01155
AWRiv2 AWRI_1338	protein _1594
LAMAP LAMAP2480_1065	subunit beta-2
CBS2499v2 CBS2499_2366	subunit beta-2
AWRiv2 AWRI_1334	
LAMAP LAMAP2480_1070	ubiquitin-protein ligase complex SLX5-SLX8 subunit SLX5
CBS2499v2 CBS2499_2372	ubiquitin-protein ligase complex SLX5-SLX8 subunit SLX5
AWRiv2 AWRI_1327	metabolism-related protein
LAMAP LAMAP2480_1084	BIG1
CBS2499v2 CBS2499_2386	BIG1
AWRiv2 AWRI_1316	BIG1
LAMAP LAMAP2480_1096	fumarate reductase, required with isoenzyme Osm1p for anaerobic growth; may interact with ribosomes, based on co-purification experiments; authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies
CBS2499v2 CBS2499_2402	fumarate reductase; required with isoenzyme Osm1p for anaerobic growth; may interact with ribosomes, based on co-purification experiments; authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies; similar to Arxula adeninovorans fumarate reductase; protein abundance increases in response to DNA replication stress; FRD1 has a paralog, OSM1, that arose from the whole genome duplication
AWRiv2 AWRI_1302	fumarate reductase; required with isoenzyme Osm1p for anaerobic growth; may interact with ribosomes, based on co-purification experiments; authentic, non-tagged protein is detected in purified mitochondria in high-throughput studies; similar to Arxula adeninovorans fumarate reductase; protein abundance increases in response to DNA replication stress; FRD1 has a paralog, OSM1, that arose from the whole genome duplication
LAMAP LAMAP2480_1097	protein _1551
CBS2499v2 CBS2499_2403	protein _1551
AWRiv2 AWRI_1301	protein _1551
LAMAP LAMAP2480_1098	4-phosphate cytidyltransferase
CBS2499v2 CBS2499_2404	4-phosphate cytidyltransferase
AWRiv2 AWRI_1300	mannose-1-phosphate guanyltransferase
LAMAP LAMAP2480_1113	translation initiation factor 3 subunit
CBS2499v2 CBS2499_2420	translation initiation factor 3 subunit
AWRiv2 AWRI_3311	translation initiation factor 3 subunit D
LAMAP LAMAP2480_1117	carboxyl-terminal hydrolase 14
CBS2499v2 CBS2499_2425	carboxyl-terminal hydrolase 14

AWRIv2 AWRI_3306	carboxyl-terminal hydrolase 14
LAMAP LAMAP2480_1128	phospholipase YOR022C, mitochondrial
CBS2499v2 CBS2499_2435	phospholipase YOR022C, mitochondrial
AWRIv2 AWRI_3295	phospholipase YOR022C, mitochondrial
LAMAP LAMAP2480_1137	protein _3945
CBS2499v2 CBS2499_2444	protein _3945
AWRIv2 AWRI_3289	protein _3945
LAMAP LAMAP2480_1141	polymerase II subunit A C-terminal domain phosphatase
CBS2499v2 CBS2499_2447	phosphatase, phosphatase domain
AWRIv2 AWRI_3287	polymerase II subunit A C-terminal domain phosphatase
LAMAP LAMAP2480_1154	RNA polymerase III subunit RPC4
CBS2499v2 CBS2499_4101	RNA polymerase III subunit RPC4
AWRIv2 AWRI_2742	rna polymerase iii subunit c4
LAMAP LAMAP2480_1199	reductase [NADPH]
CBS2499v2 CBS2499_5053	reductase [NADPH]
AWRIv2 AWRI_4108	reductase [NADPH]
LAMAP LAMAP2480_1200	reductase [NAD(P)H], large subunit
CBS2499v2 CBS2499_5054	reductase [NAD(P)H], large subunit
AWRIv2 AWRI_4109	reductase [NAD(P)H], large subunit
LAMAP LAMAP2480_1201	transporter
CBS2499v2 CBS2499_5055	transporter
AWRIv2 AWRI_4110	transporter
LAMAP LAMAP2480_1202	isomaltase (alpha-1,6-glucosidase) required for isomaltose utilization; has specificity for isomaltose, palatinose, and methyl-alpha-glucoside; member of the IMA isomaltase family
CBS2499v2 CBS2499_5056	isomaltase (alpha-1,6-glucosidase/alpha-methylglucosidase); required for isomaltose utilization; preferred specificity for isomaltose, alpha-methylglucoside, and palatinose, but also exhibits alpha-1,2 glucosidase activity on sucrose and kojibiose, and can cleave the 1,3-alpha linkage of nigerose and turanose and the alpha-1,5 linkage of leucrose in vitro; member of the IMA isomaltase family
AWRIv2 AWRI_4111	isomaltase (alpha-1,6-glucosidase/alpha-methylglucosidase); required for isomaltose utilization; preferred specificity for isomaltose, alpha-methylglucoside, and palatinose, but also exhibits alpha-1,2 glucosidase activity on sucrose and kojibiose, and can cleave the 1,3-alpha linkage of nigerose and turanose and the alpha-1,5 linkage of leucrose in vitro; member of the IMA isomaltase family
LAMAP LAMAP2480_1203	phosphodiesterase 2
CBS2499v2 CBS2499_5057	phosphodiesterase 2
AWRIv2 AWRI_4112	phosphodiesterase 2
LAMAP LAMAP2480_1225	chaperone required for correct maturation of the 20S proteasome; may inhibit premature dimerization of proteasome half-mers; degraded by proteasome upon completion of its assembly
CBS2499v2 CBS2499_4205	required for correct maturation of the 20S proteasome; short-lived chaperone; may inhibit premature dimerization of proteasome half-mers; degraded by proteasome upon completion of its assembly
AWRIv2 AWRI_3062	required for correct maturation of the 20S proteasome; short-lived chaperone; may inhibit premature dimerization of proteasome half-mers; degraded by proteasome upon completion of its assembly
LAMAP LAMAP2480_1243	PEP12

CBS2499v2 CBS2499_4189 AWRIv2 AWRI_3074	PEP12 PEP12 repeat protein involved in assembly of cytosolic and nuclear iron-sulfur proteins; similar to the human Ciao1 protein; YDR267C is an essential gene
LAMAP LAMAP2480_1244	
	of cytosolic iron-sulfur protein assembly (CIA) machinery; acts at a late step of Fe-S cluster assembly; forms the CIA targeting complex with Cia2p and Met18p that directs Fe-S cluster incorporation into a subset of proteins involved in methionine biosynthesis, DNA replication and repair, transcription, and telomere maintenance; contains WD40 repeats; ortholog of human Ciao1 protein
CBS2499v2 CBS2499_4188	
	of cytosolic iron-sulfur protein assembly (CIA) machinery; acts at a late step of Fe-S cluster assembly; forms the CIA targeting complex with Cia2p and Met18p that directs Fe-S cluster incorporation into a subset of proteins involved in methionine biosynthesis, DNA replication and repair, transcription, and telomere maintenance; contains WD40 repeats; ortholog of human Ciao1 protein
AWRIv2 AWRI_3075 LAMAP LAMAP2480_1248 CBS2499v2 CBS2499_4184 AWRIv2 AWRI_3078 LAMAP LAMAP2480_1280 CBS2499v2 CBS2499_4155 AWRIv2 AWRI_3469 LAMAP LAMAP2480_1314 CBS2499v2 CBS2499_3305 AWRIv2 AWRI_2309 LAMAP LAMAP2480_1346 CBS2499v2 CBS2499_3338 AWRIv2 AWRI_0186 LAMAP LAMAP2480_1347 CBS2499v2 CBS2499_3339 AWRIv2 AWRI_0187 LAMAP LAMAP2480_1350 CBS2499v2 CBS2499_3342 AWRIv2 AWRI_0190 LAMAP LAMAP2480_1354 CBS2499v2 CBS2499_3346 AWRIv2 AWRI_0194 LAMAP LAMAP2480_1373 CBS2499v2 CBS2499_3914 AWRIv2 AWRI_0204 LAMAP LAMAP2480_1381	HIR2 hir1 HIR2 protein _4165 protein _4165 protein _4165 protein _2764 protein _2764 protein _2764 protein sorting-associated protein VTA1 homolog HOMOLOG OF MAMMALIAN LYST-INTERACTING PROTEIN 5 HOMOLOG OF MAMMALIAN LYST-INTERACTING PROTEIN 5 BNI1 BNI1 BNI1 cysteine protease ATG4 cysteine protease ATG4 cysteine protease ATG4 dehydrogenase dehydrogenase dehydrogenase domain-containing protein FUN19 domain-containing protein FUN19 domain-containing protein FUN19 co-chaperone AHA1 that binds Hsp82p and activates its ATPase activity; plays a role in determining prion variants; similar to Hch1p; expression is regulated by stresses such as heat shock; protein abundance increases in response to DNA replication stress co-chaperone AHA1
CBS2499v2 CBS2499_3922 AWRIv2 AWRI_0215 LAMAP LAMAP2480_1386	

CBS2499v2 CBS2499_5084		3
AWRIv2 AWRI_0219		2
LAMAP LAMAP2480_1387	protein YLR287C	
CBS2499v2 CBS2499_5085	protein YLR287C	
AWRIv2 AWRI_0221	protein YLR287C	
LAMAP LAMAP2480_1394	complex subunit 2	
CBS2499v2 CBS2499_3934	complex subunit 2	
AWRIv2 AWRI_0223	complex subunit 2	
LAMAP LAMAP2480_1401	resistance MFS transporter, drug:H+ antiporter-2 (14 Spanner) (DHA2) family	
CBS2499v2 CBS2499_3940	resistance MFS transporter, drug:H+ antiporter-2 (14 Spanner) (DHA2) family	
AWRIv2 AWRI_0229	resistance MFS transporter, drug:H+ antiporter-2 (14 Spanner) (DHA2) family	
LAMAP LAMAP2480_1405	factor SYF1	
CBS2499v2 CBS2499_3944	factor SYF1	
AWRIv2 AWRI_0232	factor syf1	
	required, along with Dph1p, Kti11p, Jjj3p, and Dph5p, for synthesis of diphthamide, which is a modified histidine residue of translation elongation factor 2 (Eft1p or Eft2p); may act in a complex with Dph1p and Kti11p	
LAMAP LAMAP2480_1416	required for synthesis of diphthamide; required along with Dph1p, Kti11p, Jjj3p, and Dph5p; diphthamide is a modified histidine residue of translation elongation factor 2 (Eft1p or Eft2p); may act in a complex with Dph1p and Kti11p	
CBS2499v2 CBS2499_3954	required for synthesis of diphthamide; required along with Dph1p, Kti11p, Jjj3p, and Dph5p; diphthamide is a modified histidine residue of translation elongation factor 2 (Eft1p or Eft2p); may act in a complex with Dph1p and Kti11p	
AWRIv2 AWRI_0240		4
LAMAP LAMAP2480_1421		4
CBS2499v2 CBS2499_3959		
AWRIv2 AWRI_0247	protein C1A6.05c	
LAMAP LAMAP2480_1429	phosphate lyase, regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases, prefers C16 dihydrosphingosine-1-phosphate as a substrate	
CBS2499v2 CBS2499_3966	phosphate lyase; regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases, prefers C16 dihydrosphingosine-1-phosphate as a substrate	
AWRIv2 AWRI_0254	phosphate lyase; regulates intracellular levels of sphingolipid long-chain base phosphates (LCBPs), degrades phosphorylated long chain bases, prefers C16 dihydrosphingosine-1-phosphate as a substrate	
LAMAP LAMAP2480_1431	preferring nucleoside hydrolase	
CBS2499v2 CBS2499_4993	preferring nucleoside hydrolase	
AWRIv2 AWRI_4181	preferring nucleoside hydrolase	
LAMAP LAMAP2480_1432	activator of proteases prtT	
CBS2499v2 CBS2499_4992	activator of proteases prtT	
AWRIv2 AWRI_4182	activator of proteases prtT	
LAMAP LAMAP2480_1433	transcriptional regulatory protein C25B8.11	
CBS2499v2 CBS2499_4991	transcriptional regulatory protein C25B8.11	
AWRIv2 AWRI_4176	transcriptional regulatory protein C25B8.11	

LAMAP LAMAP2480_1434	b2 (L-lactate cytochrome-c oxidoreductase), component of the mitochondrial intermembrane space, required for lactate utilization; expression is repressed by glucose and anaerobic conditions
CBS2499v2 CBS2499_4990	b2 (L-lactate cytochrome-c oxidoreductase); component of the mitochondrial intermembrane space, required for lactate utilization; expression is repressed by glucose and anaerobic conditions
AWRiv2 AWRI_4175	b2 (L-lactate cytochrome-c oxidoreductase); component of the mitochondrial intermembrane space, required for lactate utilization; expression is repressed by glucose and anaerobic conditions
LAMAP LAMAP2480_1444	of the NineTeen Complex (NTC) that contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 snRNAs
CBS2499v2 CBS2499_1619	of the NineTeen Complex (NTC); this complex contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 snRNAs
AWRiv2 AWRI_2140	factor prp46
LAMAP LAMAP2480_1445	protein 3
CBS2499v2 CBS2499_1620	protein 3
AWRiv2 AWRI_2141	protein 3
LAMAP LAMAP2480_1454	protein Mis14/NSL1
CBS2499v2 CBS2499_1630	protein Mis14/NSL1
AWRiv2 AWRI_2146	protein _2565
LAMAP LAMAP2480_1463	MNN2
CBS2499v2 CBS2499_1641	MNN21
AWRiv2 AWRI_2155	responsible for addition of the first alpha-1,2-linked mannose to form the branches on the mannan backbone of oligosaccharides, localizes to an early Golgi compartment
LAMAP LAMAP2480_1466	oxidoreductase 12 kDa subunit, mitochondrial
CBS2499v2 CBS2499_1645	oxidoreductase 12 kDa subunit, mitochondrial
AWRiv2 AWRI_2158	oxidoreductase 12 kDa subunit, mitochondrial
LAMAP LAMAP2480_1468	permease, required for high-affinity transport of proline; also transports the toxic proline analog azetidine-2-carboxylate (AzC); PUT4 transcription is repressed in ammonia-grown cells
CBS2499v2 CBS2499_1647	permease; required for high-affinity transport of proline; also transports the toxic proline analog azetidine-2-carboxylate (AzC); PUT4 transcription is repressed in ammonia-grown cells
AWRiv2 AWRI_2160	permease; required for high-affinity transport of proline; also transports the toxic proline analog azetidine-2-carboxylate (AzC); PUT4 transcription is repressed in ammonia-grown cells
LAMAP LAMAP2480_1469	protein _2581
CBS2499v2 CBS2499_1648	protein _2581
AWRiv2 AWRI_2161	protein _2581
LAMAP LAMAP2480_1481	protein _2593
CBS2499v2 CBS2499_1661	protein _2593
AWRiv2 AWRI_2171	protein _2593
LAMAP LAMAP2480_1500	metabolite transport protein C1271.09
CBS2499v2 CBS2499_1679	metabolite transport protein C1271.09
AWRiv2 AWRI_2186	metabolite transport protein C1271.09
LAMAP LAMAP2480_1503	regulator MET32

CBS2499v2 CBS2499_1682	regulator MET32
AWRIv2 AWRI_2189	regulator MET32
LAMAP LAMAP2480_1509	ferric reductase transmembrane component
CBS2499v2 CBS2499_1687	ferric reductase transmembrane component
AWRIv2 AWRI_1397	ferric reductase transmembrane component 8
LAMAP LAMAP2480_1518	membrane protein YDL133W
CBS2499v2 CBS2499_1696	of phospholipase D SRF1
AWRIv2 AWRI_1403	of phospholipase D SRF1
LAMAP LAMAP2480_1538	enzyme
CBS2499v2 CBS2499_1716	enzyme
AWRIv2 AWRI_1417	domain-containing protein C57A10.08c
LAMAP LAMAP2480_1541	protein YKR023W
CBS2499v2 CBS2499_1719	protein YKR023W
AWRIv2 AWRI_1419	protein C1A6.01c
LAMAP LAMAP2480_1543	domain-containing protein 3
CBS2499v2 CBS2499_1721	domain-containing protein 3
AWRIv2 AWRI_1421	domain-containing protein 3
LAMAP LAMAP2480_1547	ligase
CBS2499v2 CBS2499_1725	ligase
AWRIv2 AWRI_1427	ligase
LAMAP LAMAP2480_1551	emergence protein 1
CBS2499v2 CBS2499_1729	emergence protein 1
AWRIv2 AWRI_1428	scd2/ral3
LAMAP LAMAP2480_1555	protein YIL096C
CBS2499v2 CBS2499_1733	rRNA (uridine(2634)-N(3))-methyltransferase
	required for m3U2634 methylation of the 25S rRNA; S-adenosylmethionine-dependent; associates with precursors of the 60S ribosomal subunit; predicted to be involved in ribosome biogenesis
AWRIv2 AWRI_1431	division protein 1
LAMAP LAMAP2480_1575	division protein 1
CBS2499v2 CBS2499_2467	division protein 1
AWRIv2 AWRI_4032	division protein 1
LAMAP LAMAP2480_1619	dioxygenase extradiol-like protein
CBS2499v2 CBS2499_2509	dioxygenase extradiol
AWRIv2 AWRI_0535	dioxygenase extradiol-like protein
LAMAP LAMAP2480_1630	mannosyltransferase
CBS2499v2 CBS2499_2521	mannosyltransferase subunit 1
AWRIv2 AWRI_0543	mannosyltransferase
LAMAP LAMAP2480_1635	endoplasmic reticulum membrane protein YNR021W
CBS2499v2 CBS2499_2525	endoplasmic reticulum membrane protein YNR021W
AWRIv2 AWRI_0548	endoplasmic reticulum membrane protein YNR021W
LAMAP LAMAP2480_1648	phosphatase 2C homolog 3
CBS2499v2 CBS2499_2539	phosphatase 2C homolog 3
AWRIv2 AWRI_0557	phosphatase 2C homolog 3

LAMAP LAMAP2480_1659	(PABA) synthase, has similarity to Escherichia coli PABA synthase components PabA and PabB; required for the synthesis of para-aminobenzoic acid, an important intermediate for folate and ubiquinone Q biosynthesis
CBS2499v2 CBS2499_2552	(PABA) synthase; has similarity to Escherichia coli PABA synthase components PabA and PabB; required for the synthesis of para-aminobenzoic acid, an important intermediate for folate and ubiquinone Q biosynthesis;
AWRIv2 AWRI_0564	protein abundance increases in response to DNA replication stress
LAMAP LAMAP2480_1662	amidotransferase of anthranilate synthase or aminodeoxychorismate synthase
CBS2499v2 CBS2499_0019	
AWRIv2 AWRI_0788	amidase C550.07
LAMAP LAMAP2480_1666	N-formyl-4-amino-5-aminomethyl-2-methylpyrimidine deformylase
CBS2499v2 CBS2499_0014	selenium metabolism hydrolase
AWRIv2 AWRI_0785	metallohydrolase YodQ
LAMAP LAMAP2480_1674	resistance MFS transporter, drug:H⁺ antiporter-2 (14 Spanner) (DHA2) family
CBS2499v2 CBS2499_4758	resistance MFS transporter, drug:H ⁺ antiporter-2 (14 Spanner) (DHA2) family
AWRIv2 AWRI_0777	of basic amino acids in the vacuolar membrane
LAMAP LAMAP2480_1684	protein _0934
CBS2499v2 CBS2499_4770	termination factor Rtf2
AWRIv2 AWRI_0768	protein _0934
LAMAP LAMAP2480_1689	differentiation protein rcd1
CBS2499v2 CBS2499_4776	N-acetyltransferase C550.08
AWRIv2 AWRI_0763	N-acetyltransferase C550.08
LAMAP LAMAP2480_1697	
CBS2499v2 CBS2499_4783	
AWRIv2 AWRI_0760	
LAMAP LAMAP2480_1703	protein _0917
CBS2499v2 CBS2499_4786	protein _0917
AWRIv2 AWRI_0756	protein _0917
LAMAP LAMAP2480_1705	protein _0916
CBS2499v2 CBS2499_4787	protein JL09_g4631
AWRIv2 AWRI_0755	protein _0916
	with similarity to members of a family of flavodoxin-like proteins; induced by oxidative stress in a Yap1p dependent manner; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
LAMAP LAMAP2480_1721	with similarity to a family of flavodoxin-like proteins; induced by oxidative stress in a Yap1p dependent manner; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; protein abundance increases in response to DNA replication stress; PST2 has a paralog, RFS1, that arose from the whole genome duplication
CBS2499v2 CBS2499_1037	with similarity to a family of flavodoxin-like proteins; induced by oxidative stress in a Yap1p dependent manner; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; protein abundance increases in response to DNA replication stress; PST2 has a paralog, RFS1, that arose from the whole genome duplication
AWRIv2 AWRI_0652	inheritance of mitochondria protein 3
LAMAP LAMAP2480_1739	inheritance of mitochondria protein 3
CBS2499v2 CBS2499_1020	

AWRIv2 AWRI_0666	inheritance of mitochondria protein 3
LAMAP LAMAP2480_1742	synthesis regulatory protein
CBS2499v2 CBS2499_1017	wall biosynthesis/cell cycle regulator smi1
AWRIv2 AWRI_0668	homolog
LAMAP LAMAP2480_1766	carboxyl-terminal hydrolase 15
	protease involved in protein deubiquitination; catalytic activity regulated by an N-terminal TRAF-like domain and and C-terminal sequences; physically interacts with anaphase-promoting complex/cyclosome (APC/C) activator, Cdh1p; forms a complex with AAA peroxins Pex1p and Pex6p
CBS2499v2 CBS2499_0993	
	protease involved in protein deubiquitination; catalytic activity regulated by an N-terminal TRAF-like domain and and C-terminal sequences; physically interacts with anaphase-promoting complex/cyclosome (APC/C) activator, Cdh1p; forms a complex with AAA peroxins Pex1p and Pex6p
AWRIv2 AWRI_0697	globin-like protein YNL234W
LAMAP LAMAP2480_1771	globin-like protein YNL234W
CBS2499v2 CBS2499_0986	globin-like protein YNL234W
AWRIv2 AWRI_0706	globin-like protein YNL234W
LAMAP LAMAP2480_1796	protein At1g78280
CBS2499v2 CBS2499_2031	protein At1g78280
AWRIv2 AWRI_0975	protein At5g06550
LAMAP LAMAP2480_1799	
CBS2499v2 CBS2499_2033	
AWRIv2 AWRI_0973	
LAMAP LAMAP2480_1800	factor
CBS2499v2 CBS2499_2034	factor
AWRIv2 AWRI_0972	factor
LAMAP LAMAP2480_1811	coactivator, component of the ADA and SAGA transcriptional adaptor/HAT (histone acetyltransferase) complexes
CBS2499v2 CBS2499_5092	coactivator; component of the ADA and SAGA transcriptional adaptor/HAT (histone acetyltransferase) complexes
AWRIv2 AWRI_0961	coactivator; component of the ADA and SAGA transcriptional adaptor/HAT (histone acetyltransferase) complexes
LAMAP LAMAP2480_1824	that stimulates the ATPase activity of the HSP70 protein Ssc1p; involved in protein folding/refolding in the mitochondrial matrix; required for proteolysis of misfolded proteins; member of the HSP40 (DnaJ) family of chaperones
CBS2499v2 CBS2499_2056	that stimulates HSP70 protein Ssc1p ATPase activity; involved in protein folding/refolding in the mitochondrial matrix; required for proteolysis of misfolded proteins; member of the HSP40 (DnaJ) family of chaperones
AWRIv2 AWRI_0948	protein DnaJ
LAMAP LAMAP2480_1831	protein _1140
CBS2499v2 CBS2499_2063	protein _1140
AWRIv2 AWRI_0941	protein _1140
LAMAP LAMAP2480_1833	

CBS2499v2 CBS2499_2065 AWRIv2 AWRI_0939 LAMAP LAMAP2480_1845 CBS2499v2 CBS2499_2077 AWRIv2 AWRI_0927	thioredoxin; highly conserved oxidoreductase required to maintain the redox homeostasis of the cell, forms the mitochondrial thioredoxin system with Trr2p, redox state is maintained by both Trr2p and Glr1p protein _1126 protein _1126 protein _1126
LAMAP LAMAP2480_1857	symporter of the plasma membrane; transport activity is dependent on the pH gradient across the membrane; mediates high-affinity uptake of carbon sources lactate, pyuvate, and acetate, and also of the micronutrient selenite, whose structure mimics that of monocarboxylates; expression and localization are tightly regulated, with transcription repression, mRNA degradation, and protein endocytosis and degradation all occurring in the presence of glucose symporter of the plasma membrane; transport activity is dependent on the pH gradient across the membrane; mediates high-affinity uptake of carbon sources lactate, pyuvate, and acetate, and also of the micronutrient selenite, whose structure mimics that of monocarboxylates; expression and localization are tightly regulated, with transcription repression, mRNA degradation, and protein endocytosis and degradation all occurring in the presence of glucose
CBS2499v2 CBS2499_2089	symporter of the plasma membrane; transport activity is dependent on the pH gradient across the membrane; mediates high-affinity uptake of carbon sources lactate, pyuvate, and acetate, and also of the micronutrient selenite, whose structure mimics that of monocarboxylates; expression and localization are tightly regulated, with transcription repression, mRNA degradation, and protein endocytosis and degradation all occurring in the presence of glucose
AWRIv2 AWRI_0919	protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
LAMAP LAMAP2480_1867	protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
CBS2499v2 CBS2499_2099	protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
AWRIv2 AWRI_0909	WRNIP1
LAMAP LAMAP2480_1911	ATPase MGS1
CBS2499v2 CBS2499_3753	WRNIP1 homolog C26H5.02c
AWRIv2 AWRI_1149	app1
LAMAP LAMAP2480_1916	protein
CBS2499v2 CBS2499_3756	protein
AWRIv2 AWRI_1147	protein _1363
LAMAP LAMAP2480_1926	protein _1363
CBS2499v2 CBS2499_3767	protein _1363
AWRIv2 AWRI_1139	protein _1351
LAMAP LAMAP2480_1939	protein _1351
CBS2499v2 CBS2499_3779	protein _1351
AWRIv2 AWRI_1127	protein _1351
LAMAP LAMAP2480_1946	polymerase epsilon subunit D
CBS2499v2 CBS2499_3787	polymerase epsilon subunit D
AWRIv2 AWRI_1119	polymerase epsilon subunit D

LAMAP LAMAP2480_1948	involved in negative regulation of transcription of iron regulon; forms an iron independent complex with Fra2p, Grx3p, and Grx4p; cytosolic; mutant fails to repress transcription of iron regulon and is defective in spore formation
CBS2499v2 CBS2499_3789	involved in negative regulation of iron regulon transcription; forms an iron independent complex with Fra2p, Grx3p, and Grx4p; cytosolic; mutant fails to repress transcription of iron regulon and is defective in spore formation
AWRIv2 AWRI_1117	N-terminal domain
LAMAP LAMAP2480_1950	sulfonate dioxygenase
CBS2499v2 CBS2499_3791	sulfonate dioxygenase
AWRIv2 AWRI_1115	alpha-ketoglutarate-dependent sulfonate dioxygenase
LAMAP LAMAP2480_1961	specificity protein phosphatase PPS1
CBS2499v2 CBS2499_3801	specificity protein phosphatase PPS1
AWRIv2 AWRI_1106	specificity protein phosphatase PPS1
LAMAP LAMAP2480_1983	of serine hydrolases 3
CBS2499v2 CBS2499_4301	of serine hydrolases 3
AWRIv2 AWRI_1560	cancer-associated gene 2 protein homolog
LAMAP LAMAP2480_1993	protein _1836
CBS2499v2 CBS2499_4290	protein _1836
AWRIv2 AWRI_1552	protein _1836
LAMAP LAMAP2480_1994	specific transcription factor domain
CBS2499v2 CBS2499_4289	specific transcription factor domain
AWRIv2 AWRI_1551	specific transcription factor domain
LAMAP LAMAP2480_1996	keto reductase
CBS2499v2 CBS2499_4287	keto reductase
AWRIv2 AWRI_1550	keto reductase
LAMAP LAMAP2480_2015	protein kinase mpkC
CBS2499v2 CBS2499_4264	kinase Bud32
AWRIv2 AWRI_1533	kinase 7
LAMAP LAMAP2480_2021	deacetylase
CBS2499v2 CBS2499_4257	deacetylase
AWRIv2 AWRI_1529	
LAMAP LAMAP2480_2024	hydantoinase/carbamoylase family
CBS2499v2 CBS2499_4254	protein
AWRIv2 AWRI_1527	hydantoinase/carbamoylase family
LAMAP LAMAP2480_2029	permease regulator 3
CBS2499v2 CBS2499_4251	permease regulator 3
AWRIv2 AWRI_1524	permease regulator 3
LAMAP LAMAP2480_2037	protein, YigZ family
CBS2499v2 CBS2499_4245	protein, YigZ family
AWRIv2 AWRI_1517	protein, YigZ family
LAMAP LAMAP2480_2038	phosphatase 5
CBS2499v2 CBS2499_4244	phosphatase 5
AWRIv2 AWRI_1516	phosphatase 5
LAMAP LAMAP2480_2041	protein C132.01c

CBS2499v2 CBS2499_4241	export mediator factor NEMF homolog
AWRIv2 AWRI_1513	export mediator factor NEMF homolog
LAMAP LAMAP2480_2044	family
CBS2499v2 CBS2499_4239	family
AWRIv2 AWRI_1511	family
LAMAP LAMAP2480_2045	transporter, sugar porter (SP) family
CBS2499v2 CBS2499_4238	transporter, sugar porter (SP) family
AWRIv2 AWRI_1510	transporter, sugar porter (SP) family
LAMAP LAMAP2480_2046	protease 1
CBS2499v2 CBS2499_4237	protease 1
AWRIv2 AWRI_1509	protease 1
LAMAP LAMAP2480_2047	protein YPP1
CBS2499v2 CBS2499_4236	protein YPP1
AWRIv2 AWRI_1507	protein YPP1
LAMAP LAMAP2480_2050	protein _1784
CBS2499v2 CBS2499_4235	protein _1784
AWRIv2 AWRI_1506	protein _1784
LAMAP LAMAP2480_2052	polymerase epsilon subunit C
CBS2499v2 CBS2499_4233	polymerase epsilon subunit C
AWRIv2 AWRI_1504	polymerase epsilon subunit C
LAMAP LAMAP2480_2054	assembly chaperone 2
CBS2499v2 CBS2499_4231	assembly chaperone 2
AWRIv2 AWRI_1502	assembly chaperone 2
LAMAP LAMAP2480_2055	domain
CBS2499v2 CBS2499_4230	protein STP22 of temperature-sensitive alpha-factor receptor and arginine permease
AWRIv2 AWRI_1501	protein STP22 of temperature-sensitive alpha-factor receptor and arginine permease
LAMAP LAMAP2480_2059	organelle assembly protein TopJ
CBS2499v2 CBS2499_4225	organelle assembly protein TopJ
	II HSP40 co-chaperone that interacts with the HSP70 protein Ssa1p; shuttles between cytosol and nucleus; mediates delivery of misfolded proteins into the nucleus for degradation; involved in proteasomal degradation of misfolded cytosolic proteins; protein abundance increases in response to DNA replication stress; polyQ aggregates sequester Sis1p and interfere with clearance of misfolded proteins; similar to bacterial DnaJ proteins and mammalian DnaJB1
AWRIv2 AWRI_1497	amidolyase, contains both urea carboxylase and allophanate hydrolase activities, degrades urea to CO ₂ and NH ₃ ; expression sensitive to nitrogen catabolite repression and induced by allophanate, an intermediate in allantoin degradation
LAMAP LAMAP2480_2061	
	amidolyase; contains both urea carboxylase and allophanate hydrolase activities, degrades urea to CO ₂ and NH ₃ ; expression sensitive to nitrogen catabolite repression and induced by allophanate, an intermediate in allantoin degradation; protein abundance increases in response to DNA replication stress
CBS2499v2 CBS2499_5012	
	amidolyase; contains both urea carboxylase and allophanate hydrolase activities, degrades urea to CO ₂ and NH ₃ ; expression sensitive to nitrogen catabolite repression and induced by allophanate, an intermediate in allantoin degradation; protein abundance increases in response to DNA replication stress
AWRIv2 AWRI_1493	

LAMAP LAMAP2480_2062	protein PYRAB09930	
CBS2499v2 CBS2499_5011	utilization protein lamB	
AWRIv2 AWRI_1492	protein SE_1287	
LAMAP LAMAP2480_2063	solute:sodium symporter (SSS) family	
CBS2499v2 CBS2499_5010	solute:sodium symporter (SSS) family	
AWRIv2 AWRI_1491	urea active transporter 1	
LAMAP LAMAP2480_2064		20
CBS2499v2 CBS2499_5009		20
AWRIv2 AWRI_1490		20
LAMAP LAMAP2480_2067	protein _1768	
CBS2499v2 CBS2499_5007	protein _1768	
AWRIv2 AWRI_1488	protein _1768	
LAMAP LAMAP2480_2068	protein _1766	
CBS2499v2 CBS2499_5006	protein _1766	
AWRIv2 AWRI_1487	protein _1766	
LAMAP LAMAP2480_2069	zinc transporter	
CBS2499v2 CBS2499_5005	transporter ZIP9	
AWRIv2 AWRI_1486	transporter ZIP9	
LAMAP LAMAP2480_2070	secreted protein	
CBS2499v2 CBS2499_5003	secreted protein	
AWRIv2 AWRI_1485	secreted protein	
LAMAP LAMAP2480_2071	5-kinase FAB1	
CBS2499v2 CBS2499_5002	3-phosphate 5-kinase FAB1	
AWRIv2 AWRI_1484	3-phosphate 5-kinase FAB1	
LAMAP LAMAP2480_2072	affecting a late Golgi compartment protein 2	
CBS2499v2 CBS2499_5001	affecting a late Golgi compartment protein 2	
AWRIv2 AWRI_1482	affecting a late Golgi compartment protein 2	
LAMAP LAMAP2480_2073	membrane protein YOL019W	
CBS2499v2 CBS2499_5000	membrane protein YOL019W	
AWRIv2 AWRI_1481	membrane protein YOL019W	
LAMAP LAMAP2480_2075	protein _1758	
CBS2499v2 CBS2499_4998	protein _1758	
AWRIv2 AWRI_1479	protein _1758	
LAMAP LAMAP2480_2077	transporter, sugar porter (SP) family	
CBS2499v2 CBS2499_4994	transporter, sugar porter (SP) family	
AWRIv2 AWRI_1475	transporter, sugar porter (SP) family	
LAMAP LAMAP2480_2085	protein MSB1	
CBS2499v2 CBS2499_4325	protein MSB1	
AWRIv2 AWRI_2609	protein MSB1	
LAMAP LAMAP2480_2089	domain and RING finger protein YDR266C	
CBS2499v2 CBS2499_4329	ubiquitin-protein ligase HEL2	
AWRIv2 AWRI_2607	ubiquitin-protein ligase HEL2	
LAMAP LAMAP2480_2116	acetate-hydrolyzing esterase, required in balance with alcohol acetyltransferase to maintain optimal amounts of isoamyl acetate, which is particularly important in sake brewing	

CBS2499v2 CBS2499_4355	acetate-hydrolyzing esterase; required in balance with alcohol acetyltransferase to maintain optimal amounts of isoamyl acetate, which is particularly important in sake brewing
AWRIv2 AWRI_2581	acetate-hydrolyzing esterase
LAMAP LAMAP2480_2147	protein REB1
CBS2499v2 CBS2499_4847	protein REB1
AWRIv2 AWRI_3415	protein _4094
LAMAP LAMAP2480_2152	domain-containing protein C1B9.03c
CBS2499v2 CBS2499_4842	of 66S pre-ribosomal particles; required for ribosomal large subunit maturation; functionally redundant with Ssf2p; member of the Brix family; SSF1 has a paralog, SSF2, that arose from the whole genome duplication
AWRIv2 AWRI_3411	biogenesis protein SSF2
LAMAP LAMAP2480_2207	amidotransferase, A subunit
CBS2499v2 CBS2499_4296	amidotransferase, A subunit
AWRIv2 AWRI_1557	amidotransferase subunit A, mitochondrial
LAMAP LAMAP2480_2210	protein of unknown function; non-tagged protein is detected in purified mitochondria; may interact with respiratory chain complex IV; null mutant is viable and displays reduced frequency of mitochondrial genome loss
CBS2499v2 CBS2499_4295	c oxidase subunit; has a role in assembly of respiratory supercomplexes; similar to Rcf1p, and either Rcf1p or Rcf2p is required for late-stage assembly of the Cox12p and Cox13p subunits and for cytochrome c oxidase activity; associates with the cytochrome c oxidase - cytochrome bc1 supercomplex; null mutant accumulates reactive oxygen species; member of the conserved hypoxia induced gene family; C. elegans homolog is functional in yeast
AWRIv2 AWRI_1556	c oxidase subunit; has a role in assembly of respiratory supercomplexes; similar to Rcf1p, and either Rcf1p or Rcf2p is required for late-stage assembly of the Cox12p and Cox13p subunits and for cytochrome c oxidase activity; associates with the cytochrome c oxidase - cytochrome bc1 supercomplex; null mutant accumulates reactive oxygen species; member of the conserved hypoxia induced gene family; C. elegans homolog is functional in yeast
LAMAP LAMAP2480_2213	nucleosidase
CBS2499v2 CBS2499_4292	nucleosidase (uridine-cytidine N-ribohydrolase); cleaves N-glycosidic bonds in nucleosides; involved in the pyrimidine salvage and nicotinamide riboside salvage pathways
AWRIv2 AWRI_1553	nucleosidase
LAMAP LAMAP2480_2247	MNN4
CBS2499v2 CBS2499_4253	protein YJR061W
AWRIv2 AWRI_1526	MNN4
LAMAP LAMAP2480_2248	protein _1804
CBS2499v2 CBS2499_4252	protein _1804
AWRIv2 AWRI_1525	protein _1804
LAMAP LAMAP2480_2290	FAM63A
CBS2499v2 CBS2499_3164	protein YPL191C
AWRIv2 AWRI_3564	protein YPL191C
LAMAP LAMAP2480_2295	oxidase required for oxidative protein folding in the endoplasmic reticulum

CBS2499v2 CBS2499_3159	oxidase required for oxidative protein folding in the ER; essential for maintaining proper redox balance in ER; feedback regulation of Ero1p occurs via reduction and oxidation of Ero1p regulatory bonds; reduced Pdi1p activates Ero1p by direct reduction of Ero1p regulatory bonds; depletion of thiol substrates and accumulation of oxidized Pdi1p results in inactivation of Ero1p by both Pdi1p-mediated oxidation and autonomous oxidation of Ero1p regulatory bonds
AWRIv2 AWRI_3559	oxidase required for oxidative protein folding in the ER; essential for maintaining proper redox balance in ER; feedback regulation of Ero1p occurs via reduction and oxidation of Ero1p regulatory bonds; reduced Pdi1p activates Ero1p by direct reduction of Ero1p regulatory bonds; depletion of thiol substrates and accumulation of oxidized Pdi1p results in inactivation of Ero1p by both Pdi1p-mediated oxidation and autonomous oxidation of Ero1p regulatory bonds
LAMAP LAMAP2480_2304	WD repeat-containing protein C227.12
CBS2499v2 CBS2499_3151	WD repeat-containing protein C227.12
AWRIv2 AWRI_3549	WD repeat-containing protein C227.12
LAMAP LAMAP2480_2306	complex subunit 3
CBS2499v2 CBS2499_3149	complex subunit 3
AWRIv2 AWRI_3547	of the HDA1 histone deacetylase complex; possibly tetrameric trichostatin A-sensitive class II histone deacetylase complex contains Hda1p homodimer and an Hda2p-Hda3p heterodimer; required for the activity of the complex; relocates to the cytosol in response to hypoxia; similar to Hda2p
LAMAP LAMAP2480_2319	binding domain of Hap4 for binding to Hap2/3/5
CBS2499v2 CBS2499_3134	protein _4457
AWRIv2 AWRI_3730	binding domain of Hap4 for binding to Hap2/3/5
LAMAP LAMAP2480_2321	aminotransferase C1771.03c
CBS2499v2 CBS2499_3132	aminotransferase C1771.03c
AWRIv2 AWRI_3734	aminotransferase C1771.03c
LAMAP LAMAP2480_2357	and RNase II family 3'-5' exoribonucleases
CBS2499v2 CBS2499_1183	and RNase II family 3'-5' exoribonucleases
AWRIv2 AWRI_2573	II, mitochondrial
LAMAP LAMAP2480_2361	protein 1
CBS2499v2 CBS2499_1187	protein 1
AWRIv2 AWRI_2570	protein 1
LAMAP LAMAP2480_2365	protein _3106
CBS2499v2 CBS2499_1173	protein _3106
AWRIv2 AWRI_2579	protein _3106
LAMAP LAMAP2480_2366	regulator CRZ1
CBS2499v2 CBS2499_1172	regulator CRZ1
AWRIv2 AWRI_4183	regulator CRZ1
LAMAP LAMAP2480_2373	alpha of assimilatory sulfite reductase, which converts sulfite into sulfide
CBS2499v2 CBS2499_1164	alpha of assimilatory sulfite reductase; complex converts sulfite into sulfide
AWRIv2 AWRI_2450	reductase [NADPH] flavoprotein component
LAMAP LAMAP2480_2386	protein insertase, YidC/Oxa1 family

CBS2499v2 CBS2499_1152	inner membrane insertase; mediates the insertion of both mitochondrial- and nuclear-encoded proteins from the matrix into the inner membrane; also has a role in insertion of carrier proteins into the inner membrane; acts as a voltage-gated ion channel, activated by substrate peptides; interacts with mitochondrial ribosomes; conserved from bacteria to animals
AWRiv2 AWRI_2461	inner membrane insertase; mediates the insertion of both mitochondrial- and nuclear-encoded proteins from the matrix into the inner membrane; also has a role in insertion of carrier proteins into the inner membrane; acts as a voltage-gated ion channel, activated by substrate peptides; interacts with mitochondrial ribosomes; conserved from bacteria to animals
LAMAP LAMAP2480_2388	snRNP component ist3
CBS2499v2 CBS2499_1150	snRNP component ist3
AWRiv2 AWRI_2463	snRNP component ist3
LAMAP LAMAP2480_2394	DCR2
	involved in downregulation of the unfolded protein response (UPR), at least in part via dephosphorylation of Ire1p; dosage-dependent positive regulator of the G1/S phase transition through control of the timing of START
CBS2499v2 CBS2499_1144	protein C1020.05
AWRiv2 AWRI_2469	protein 3
LAMAP LAMAP2480_2403	protein 3
CBS2499v2 CBS2499_1136	homolog spn4
AWRiv2 AWRI_2472	inducibility protein 3
LAMAP LAMAP2480_2432	inducibility protein 3
CBS2499v2 CBS2499_3546	inducibility protein 3
AWRiv2 AWRI_3896	involved in cell wall beta-glucan assembly; null mutation leads to severe growth defects, aberrant multibudded morphology, and mating defects
LAMAP LAMAP2480_2441	involved in cell wall beta-glucan assembly; null mutation leads to severe growth defects, aberrant multibudded morphology, and mating defects
CBS2499v2 CBS2499_3554	involved in cell wall beta-glucan assembly; null mutation leads to severe growth defects, aberrant multibudded morphology, and mating defects
AWRiv2 AWRI_3901	involved in cell wall beta-glucan assembly; null mutation leads to severe growth defects, aberrant multibudded morphology, and mating defects
LAMAP LAMAP2480_2453	shock protein 26
	heat shock protein (sHSP) with chaperone activity; forms hollow, sphere-shaped oligomers that suppress unfolded proteins aggregation; long-lived protein that is preferentially retained in mother cells and forms cytoplasmic foci; oligomer activation requires heat-induced conformational change; also has mRNA binding activity
CBS2499v2 CBS2499_3570	shock protein 26
AWRiv2 AWRI_3912	DNA-binding domain
LAMAP LAMAP2480_2455	regulator of yeast form adherence 6
CBS2499v2 CBS2499_3572	regulator of yeast form adherence 6
AWRiv2 AWRI_4157	maintenance of chromosomes protein 4
LAMAP LAMAP2480_2461	maintenance of chromosomes protein 4
CBS2499v2 CBS2499_3584	maintenance of chromosomes protein 4
AWRiv2 AWRI_2720	kinase 1
LAMAP LAMAP2480_2466	kinase 1
CBS2499v2 CBS2499_3590	kinase 1
AWRiv2 AWRI_2716	kinase ssp1

LAMAP LAMAP2480_2479	subunit (145 kDa), involved in RNA polymerase II transcription initiation; possesses in vitro histone acetyltransferase activity but its role in vivo appears to be minor; involved in promoter binding and G1/S progression
CBS2499v2 CBS2499_3625	subunit, involved in RNA pol II transcription initiation; possesses in vitro histone acetyltransferase activity but its role in vivo appears to be minor; involved in promoter binding and G1/S progression; relocalizes to the cytosol in response to hypoxia
AWRIv2 AWRI_2683	initiation factor TFIID subunit 1
LAMAP LAMAP2480_2484	repeat-containing protein 40
CBS2499v2 CBS2499_3630	repeat-containing protein 58
AWRIv2 AWRI_2679	protein _3222
LAMAP LAMAP2480_2491	site selection protein RAX2
CBS2499v2 CBS2499_3636	site selection protein RAX2
AWRIv2 AWRI_1761	site selection protein RAX2
LAMAP LAMAP2480_2501	N-lysine methyltransferase 1
CBS2499v2 CBS2499_3645	lysine N-methyltransferase 1
AWRIv2 AWRI_1769	lysine N-methyltransferase 1
LAMAP LAMAP2480_2504	non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; has similarity to E. coli RNase PH and to human hRrp42p (EXOSC7)
CBS2499v2 CBS2499_3648	non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; has similarity to E. coli RNase PH and to human hRrp42p (EXOSC7)
AWRIv2 AWRI_1771	non-catalytic core component; involved in 3'-5' RNA processing and degradation in both the nucleus and the cytoplasm; has similarity to E. coli RNase PH and to human hRrp42p (EXOSC7)
LAMAP LAMAP2480_2524	trafficking adapter 3
CBS2499v2 CBS2499_1030	trafficking adapter 3
AWRIv2 AWRI_0659	trafficking adapter 3
LAMAP LAMAP2480_2531	ligase, required for tRNA splicing and for both splicing and translation of HAC1 mRNA in the UPR; has phosphodiesterase, polynucleotide kinase, and ligase activities; localized at the inner nuclear envelope and partially to polysomes
CBS2499v2 CBS2499_1024	ligase; required for tRNA splicing and for both splicing and translation of HAC1 mRNA in the UPR; has phosphodiesterase, polynucleotide kinase, and ligase activities; localized at the inner nuclear envelope and partially to polysomes
AWRIv2 AWRI_0664	ligase; required for tRNA splicing and for both splicing and translation of HAC1 mRNA in the UPR; has phosphodiesterase, polynucleotide kinase, and ligase activities; localized at the inner nuclear envelope and partially to polysomes
LAMAP LAMAP2480_2536	kinase and DNA damage checkpoint effector, mediates cell cycle arrest via phosphorylation of Pds1p; phosphorylated by checkpoint signal transducer Mec1p; homolog of S. pombe and mammalian Chk1 checkpoint kinase
CBS2499v2 CBS2499_1019	kinase and DNA damage checkpoint effector; mediates cell cycle arrest via phosphorylation of Pds1p; phosphorylated by checkpoint signal transducer Mec1p; homolog of S. pombe and mammalian Chk1 checkpoint kinase
AWRIv2 AWRI_0667	kinase and DNA damage checkpoint effector; mediates cell cycle arrest via phosphorylation of Pds1p; phosphorylated by checkpoint signal transducer Mec1p; homolog of S. pombe and mammalian Chk1 checkpoint kinase
LAMAP LAMAP2480_2545	IME4

CBS2499v2 CBS2499_1008	IME4
AWRIv2 AWRI_0677	IME4
LAMAP LAMAP2480_2549	factor GTPase-activating protein GLO3
CBS2499v2 CBS2499_1004	factor GTPase-activating protein GLO3
AWRIv2 AWRI_0681	factor GTPase-activating protein GLO3
LAMAP LAMAP2480_2550	complex subunit 2
CBS2499v2 CBS2499_1003	complex subunit 2
AWRIv2 AWRI_0682	complex subunit 2
LAMAP LAMAP2480_2554	transporter liz1
CBS2499v2 CBS2499_5032	transporter liz1
AWRIv2 AWRI_4184	transporter liz1
LAMAP LAMAP2480_2555	dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane
CBS2499v2 CBS2499_5033	dehydrogenase; oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane
AWRIv2 AWRI_4185	dehydrogenase; oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane
LAMAP LAMAP2480_2557	protein y4sH
CBS2499v2 CBS2499_5035	protein y4sH
AWRIv2 AWRI_4187	protein y4sH
LAMAP LAMAP2480_2582	carboxyl-terminal hydrolase 12
CBS2499v2 CBS2499_4698	carboxyl-terminal hydrolase 12
AWRIv2 AWRI_2403	carboxyl-terminal hydrolase 12
LAMAP LAMAP2480_2589	initiation factor TFIID subunit 10
CBS2499v2 CBS2499_4704	initiation factor TFIID subunit 10
AWRIv2 AWRI_2397	initiation factor TFIID subunit 10
LAMAP LAMAP2480_2601	ldg family protein 7
CBS2499v2 CBS2499_3136	wall protein RHD3
AWRIv2 AWRI_3729	wall protein RHD3
LAMAP LAMAP2480_2613	membrane protein PEX29
CBS2499v2 CBS2499_3125	membrane protein PEX29
AWRIv2 AWRI_3742	membrane protein PEX29
LAMAP LAMAP2480_2614	checkpoint protein BUB3
CBS2499v2 CBS2499_3124	checkpoint protein BUB3.1
AWRIv2 AWRI_3743	checkpoint protein BUB3.1
LAMAP LAMAP2480_2616	finger protein C144.02
CBS2499v2 CBS2499_3122	complex subunit 1
AWRIv2 AWRI_3745	complex subunit 1
LAMAP LAMAP2480_2626	transferase 3
CBS2499v2 CBS2499_3116	transferase 3
AWRIv2 AWRI_3750	transferase 3
LAMAP LAMAP2480_2631	oxidase
CBS2499v2 CBS2499_3111	oxidase
AWRIv2 AWRI_1195	oxidase

LAMAP|LAMAP2480_2643
 CBS2499v2|CBS2499_3095
 AWRiv2|AWRI_1208
 LAMAP|LAMAP2480_2649
 CBS2499v2|CBS2499_3088
 AWRiv2|AWRI_1217
 LAMAP|LAMAP2480_2654
 CBS2499v2|CBS2499_3083
 AWRiv2|AWRI_1221
 LAMAP|LAMAP2480_2660
 CBS2499v2|CBS2499_3073
 AWRiv2|AWRI_1228

 LAMAP|LAMAP2480_2663

 CBS2499v2|CBS2499_3069

 AWRiv2|AWRI_1231
 LAMAP|LAMAP2480_2666
 CBS2499v2|CBS2499_3064
 AWRiv2|AWRI_1238
 LAMAP|LAMAP2480_2668
 CBS2499v2|CBS2499_3060
 AWRiv2|AWRI_1242
 LAMAP|LAMAP2480_2669
 CBS2499v2|CBS2499_3059
 AWRiv2|AWRI_1243
 LAMAP|LAMAP2480_2671
 CBS2499v2|CBS2499_3056
 AWRiv2|AWRI_1245

 LAMAP|LAMAP2480_2673
 CBS2499v2|CBS2499_3052
 AWRiv2|AWRI_1248
 LAMAP|LAMAP2480_2675
 CBS2499v2|CBS2499_3050
 AWRiv2|AWRI_1250
 LAMAP|LAMAP2480_2677
 CBS2499v2|CBS2499_3047
 AWRiv2|AWRI_1254
 LAMAP|LAMAP2480_2712
 CBS2499v2|CBS2499_0748
 AWRiv2|AWRI_0098
 LAMAP|LAMAP2480_2713

ubiquitin-protein ligase UBR1
 ubiquitin-protein ligase UBR1
 ubiquitin-protein ligase UBR1
 MNT3
 alpha-1,3-mannosyltransferase MNN15
 alpha-1,3-mannosyltransferase MNN14
 protein _1462
 protein _1462
 protein _1462
 snRNP component prp10
 snRNP component prp10
 snRNP component prp10
xylose and arabinose reductase; member of the aldo-keto reductase (AKR) family; GFP-fusion protein is induced in response to the DNA-damaging agent MMS
 and arabinose reductase; member of the aldo-keto reductase (AKR) family; GFP-fusion protein is induced in response to the DNA-damaging agent MMS
 and arabinose reductase; member of the aldo-keto reductase (AKR) family; GFP-fusion protein is induced in response to the DNA-damaging agent MMS
 transcription activator TEC1
 transcription activator TEC1
 tea atts type DNA binding protein
 protein _1485
 protein HPODL_00938
 protein _1485
 rna annealing mrna export
 rna annealing mrna export
 rna annealing mrna export
 membrane protein PMP47A
 membrane protein PMP47A
 membrane protein PMP47A
 of U3-containing Small Subunit (SSU) processome complex involved in production of 18S rRNA and assembly of small ribosomal subunit
 protein C57A7.06
 protein C57A7.06
 protein HPODL_00947
 protein HPODL_00947
 of six subunits of rna polymerase iii transcription initiation factor complex
 protein involved in pre-rRNA processing; depletion causes severely decreased 18S rRNA levels
 protein ESF1
 protein ESF1
 protein C31F10.16
 protein C31F10.16
 protein C31F10.16
 protein SAP190

CBS2499v2|CBS2499_0747
AWRIv2|AWRI_0099
LAMAP|LAMAP2480_2725
CBS2499v2|CBS2499_0735
AWRIv2|AWRI_0106
LAMAP|LAMAP2480_2732
CBS2499v2|CBS2499_0729
AWRIv2|AWRI_0110
LAMAP|LAMAP2480_2733
CBS2499v2|CBS2499_0728
AWRIv2|AWRI_0111
LAMAP|LAMAP2480_2734
CBS2499v2|CBS2499_0727
AWRIv2|AWRI_0112
LAMAP|LAMAP2480_2738
CBS2499v2|CBS2499_0722
AWRIv2|AWRI_0117
LAMAP|LAMAP2480_2741
CBS2499v2|CBS2499_0719
AWRIv2|AWRI_0120
LAMAP|LAMAP2480_2751
CBS2499v2|CBS2499_0710
AWRIv2|AWRI_0130
LAMAP|LAMAP2480_2753
CBS2499v2|CBS2499_0708
AWRIv2|AWRI_0132
LAMAP|LAMAP2480_2754
CBS2499v2|CBS2499_0707
AWRIv2|AWRI_0133
LAMAP|LAMAP2480_2765
CBS2499v2|CBS2499_1409
AWRIv2|AWRI_2010
LAMAP|LAMAP2480_2766
CBS2499v2|CBS2499_1408
AWRIv2|AWRI_2011
LAMAP|LAMAP2480_2767
CBS2499v2|CBS2499_1407
AWRIv2|AWRI_2012
LAMAP|LAMAP2480_2768
CBS2499v2|CBS2499_1406
AWRIv2|AWRI_2013

protein SAP190
protein SAP190
N-methyltransferase, H3 lysine-4 specific
N-methyltransferase, H3 lysine-4 specific
N-methyltransferase, H3 lysine-4 specific
protein MAG2
protein MAG2
protein MAG2
mannosyltransferase 1
mannosyltransferase 1
mannosyltransferase 1
of RNA polymerase II transcription subunit 21
of RNA polymerase II transcription subunit 21
of RNA polymerase II transcription subunit 21
protein 2
protein 2
protein 2
atp synthase epsilon chain domain-containing protein
atp synthase epsilon chain domain-containing protein
atp synthase epsilon chain domain-containing protein
specific transcription factor domain
specific transcription factor domain
transcription
domain
domain
and polytropic retrovirus receptor 1
protein _0157
protein _0157
protein _0157
FMP25, mitochondrial
FMP25, mitochondrial
FMP25, mitochondrial
protein _2408
protein _2408
protein _2408
protein _2409
protein _2409
protein _2409
domain-containing protein DEHA2G15708g
domain-containing protein DEHA2G15708g
domain-containing protein YALI0D26906g

LAMAP|LAMAP2480_2780

phosphoribosyl transferase of the tryptophan biosynthetic pathway, catalyzes the phosphoribosylation of anthranilate, subject to the general control system of amino acid biosynthesis

CBS2499v2 CBS2499_1390	phosphoribosyl transferase; transferase of the tryptophan biosynthetic pathway; catalyzes the phosphoribosylation of anthranilate; subject to the general control system of amino acid biosynthesis
AWRlv2 AWRI_2027	phosphoribosyl transferase; transferase of the tryptophan biosynthetic pathway; catalyzes the phosphoribosylation of anthranilate; subject to the general control system of amino acid biosynthesis
LAMAP LAMAP2480_2789	gras liver health family 1
CBS2499v2 CBS2499_1381	gras liver health family 1
AWRlv2 AWRI_2037	protein
LAMAP LAMAP2480_2790	amino-acid permease C584.13
CBS2499v2 CBS2499_1379	amino-acid permease C584.13
AWRlv2 AWRI_2038	amino-acid permease C584.13
	matrix iron chaperone; oxidizes and stores iron; interacts with Isu1p to promote Fe-S cluster assembly; mutation results in multiple Fe/S-dependent enzyme deficiencies; human frataxin homolog is mutated in Friedrich's ataxia
LAMAP LAMAP2480_2791	matrix iron chaperone; oxidizes and stores iron; interacts with Isu1p to promote Fe-S cluster assembly; mutation results in multiple Fe/S-dependent enzyme deficiencies; human frataxin homolog is mutated in Friedrich's ataxia
	donor protein CyaY
CBS2499v2 CBS2499_1378	protein _2441
AWRlv2 AWRI_2039	protein _2441
LAMAP LAMAP2480_2794	protein
CBS2499v2 CBS2499_1375	esterase TGL1
AWRlv2 AWRI_2041	esterase TGL1
LAMAP LAMAP2480_2795	protein _2443
CBS2499v2 CBS2499_1374	protein _2443
AWRlv2 AWRI_2042	protein _2443
LAMAP LAMAP2480_2796	of ubiquitin conjugation to ER degradation protein 1
CBS2499v2 CBS2499_1373	of ubiquitin conjugation to ER degradation protein 1
AWRlv2 AWRI_2043	of ubiquitin conjugation to ER degradation protein 1
LAMAP LAMAP2480_2798	regulatory protein SAP30
CBS2499v2 CBS2499_1371	regulatory protein SAP30
AWRlv2 AWRI_2045	of a histone deacetylase complex
LAMAP LAMAP2480_2799	2-reductase
CBS2499v2 CBS2499_1370	2-reductase
AWRlv2 AWRI_2046	2-reductase
LAMAP LAMAP2480_2800	protein _2447
CBS2499v2 CBS2499_1369	of G protein signaling domain
AWRlv2 AWRI_2047	of G protein signaling domain
LAMAP LAMAP2480_2801	expression activator
CBS2499v2 CBS2499_1368	wall transcription factor ACE2
AWRlv2 AWRI_2048	wall transcription factor ACE2
LAMAP LAMAP2480_2808	protein _2465
CBS2499v2 CBS2499_1362	
AWRlv2 AWRI_2053	
LAMAP LAMAP2480_2821	

CBS2499v2 CBS2499_1347	protein _2465
AWRiv2 AWRI_2064	protein _2465
LAMAP LAMAP2480_2830	cardiolipin-specific deacylase, mitochondrial
CBS2499v2 CBS2499_1337	cardiolipin-specific deacylase, mitochondrial
AWRiv2 AWRI_2072	cardiolipin-specific deacylase, mitochondrial
LAMAP LAMAP2480_2836	ligase, beta subunit
CBS2499v2 CBS2499_1331	ligase, beta subunit
AWRiv2 AWRI_3602	ligase, beta subunit
LAMAP LAMAP2480_2839	of Elongator complex, which is required for modification of wobble nucleosides in tRNA; required for Elongator structural integrity
CBS2499v2 CBS2499_1327	of hexameric RecA-like ATPase Elp456 Elongator subcomplex; which is required for modification of wobble nucleosides in tRNA; required for Elongator structural integrity
AWRiv2 AWRI_3599	complex protein 4
LAMAP LAMAP2480_2849	acetyltransferase TAN1
CBS2499v2 CBS2499_1315	acetyltransferase TAN1
AWRiv2 AWRI_3586	acetyltransferase TAN1
LAMAP LAMAP2480_2850	protein _4282
CBS2499v2 CBS2499_1314	protein _4282
AWRiv2 AWRI_3585	protein _4282
LAMAP LAMAP2480_2852	hydrolase family
CBS2499v2 CBS2499_1310	protein YJR098C
AWRiv2 AWRI_3582	hydrolase family
LAMAP LAMAP2480_2853	biosynthesis protein 4
CBS2499v2 CBS2499_1309	biosynthesis protein 4
AWRiv2 AWRI_3581	biosynthesis protein 4
LAMAP LAMAP2480_2855	of telomere capping protein 1
CBS2499v2 CBS2499_1303	of telomere capping protein 1
AWRiv2 AWRI_3575	of telomere capping protein 1
LAMAP LAMAP2480_2858	protein _2313
CBS2499v2 CBS2499_3222	protein HPODL_03172
AWRiv2 AWRI_1939	protein _2313
LAMAP LAMAP2480_2860	protein SAP155
CBS2499v2 CBS2499_3220	protein SAP155
AWRiv2 AWRI_1936	protein SAP155
LAMAP LAMAP2480_2878	membrane protein YOL107W
CBS2499v2 CBS2499_2217	protein 115 homolog
AWRiv2 AWRI_2824	protein 115 homolog
LAMAP LAMAP2480_2883	catalyzes the eighth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; transcription is regulated by general amino acid control
CBS2499v2 CBS2499_2222	catalyzes the eighth step in histidine biosynthesis; mutations cause histidine auxotrophy and sensitivity to Cu, Co, and Ni salts; transcription is regulated by general amino acid control
AWRiv2 AWRI_2827	phosphate phosphatase HisJ family
LAMAP LAMAP2480_2899	resistance protein SNG1
CBS2499v2 CBS2499_2238	resistance protein SNG1

AWRIv2 AWRI_2837	endoplasmic reticulum membrane protein YJR015W
LAMAP LAMAP2480_2906	protein 1
CBS2499v2 CBS2499_2244	regulator CBF1
AWRIv2 AWRI_2841	regulator CBF1
LAMAP LAMAP2480_2909	protein _3418
CBS2499v2 CBS2499_2247	protein _3418
AWRIv2 AWRI_2843	protein _3418
LAMAP LAMAP2480_2918	PEP-CTERM system TPR-repeat lipoprotein
CBS2499v2 CBS2499_2259	IV pilus biogenesis/stability protein PilW
AWRIv2 AWRI_2846	transcriptional corepressor CYC8
LAMAP LAMAP2480_2920	complex subunit mu
CBS2499v2 CBS2499_2262	complex subunit mu
AWRIv2 AWRI_2849	complex subunit mu
LAMAP LAMAP2480_2923	transport transcription regulator RGT1
CBS2499v2 CBS2499_2265	transport transcription regulator RGT1
AWRIv2 AWRI_2851	protein HPODL_03195
LAMAP LAMAP2480_2926	protein
CBS2499v2 CBS2499_2268	protein
AWRIv2 AWRI_2854	protein
LAMAP LAMAP2480_2928	domain-containing protein 1
CBS2499v2 CBS2499_2270	protein 45
AWRIv2 AWRI_2856	protein 45
LAMAP LAMAP2480_2929	repression protein creC
CBS2499v2 CBS2499_2271	repression protein creC
AWRIv2 AWRI_3827	repression protein creC
LAMAP LAMAP2480_2939	RNA polymerase III subunit RPC7
CBS2499v2 CBS2499_2281	RNA polymerase III subunit RPC7
AWRIv2 AWRI_3835	RNA polymerase III subunit RPC7
LAMAP LAMAP2480_2957	
CBS2499v2 CBS2499_3017	cellobiohydrolase CEL6A
AWRIv2 AWRI_1283	cellobiohydrolase CEL6A
LAMAP LAMAP2480_2971	transcription factor YER064C
CBS2499v2 CBS2499_3002	factor VHR2
AWRIv2 AWRI_1295	factor VHR2
LAMAP LAMAP2480_2980	domain-containing protein 3
CBS2499v2 CBS2499_4943	domain-containing protein 3
AWRIv2 AWRI_3115	domain-containing protein 3
LAMAP LAMAP2480_2981	recognition particle 14kd protein
CBS2499v2 CBS2499_4942	recognition particle subunit SRP14
AWRIv2 AWRI_3114	recognition particle 14kd protein
LAMAP LAMAP2480_2984	ASM4
CBS2499v2 CBS2499_4940	ASM4
AWRIv2 AWRI_3113	ASM4
LAMAP LAMAP2480_2986	integral to the mitochondrial membrane; has a conserved methyltransferase motif; multicopy suppressor of respiratory defects caused by OXA1 mutations

CBS2499v2 CBS2499_4939	integral to the mitochondrial membrane; has a conserved methyltransferase motif and is predicted to be an RNA methyltransferase; multicopy suppressor of respiratory defects caused by OXA1 mutations
AWRlv2 AWRI_3112	integral to the mitochondrial membrane; has a conserved methyltransferase motif and is predicted to be an RNA methyltransferase; multicopy suppressor of respiratory defects caused by OXA1 mutations
LAMAP LAMAP2480_2993	alpha mannosidase, involved in free oligosaccharide (fOS) degradation; delivered to the vacuole in a novel pathway separate from the secretory pathway
CBS2499v2 CBS2499_2156	alpha mannosidase; involved in free oligosaccharide (fOS) degradation; delivered to the vacuole in a novel pathway separate from the secretory pathway
AWRlv2 AWRI_2893	alpha mannosidase; involved in free oligosaccharide (fOS) degradation; delivered to the vacuole in a novel pathway separate from the secretory pathway
LAMAP LAMAP2480_2996	domain-containing protein WWM1
CBS2499v2 CBS2499_2153	domain-containing protein WWM1
AWRlv2 AWRI_2894	domain-containing protein WWM1
LAMAP LAMAP2480_2997	metalloprotease of the mitochondrial intermembrane space, member of the pitrilysin family; degrades proteins and presequence peptides cleaved from imported proteins; required for normal mitochondrial morphology
CBS2499v2 CBS2499_2152	metalloprotease of the pitrilysin family; metalloprotease of the intermembrane space; degrades proteins and presequence peptides cleaved from imported proteins; required for normal mitochondrial morphology
AWRlv2 AWRI_2895	metalloprotease of the pitrilysin family; metalloprotease of the intermembrane space; degrades proteins and presequence peptides cleaved from imported proteins; required for normal mitochondrial morphology
LAMAP LAMAP2480_3012	protein _1061
CBS2499v2 CBS2499_2134	protein _1061
AWRlv2 AWRI_0873	protein _1061
LAMAP LAMAP2480_3015	of rapamycin complex 2 subunit AVO2
CBS2499v2 CBS2499_2132	of rapamycin complex 2 subunit AVO2
AWRlv2 AWRI_0875	ankyrin repeat protein FPV245
LAMAP LAMAP2480_3016	RING finger protein C2F3.16
CBS2499v2 CBS2499_2131	RING finger protein C2F3.16
AWRlv2 AWRI_0876	RING finger protein C2F3.16
LAMAP LAMAP2480_3017	membrane protein localized to late Golgi vesicles along with the v-SNARE Tlg2p; may interact with ribosomes, based on co-purification experiments
CBS2499v2 CBS2499_2130	membrane protein; localized to late Golgi vesicles along with the v-SNARE Tlg2p; may interact with ribosomes, based on co-purification experiments; may have a role in intracellular sterol transport
AWRlv2 AWRI_0877	membrane protein; localized to late Golgi vesicles along with the v-SNARE Tlg2p; may interact with ribosomes, based on co-purification experiments; may have a role in intracellular sterol transport
LAMAP LAMAP2480_3033	elongation factor SPT5
CBS2499v2 CBS2499_2113	elongation factor SPT5
AWRlv2 AWRI_0894	elongation factor SPT5
LAMAP LAMAP2480_3043	protein product
CBS2499v2 CBS2499_4438	protein product

AWRIv2 AWRI_2112	protein _2527	
LAMAP LAMAP2480_3052	poly(A)-specific ribonuclease subunit PAN3	
CBS2499v2 CBS2499_4446	poly(A)-specific ribonuclease subunit PAN3	
AWRIv2 AWRI_2118	poly(A)-specific ribonuclease subunit pan3	
LAMAP LAMAP2480_3066	RNA polymerase III subunit RPC5	
CBS2499v2 CBS2499_4467	RNA polymerase III subunit RPC5	
AWRIv2 AWRI_3148	RNA polymerase III subunit RPC5	
LAMAP LAMAP2480_3097	regulatory protein DEP1	
CBS2499v2 CBS2499_4971	regulatory protein DEP1	
AWRIv2 AWRI_3124	regulatory protein DEP1	
LAMAP LAMAP2480_3101	protein _3737	
CBS2499v2 CBS2499_4968	protein _3737	
AWRIv2 AWRI_3122	protein _3737	
	NAPDH-dependent diflavin reductase, component of an early step in the cytosolic Fe-S protein assembly (CIA) machinery; transfers electrons from NADPH to the Fe-S cluster of Dre2p; plays a pro-death role under oxidative stress	
LAMAP LAMAP2480_3114	NAPDH-dependent diflavin reductase; component of an early step in the cytosolic Fe-S protein assembly (CIA) machinery; transfers electrons from NADPH to the Fe-S cluster of Dre2p; plays a pro-death role under oxidative stress; Tah18p-dependent nitric oxide synthesis confers high-temperature stress tolerance; possible target for development of antifungal drugs	
	NAPDH-dependent diflavin reductase; component of an early step in the cytosolic Fe-S protein assembly (CIA) machinery; transfers electrons from NADPH to the Fe-S cluster of Dre2p; plays a pro-death role under oxidative stress; Tah18p-dependent nitric oxide synthesis confers high-temperature stress tolerance; possible target for development of antifungal drugs	
CBS2499v2 CBS2499_4955	NAPDH-dependent diflavin reductase; component of an early step in the cytosolic Fe-S protein assembly (CIA) machinery; transfers electrons from NADPH to the Fe-S cluster of Dre2p; plays a pro-death role under oxidative stress; Tah18p-dependent nitric oxide synthesis confers high-temperature stress tolerance; possible target for development of antifungal drugs	
	NAPDH-dependent diflavin reductase; component of an early step in the cytosolic Fe-S protein assembly (CIA) machinery; transfers electrons from NADPH to the Fe-S cluster of Dre2p; plays a pro-death role under oxidative stress; Tah18p-dependent nitric oxide synthesis confers high-temperature stress tolerance; possible target for development of antifungal drugs	
AWRIv2 AWRI_3087	V, beta subunit	
LAMAP LAMAP2480_3125	V, beta subunit	
CBS2499v2 CBS2499_3231	V, beta subunit	
AWRIv2 AWRI_1946	V, beta subunit	
LAMAP LAMAP2480_3126	transporter ESBP6	
CBS2499v2 CBS2499_3232	transporter ESBP6	
AWRIv2 AWRI_1947	transporter ESBP6	
	permease, mediates purine (adenine, guanine, and hypoxanthine) and cytosine accumulation	
LAMAP LAMAP2480_3150	permease; mediates purine (adenine, guanine, and hypoxanthine) and cytosine accumulation; relative distribution to the vacuole increases upon DNA replication stress	
CBS2499v2 CBS2499_1089	purine-cytosine permease; very similar to Fcy2p but cannot substitute for its function	
AWRIv2 AWRI_0610	wry family protein 8	7
LAMAP LAMAP2480_3159		7
CBS2499v2 CBS2499_1081		
AWRIv2 AWRI_0615		
LAMAP LAMAP2480_3160	wry family protein 8	1
CBS2499v2 CBS2499_1080		4
AWRIv2 AWRI_0616		
LAMAP LAMAP2480_3165	protein	
CBS2499v2 CBS2499_1075	protein HPODL_00030	
AWRIv2 AWRI_0620	protein _0763	

LAMAP LAMAP2480_3173	protein
CBS2499v2 CBS2499_1067	protein
AWRlv2 AWRI_0628	protein
	light chain, subunit of the major coat protein involved in intracellular protein transport and endocytosis; thought to regulate clathrin function; two Clathrin heavy chains (CHC1) form the clathrin triskelion structural component
LAMAP LAMAP2480_3191	light chain; subunit of the major coat protein involved in intracellular protein transport and endocytosis; regulates endocytic progression; thought to regulate clathrin function; the clathrin triskelion is a trimeric molecule composed of three heavy chains that radiate from a vertex and three light chains which bind noncovalently near the vertex of the triskelion
CBS2499v2 CBS2499_1820	light chain
AWRlv2 AWRI_2258	polymerase (pol2)
LAMAP LAMAP2480_3209	polymerase (pol2)
CBS2499v2 CBS2499_1803	polymerase (pol2)
AWRlv2 AWRI_4118	protein
LAMAP LAMAP2480_3210	protein
CBS2499v2 CBS2499_1802	protein
AWRlv2 AWRI_4119	ribosomal protein of the large subunit, homolog of prokaryotic L29 ribosomal protein; located at the ribosomal tunnel exit
LAMAP LAMAP2480_3216	ribosomal protein of the large subunit; homolog of prokaryotic L29 ribosomal protein; located at the ribosomal tunnel exit
CBS2499v2 CBS2499_1797	ribosomal protein of the large subunit; homolog of prokaryotic L29 ribosomal protein; located at the ribosomal tunnel exit
AWRlv2 AWRI_4123	ribosomal protein of the large subunit; homolog of prokaryotic L29 ribosomal protein; located at the ribosomal tunnel exit
LAMAP LAMAP2480_3218	protein RAP1
CBS2499v2 CBS2499_1795	protein RAP1
AWRlv2 AWRI_4124	DNA-binding
LAMAP LAMAP2480_3220	machinery-associated protein 64
CBS2499v2 CBS2499_1793	machinery-associated protein 64
AWRlv2 AWRI_1474	machinery-associated protein 64
LAMAP LAMAP2480_3223	organelle assembly protein TopJ
CBS2499v2 CBS2499_1789	organelle assembly protein TopJ
AWRlv2 AWRI_1471	organelle assembly protein TopJ
LAMAP LAMAP2480_3229	proton ATPase subunit H
CBS2499v2 CBS2499_1782	proton ATPase subunit H
AWRlv2 AWRI_1467	proton ATPase subunit H
LAMAP LAMAP2480_3244	EBS1
CBS2499v2 CBS2499_1766	EBS1
AWRlv2 AWRI_1454	EBS1
LAMAP LAMAP2480_3271	membrane protein YGR026W
CBS2499v2 CBS2499_2052	membrane protein YGR026W
AWRlv2 AWRI_0952	membrane protein YGR026W
LAMAP LAMAP2480_3273	SUMO-protein ligase RanBP2
CBS2499v2 CBS2499_2054	SUMO-protein ligase RanBP2
AWRlv2 AWRI_0950	NUP2

LAMAP LAMAP2480_3290	protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YDL144C is not an essential gene.
CBS2499v2 CBS2499_2075	of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YDL144C is not an essential gene; protein abundance increases in response to DNA replication stress
AWRlv2 AWRI_0929	of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; YDL144C is not an essential gene; protein abundance increases in response to DNA replication stress
LAMAP LAMAP2480_3299	intermediate peptidase, cleaves destabilizing N-terminal residues of a subset of proteins upon import, after their cleavage by mitochondrial processing peptidase (Mas1p-Mas2p); may contribute to mitochondrial iron homeostasis
CBS2499v2 CBS2499_2085	intermediate peptidase; cleaves destabilizing N-terminal residues of a subset of proteins upon import, after their cleavage by mitochondrial processing peptidase (Mas1p-Mas2p); may contribute to mitochondrial iron homeostasis
AWRlv2 AWRI_0921	intermediate peptidase; cleaves destabilizing N-terminal residues of a subset of proteins upon import, after their cleavage by mitochondrial processing peptidase (Mas1p-Mas2p); may contribute to mitochondrial iron homeostasis
LAMAP LAMAP2480_3305	family/GOLD
CBS2499v2 CBS2499_2091	family/GOLD
AWRlv2 AWRI_0917	family/GOLD
LAMAP LAMAP2480_3312	biosynthesis protein CHS5
CBS2499v2 CBS2499_2097	biosynthesis protein CHS5
AWRlv2 AWRI_0911	biosynthesis protein CHS5
LAMAP LAMAP2480_3314	protein 1
CBS2499v2 CBS2499_2100	protein 1
AWRlv2 AWRI_0908	protein C21B10.03c
LAMAP LAMAP2480_3316	protein _1101
CBS2499v2 CBS2499_2101	protein
AWRlv2 AWRI_0907	protein _1101
LAMAP LAMAP2480_3323	RNA polymerase, mitochondrial
CBS2499v2 CBS2499_2106	RNA polymerase, mitochondrial
AWRlv2 AWRI_0903	RNA polymerase; single subunit enzyme similar to those of T3 and T7 bacteriophages; requires a specificity subunit encoded by MTF1 for promoter recognition; Mtf1p interacts with and stabilizes the Rpo41p-promoter complex, enhancing DNA bending and melting to facilitate pre-initiation open complex formation
LAMAP LAMAP2480_3333	protein HPODL_01719
CBS2499v2 CBS2499_2114	protein HPODL_01719
AWRlv2 AWRI_0892	threonine protein kinase
LAMAP LAMAP2480_3339	finger protein REH1
CBS2499v2 CBS2499_2121	60S subunit biogenesis factor REH1
AWRlv2 AWRI_0884	60S subunit biogenesis factor REH1
LAMAP LAMAP2480_3340	of the GINS complex (Sld5p, Psf1p, Psf2p, Psf3p), which is localized to DNA replication origins and implicated in assembly of the DNA replication machinery

CBS2499v2|CBS2499_2122
AWRIv2|AWRI_0883
LAMAP|LAMAP2480_3343
CBS2499v2|CBS2499_2125
AWRIv2|AWRI_0881
LAMAP|LAMAP2480_3344
CBS2499v2|CBS2499_2126
AWRIv2|AWRI_0880
LAMAP|LAMAP2480_3350
CBS2499v2|CBS2499_2133
AWRIv2|AWRI_0874
LAMAP|LAMAP2480_3357
CBS2499v2|CBS2499_1934
AWRIv2|AWRI_1627
LAMAP|LAMAP2480_3390
CBS2499v2|CBS2499_1967
AWRIv2|AWRI_1603
LAMAP|LAMAP2480_3391
CBS2499v2|CBS2499_1968
AWRIv2|AWRI_1602
LAMAP|LAMAP2480_3401
CBS2499v2|CBS2499_1977
AWRIv2|AWRI_1592
LAMAP|LAMAP2480_3403
CBS2499v2|CBS2499_1979
AWRIv2|AWRI_1589
LAMAP|LAMAP2480_3411
CBS2499v2|CBS2499_1987
AWRIv2|AWRI_1584
LAMAP|LAMAP2480_3412
CBS2499v2|CBS2499_1988
AWRIv2|AWRI_1583
LAMAP|LAMAP2480_3413
CBS2499v2|CBS2499_1989
AWRIv2|AWRI_1582
LAMAP|LAMAP2480_3414
CBS2499v2|CBS2499_1990
AWRIv2|AWRI_1581
LAMAP|LAMAP2480_3417
CBS2499v2|CBS2499_1996
AWRIv2|AWRI_1575

LAMAP|LAMAP2480_3420

of the GINS complex (Sld5p, Psf1p, Psf2p, Psf3p); complex is localized to DNA replication origins and implicated in assembly of the DNA replication machinery
formyltransferase
protein _1070
protein _1070
protein _1070
factor subunit NURF301-like
factor subunit NURF301-like
adjacent to zinc finger domain protein 2B
nicotinic acid transporter
nicotinic acid transporter
transporter C1002.16c
transporter AQR1
transporter AQR1
transporter AQR1
domain-containing protein 5
domain-containing protein 5
domain-containing protein 5
protein _1886
protein _1886
protein _1886
protein sorting-associated protein 3
protein sorting-associated protein 3
protein sorting-associated protein 3
LTV1
LTV1
LTV1
factor 3
protein RMD8
factor 3
polymerase-associated protein C651.09c
polymerase-associated protein C651.09c
polymerase-associated protein C651.09c
subunit beta-5
subunit beta-5
subunit beta-5
negative regulator of transcription subunit 4
negative regulator of transcription subunit 4
negative regulator of transcription subunit 4
enzyme subunit 1
enzyme subunit 1
enzyme subunit 1
subunit of the coatomer complex (COPI), which coats Golgi-derived transport vesicles; involved in retrograde transport between Golgi and ER

CBS2499v2 CBS2499_1999 AWRIv2 AWRI_1572	subunit of the coatomer complex (COPI); COPI coats Golgi-derived transport vesicles; involved in retrograde transport between Golgi and ER subunit delta
LAMAP LAMAP2480_3432	subunit of the heteromeric nascent polypeptide-associated complex (NAC) involved in protein sorting and translocation, associated with cytoplasmic ribosomes
CBS2499v2 CBS2499_0220	subunit of the nascent polypeptide-associated complex (NAC); involved in protein sorting and translocation; associated with cytoplasmic ribosomes
AWRIv2 AWRI_2243 LAMAP LAMAP2480_3433 CBS2499v2 CBS2499_0219 AWRIv2 AWRI_2242	subunit of the nascent polypeptide-associated complex (NAC); involved in protein sorting and translocation; associated with cytoplasmic ribosomes membrane protein YHR192W transmembrane protein transmembrane protein
LAMAP LAMAP2480_3440	with a potential role in cell survival pathways, required for the diauxic growth shift; expression in mammalian cells increases survival under conditions inducing apoptosis; mutant has increased aneuploidy tolerance
CBS2499v2 CBS2499_0211	with a potential role in cell survival pathways; required for the diauxic growth shift; expression in mammalian cells increases survival under conditions inducing apoptosis; mutant has increased aneuploidy tolerance
AWRIv2 AWRI_2237 LAMAP LAMAP2480_3489 CBS2499v2 CBS2499_3331 AWRIv2 AWRI_0181 LAMAP LAMAP2480_3510 CBS2499v2 CBS2499_3523 AWRIv2 AWRI_3335	with a potential role in cell survival pathways; required for the diauxic growth shift; expression in mammalian cells increases survival under conditions inducing apoptosis; mutant has increased aneuploidy tolerance cyclin CLN1 cyclin CCN1 cyclin CCN1 factor tau subunit sfc1 factor tau subunit sfc1 factor tau 95 kDa subunit
LAMAP LAMAP2480_3514	subunit of the capping protein (CP) heterodimer (Cap1p and Cap2p) which binds to the barbed ends of actin filaments preventing further polymerization; localized predominantly to cortical actin patches
CBS2499v2 CBS2499_3519	subunit of the capping protein heterodimer (Cap1p and Cap2p); capping protein (CP) binds to the barbed ends of actin filaments preventing further polymerization; localized predominantly to cortical actin patches; protein increases in abundance and relocalizes from bud neck to plasma membrane upon DNA replication stress
AWRIv2 AWRI_3330 LAMAP LAMAP2480_3517 CBS2499v2 CBS2499_3516 AWRIv2 AWRI_3328 LAMAP LAMAP2480_3519 CBS2499v2 CBS2499_3514 AWRIv2 AWRI_3326	subunit of the capping protein heterodimer (Cap1p and Cap2p); capping protein (CP) binds to the barbed ends of actin filaments preventing further polymerization; localized predominantly to cortical actin patches; protein increases in abundance and relocalizes from bud neck to plasma membrane upon DNA replication stress translation elongation factor translation elongation factor elongation factor Tu protein sorting-associated protein vps5 nexin-2 protein sorting-associated protein 5

LAMAP LAMAP2480_3522	acetyltransferase B complex subunit MDM20
CBS2499v2 CBS2499_3512	acetyltransferase B complex subunit MDM20
AWRIv2 AWRI_3324	inheritance and actin cytoskeleton organization protein
LAMAP LAMAP2480_3542	proteinase yapsin-7
CBS2499v2 CBS2499_3494	proteinase yapsin-7
AWRIv2 AWRI_3529	proteinase yapsin-7
LAMAP LAMAP2480_3545	protein 1
CBS2499v2 CBS2499_3491	
AWRIv2 AWRI_3525	
LAMAP LAMAP2480_3603	membrane H⁺-pantothenate symporter; confers sensitivity to the antifungal agent fenpropimorph
CBS2499v2 CBS2499_4923	membrane H ⁺ -pantothenate symporter; confers sensitivity to the antifungal agent fenpropimorph; relocalizes from vacuole to cytoplasm upon DNA replication stress
AWRIv2 AWRI_3099	membrane H ⁺ -pantothenate symporter; confers sensitivity to the antifungal agent fenpropimorph; relocalizes from vacuole to cytoplasm upon DNA replication stress
LAMAP LAMAP2480_3622	cytoplasmic protein that serves as a scaffold for binding Get4/5p and other proteins required to mediate posttranslational insertion of tail-anchored proteins into the ER membrane; has similarity to human cochaperone SGT
CBS2499v2 CBS2499_4952	cytoplasmic cochaperone; serves as a scaffold bringing together Get4, Get5p, and other TRC complex members that are required to mediate posttranslational insertion of tail-anchored proteins into the ER membrane; interacts with the prion domain of Sup35p; amyloid sensor; plays a role in targeting chaperones to prion aggregates; has similarity to human cochaperone SGT; forms cytoplasmic foci upon DNA replication stress
AWRIv2 AWRI_3084	cytoplasmic cochaperone; serves as a scaffold bringing together Get4, Get5p, and other TRC complex members that are required to mediate posttranslational insertion of tail-anchored proteins into the ER membrane; interacts with the prion domain of Sup35p; amyloid sensor; plays a role in targeting chaperones to prion aggregates; has similarity to human cochaperone SGT; forms cytoplasmic foci upon DNA replication stress
LAMAP LAMAP2480_3625	helicase proposed to promote replication fork regression during postreplication repair by template switching; RING finger containing ubiquitin ligase; stimulates the synthesis of free and PCNA-bound polyubiquitin chains by Ubc13p-Mms2p
CBS2499v2 CBS2499_0025	helicase/Ubiquitin ligase; involved in error-free branch of DNA damage tolerance (DDT) pathway; proposed to promote replication fork regression during postreplication repair by template switching; stimulates synthesis of free and PCNA-bound polyubiquitin chains by Ubc13p-Mms2p; required for error-prone translesion synthesis; forms nuclear foci upon DNA replication stress; associates with native telomeres, cooperates with homologous recombination in senescent cells
AWRIv2 AWRI_0796	repair protein RAD5
LAMAP LAMAP2480_3655	protein HRT3
CBS2499v2 CBS2499_0055	protein HRT3
AWRIv2 AWRI_0824	protein JL09_g3662
LAMAP LAMAP2480_3684	protein _1033
CBS2499v2 CBS2499_0082	protein _1033
AWRIv2 AWRI_0848	protein _1033

LAMAP LAMAP2480_3693	integral inner membrane protein required for membrane insertion of C-terminus of Cox2p; interacts genetically and physically with Mss2p and Pnt1p; similar to <i>S. cerevisiae</i> Oxa1, <i>N. crassa</i> Oxa2p, and <i>E. coli</i> YidC
CBS2499v2 CBS2499_0928	required for membrane insertion of C-terminus of Cox2p; mitochondrial integral inner membrane protein; interacts genetically and physically with Mss2p and Pnt1p; similar to <i>S. cerevisiae</i> Oxa1, <i>N. crassa</i> Oxa2p, and <i>E. coli</i> YidC
AWRiv2 AWRI_2498	required for membrane insertion of C-terminus of Cox2p; mitochondrial integral inner membrane protein; interacts genetically and physically with Mss2p and Pnt1p; similar to <i>S. cerevisiae</i> Oxa1, <i>N. crassa</i> Oxa2p, and <i>E. coli</i> YidC
LAMAP LAMAP2480_3700	protein
CBS2499v2 CBS2499_0921	protein JL09_g666
AWRiv2 AWRI_2504	protein JL09_g666
LAMAP LAMAP2480_3702	protease 2
CBS2499v2 CBS2499_0918	protease 2
AWRiv2 AWRI_2507	protease 2
LAMAP LAMAP2480_3705	aldehyde-forming enzyme
CBS2499v2 CBS2499_0915	lipoprotein A (RlpA)-like double-psi beta-barrel
AWRiv2 AWRI_2510	lipoprotein A (RlpA)-like double-psi beta-barrel
LAMAP LAMAP2480_3708	protein
CBS2499v2 CBS2499_0912	protein
AWRiv2 AWRI_2512	protein
LAMAP LAMAP2480_3717	oxidase
CBS2499v2 CBS2499_0904	oxidase
AWRiv2 AWRI_2518	oxidase
LAMAP LAMAP2480_3724	recognition complex subunit 1
CBS2499v2 CBS2499_0897	recognition complex subunit 1
AWRiv2 AWRI_2523	recognition complex subunit 1
LAMAP LAMAP2480_3730	peptidase complex subunit SPC2
CBS2499v2 CBS2499_0889	peptidase complex subunit SPC2
AWRiv2 AWRI_2531	peptidase complex subunit SPC2
LAMAP LAMAP2480_3734	protein _3045
CBS2499v2 CBS2499_0885	protein _3045
AWRiv2 AWRI_2534	protein _3045
LAMAP LAMAP2480_3738	RNA-processing protein 1
CBS2499v2 CBS2499_0881	RNA-processing protein 1
AWRiv2 AWRI_2538	RNA processing protein 1 homolog B
LAMAP LAMAP2480_3751	factor 39
CBS2499v2 CBS2499_0867	factor 39
AWRiv2 AWRI_0004	factor 39
LAMAP LAMAP2480_3755	protein _0009
CBS2499v2 CBS2499_0862	protein _0009
AWRiv2 AWRI_0008	protein _0009

LAMAP|LAMAP2480_3757

CBS2499v2|CBS2499_0860
AWRIv2|AWRI_0009
LAMAP|LAMAP2480_3766
CBS2499v2|CBS2499_2609
AWRIv2|AWRI_3949
LAMAP|LAMAP2480_3800
CBS2499v2|CBS2499_2574
AWRIv2|AWRI_0584
LAMAP|LAMAP2480_3803
CBS2499v2|CBS2499_2571
AWRIv2|AWRI_0580
LAMAP|LAMAP2480_3824
CBS2499v2|CBS2499_1717
AWRIv2|AWRI_1418
LAMAP|LAMAP2480_3864
CBS2499v2|CBS2499_1749
AWRIv2|AWRI_1445
LAMAP|LAMAP2480_3869
CBS2499v2|CBS2499_1754
AWRIv2|AWRI_1449

LAMAP|LAMAP2480_3875
CBS2499v2|CBS2499_1761
AWRIv2|AWRI_1452
LAMAP|LAMAP2480_3886
CBS2499v2|CBS2499_1772
AWRIv2|AWRI_1459
LAMAP|LAMAP2480_3903
CBS2499v2|CBS2499_1790
AWRIv2|AWRI_1472
LAMAP|LAMAP2480_3938
CBS2499v2|CBS2499_2174
AWRIv2|AWRI_2875

LAMAP|LAMAP2480_3944

of the multi-drug and toxin extrusion (MATE) family of the multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) exporter superfamily; overproduction confers ethionine resistance and accumulation of S-adenosylmethionine

of the multi-drug and toxin extrusion (MATE) family; the MATE family is part of the multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) exporter superfamily; overproduction confers ethionine resistance and accumulation of S-adenosylmethionine

efflux family protein

HYM1

HYM1

HYM1

RNA polymerase I subunit RPA43

RNA polymerase I subunit RPA43

RNA polymerase I subunit RPA43

factor IWS1

factor IWS1

factor IWS1

induction protein kinase IME2/SME1

induction protein kinase IME2/SME1

induction protein kinase IME2/SME1

glucosyltransferase

glucosyltransferase

glucosyltransferase

protein 1

protein 1

protein 1

ligase, involved in the modification of mitochondrial enzymes by the attachment of lipoic acid groups

transferase

transferase

protein _1734

protein _1734

protein _1734

protein _1749

protein _1749

protein _1749

family protein

family protein

family protein

conserved mitochondrial protein, essential for t6A modification of mitochondrial tRNAs that decode ANN codons; similar to Kae1p and E. coli YgiD, both of which are also required for tRNA t6A modification

CBS2499v2 CBS2499_2168	involved in threonylcarbamoyl adenosine biosynthesis; Sua5p and Qri7p are necessary and sufficient for RNA t6A modification in vitro; highly conserved mitochondrial protein; essential for t6A modification of mitochondrial tRNAs that decode ANN codons; similar to Kae1p and E. coli YgjD, both of which are also required for tRNA t6A modification; when directed to the cytoplasm, complements the essential function of Kae1p in the KEOPS complex
AWRiv2 AWRI_2881	involved in threonylcarbamoyl adenosine biosynthesis; Sua5p and Qri7p are necessary and sufficient for RNA t6A modification in vitro; highly conserved mitochondrial protein; essential for t6A modification of mitochondrial tRNAs that decode ANN codons; similar to Kae1p and E. coli YgjD, both of which are also required for tRNA t6A modification; when directed to the cytoplasm, complements the essential function of Kae1p in the KEOPS complex
LAMAP LAMAP2480_3945	protein _3466
CBS2499v2 CBS2499_2167	protein _3466
AWRiv2 AWRI_2882	protein _3466
LAMAP LAMAP2480_3955	domain-containing protein CBSCBSPB3
CBS2499v2 CBS2499_2158	domain-containing protein CBSCBSPB3
AWRiv2 AWRI_2891	domain-containing protein CBSCBSPB3
LAMAP LAMAP2480_3972	factor atf1
CBS2499v2 CBS2499_1538	factor atf1
AWRiv2 AWRI_2671	osmotic stress response (OSM) domain
LAMAP LAMAP2480_3977	RNA-processing protein 7
CBS2499v2 CBS2499_1533	RNA-processing protein 7
AWRiv2 AWRI_2675	RNA-processing protein 7
LAMAP LAMAP2480_3978	STE50
CBS2499v2 CBS2499_1532	STE50
AWRiv2 AWRI_2676	STE50
LAMAP LAMAP2480_3981	synthase, catalyzes pseudouridylation at positions 35 and 56 in U2 snRNA, position 50 in 5S rRNA, position 13 in cytoplasmic tRNAs, and position 35 in pre-tRNA(Tyr); conserved in archaea, vertebrates, and some bacteria
CBS2499v2 CBS2499_1529	pseudouridine synthase, TruD family
AWRiv2 AWRI_3944	synthase; catalyzes pseudouridylation at positions 35 and 56 in U2 snRNA, position 50 in 5S rRNA, position 13 in cytoplasmic tRNAs, and position 35 in pre-tRNA(Tyr); also pseudouridylates some mRNAs; relocates from nucleus to cytoplasm during heat shock and differentially modifies some mRNAs during heat shock; conserved in archaea, vertebrates, and some bacteria
LAMAP LAMAP2480_3985	of evolutionarily-conserved CCR4-NOT regulatory complex; contains single ABC-type ATPase domain but no transmembrane domain; interacts with several subunits of Mediator
CBS2499v2 CBS2499_1523	ABC transporter ATP-binding protein C20G4.01
AWRiv2 AWRI_3939	of evolutionarily-conserved CCR4-NOT regulatory complex; contains single ABC-type ATPase domain but no transmembrane domain; interacts with several subunits of Mediator
LAMAP LAMAP2480_4034	oxidoreductase 2
CBS2499v2 CBS2499_0526	oxidoreductase 2
AWRiv2 AWRI_2390	protein
LAMAP LAMAP2480_4036	protein, cytoplasmic and nuclear
CBS2499v2 CBS2499_0524	binding domain-containing protein
AWRiv2 AWRI_2391	binding domain-containing protein

LAMAP LAMAP2480_4038	protein YEL043W
CBS2499v2 CBS2499_0522	protein YEL043W
AWRIv2 AWRI_2393	protein
LAMAP LAMAP2480_4043	protein _4611
CBS2499v2 CBS2499_0518	protein _4611
AWRIv2 AWRI_3865	protein _4611
LAMAP LAMAP2480_4044	protein
CBS2499v2 CBS2499_0517	protein
AWRIv2 AWRI_3864	protein
	subunit of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); interacts with the Translocase of the Outer Mitochondrial membrane (TOM complex) and with respiratory enzymes; may regulate TIM23 complex activity
LAMAP LAMAP2480_4076	import inner membrane translocase subunit TIM21
CBS2499v2 CBS2499_2862	import inner membrane translocase subunit TIM21
AWRIv2 AWRI_2931	nucleotide exchange factor LTE1
LAMAP LAMAP2480_4079	nucleotide exchange factor LTE1
CBS2499v2 CBS2499_2865	nucleotide exchange factor LTE1
AWRIv2 AWRI_2933	nucleotide exchange factor LTE1
LAMAP LAMAP2480_4081	protein _3520
CBS2499v2 CBS2499_2866	protein _3520
AWRIv2 AWRI_2934	protein _3520
	membrane receptor protein (v-SNARE) involved in the fusion between Golgi-derived secretory vesicles with the plasma membrane; proposed to be involved in endocytosis; member of the synaptobrevin/VAMP family of R-type v-SNARE proteins
LAMAP LAMAP2480_4084	
	membrane receptor protein (v-SNARE); involved in the fusion between Golgi-derived secretory vesicles with the plasma membrane; proposed to be involved in endocytosis; member of the synaptobrevin/VAMP family of R-type v-SNARE proteins; SNC1 has a paralog, SNC2, that arose from the whole genome duplication
CBS2499v2 CBS2499_2868	
	membrane receptor protein (v-SNARE); involved in the fusion between Golgi-derived secretory vesicles with the plasma membrane; proposed to be involved in endocytosis; member of the synaptobrevin/VAMP family of R-type v-SNARE proteins; SNC1 has a paralog, SNC2, that arose from the whole genome duplication
AWRIv2 AWRI_2936	secreted protein
LAMAP LAMAP2480_4090	nucleoside permease
CBS2499v2 CBS2499_2873	nucleoside permease
AWRIv2 AWRI_2942	a carrier protein involved in nuclear import of proteins; importin beta homolog
LAMAP LAMAP2480_4097	mRNA decay protein 5
CBS2499v2 CBS2499_2877	mRNA decay protein 5
AWRIv2 AWRI_2946	protein _3543
LAMAP LAMAP2480_4109	protein _3543
CBS2499v2 CBS2499_2888	protein _3543
AWRIv2 AWRI_2957	transferase type-2 subunit alpha
LAMAP LAMAP2480_4115	transferase type-2 subunit alpha
CBS2499v2 CBS2499_2899	transferase type-2 subunit alpha
AWRIv2 AWRI_2972	kinase subunit beta
LAMAP LAMAP2480_4116	

CBS2499v2 CBS2499_2900	kinase subunit beta	
AWRiv2 AWRI_2973	protein HPODL_02414	
LAMAP LAMAP2480_4119	specific transcription factor domain	
CBS2499v2 CBS2499_2908	specific transcription factor domain	
AWRiv2 AWRI_2981	specific transcription factor domain	
LAMAP LAMAP2480_4121	debranching enzyme	
CBS2499v2 CBS2499_2911	debranching enzyme	
	lariat debranching enzyme; catalyzes debranching of lariat introns formed during pre-mRNA splicing; required for efficient Ty1 transposition; knockdown of human homolog Dbr1 rescues toxicity of RNA-binding proteins TDP-43 and FUS which are implicated in amyotrophic lateral sclerosis (ALS), suggests potential therapeutic target for ALS and related TDP-43 proteinopathies	
AWRiv2 AWRI_2985		
LAMAP LAMAP2480_4125		3
CBS2499v2 CBS2499_2920		3
AWRiv2 AWRI_2996		3
LAMAP LAMAP2480_4140	repeat-containing protein SOG2	
CBS2499v2 CBS2499_2939	repeat-containing protein SOG2	
AWRiv2 AWRI_3013	repeat-containing protein SOG2	
LAMAP LAMAP2480_4167	-mannosyltransferase	
CBS2499v2 CBS2499_1082		3
AWRiv2 AWRI_0614		4
LAMAP LAMAP2480_4205	ribosomal protein L15, mitochondrial	
CBS2499v2 CBS2499_0093	ribosomal protein L15, mitochondrial	
AWRiv2 AWRI_0860	ribosomal protein L15, mitochondrial	
LAMAP LAMAP2480_4268	midA homolog	
CBS2499v2 CBS2499_1651	dehydrogenase [ubiquinone] complex I, assembly factor 7 homolog	
AWRiv2 AWRI_2163	dehydrogenase [ubiquinone] complex I, assembly factor 7 homolog	
LAMAP LAMAP2480_4272	protein YCR015C	
CBS2499v2 CBS2499_1642	protein YCR015C	
AWRiv2 AWRI_2156	hydrolase	
LAMAP LAMAP2480_4277	3-methyltransferase	
CBS2499v2 CBS2499_1635	3-methyltransferase	
AWRiv2 AWRI_2151	3-methyltransferase	
LAMAP LAMAP2480_4295	alpha-keto amide reductase; reduces aromatic alpha-keto amides, aliphatic alpha-keto esters, and aromatic alpha-keto esters; member of the aldo-keto reductase (AKR) family	
CBS2499v2 CBS2499_1608	alpha-keto amide reductase; reduces aromatic alpha-keto amides, aliphatic alpha-keto esters, and aromatic alpha-keto esters; member of the aldo-keto reductase (AKR) family; protein abundance increases in response to DNA replication stress	
AWRiv2 AWRI_2131	alpha-keto amide reductase; reduces aromatic alpha-keto amides, aliphatic alpha-keto esters, and aromatic alpha-keto esters; member of the aldo-keto reductase (AKR) family; protein abundance increases in response to DNA replication stress	
LAMAP LAMAP2480_4312	enzyme is ATP-dependent and functions as a dimer; similar to mouse Oplah gene; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm	

CBS2499v2|CBS2499_2190

AWRlv2|AWRI_3622
LAMAP|LAMAP2480_4314
CBS2499v2|CBS2499_2192
AWRlv2|AWRI_3623
LAMAP|LAMAP2480_4316
CBS2499v2|CBS2499_2194
AWRlv2|AWRI_3625
LAMAP|LAMAP2480_4331
CBS2499v2|CBS2499_3212
AWRlv2|AWRI_1930
LAMAP|LAMAP2480_4336
CBS2499v2|CBS2499_3207
AWRlv2|AWRI_1926
LAMAP|LAMAP2480_4338
CBS2499v2|CBS2499_3205
AWRlv2|AWRI_1925
LAMAP|LAMAP2480_4339
CBS2499v2|CBS2499_3204
AWRlv2|AWRI_1924
LAMAP|LAMAP2480_4365
CBS2499v2|CBS2499_3182
AWRlv2|AWRI_1900
LAMAP|LAMAP2480_4372
CBS2499v2|CBS2499_3175
AWRlv2|AWRI_1894
LAMAP|LAMAP2480_4383
CBS2499v2|CBS2499_4391
AWRlv2|AWRI_4167
LAMAP|LAMAP2480_4400
CBS2499v2|CBS2499_4376
AWRlv2|AWRI_4074
LAMAP|LAMAP2480_4412
CBS2499v2|CBS2499_3700
AWRlv2|AWRI_1186
LAMAP|LAMAP2480_4423
CBS2499v2|CBS2499_3708
AWRlv2|AWRI_1177
LAMAP|LAMAP2480_4535
CBS2499v2|CBS2499_4528

enzyme is ATP-dependent and functions as a dimer; similar to mouse Oplah gene; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; protein abundance increases in response to DNA replication stress

enzyme is ATP-dependent and functions as a dimer; similar to mouse Oplah gene; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; protein abundance increases in response to DNA replication stress

activator HAP3

activator HAP3

activator HAP3

inheritance rate of mitochondria protein 38

supercomplex factor 2, mitochondrial

supercomplex factor 2, mitochondrial

protein _2303

protein _2303

protein _2303

shock factor protein

shock transcription factor

shock transcription factor

transporter MCH2

transporter ESBP6

transporter ESBP6

transporter ESBP6

transporter ESBP6

transporter ESBP6

site selection protein 22

site selection protein 22

site selection protein

ribosome biogenesis protein C8F11.04

ribosome biogenesis protein C8F11.04

ribosome biogenesis protein C8F11.04

protein TCA17

protein TCA17

membrane protein yol092w

ribosomal protein S24, mitochondrial

ribosomal protein S24, mitochondrial

ribosomal protein S24, mitochondrial

complex exonuclease RRP6

complex exonuclease RRP6

complex exonuclease RRP6

transcriptional regulator ZAP1

transcriptional regulator ZAP1

finger protein csr1p

complex component snt2

complex component snt2

AWRIv2 AWRI_1044	complex component snt2
LAMAP LAMAP2480_4545	protein C3orf37 homolog
CBS2499v2 CBS2499_4538	peptidase YMR114C
AWRIv2 AWRI_1053	peptidase YMR114C
	DNA helicase involved in sister-chromatid cohesion and genome integrity; interacts with ECO1 and CTF18; mutants are defective in silencing, rDNA recombination, aging and the heat shock response; FANCI-like helicase family member
LAMAP LAMAP2480_4558	
	DNA helicase; involved in sister-chromatid cohesion and genome integrity and interstrand cross-link repair; interacts with ECO1 and CTF18; mutants are defective in silencing, rDNA recombination, aging and the heat shock response; FANCI-like helicase family member; mutations in the human homolog, DDX11/ChLR1, cause Warsaw breakage syndrome
CBS2499v2 CBS2499_4402	
	DNA helicase; involved in sister-chromatid cohesion and genome integrity and interstrand cross-link repair; interacts with ECO1 and CTF18; mutants are defective in silencing, rDNA recombination, aging and the heat shock response; FANCI-like helicase family member; mutations in the human homolog, DDX11/ChLR1, cause Warsaw breakage syndrome
AWRIv2 AWRI_2081	transporter YBR287W
LAMAP LAMAP2480_4565	transporter YBR287W
CBS2499v2 CBS2499_4410	transporter YBR287W
AWRIv2 AWRI_2084	transporter YBR287W
LAMAP LAMAP2480_4579	cofactor synthesis domain
CBS2499v2 CBS2499_4424	cofactor synthesis domain
AWRIv2 AWRI_2097	cofactor synthesis domain
LAMAP LAMAP2480_4583	SNQ2
CBS2499v2 CBS2499_4428	SNQ2
AWRIv2 AWRI_2103	SNQ2
LAMAP LAMAP2480_4592	ribosomal protein S22, mitochondrial
CBS2499v2 CBS2499_4437	ribosomal protein S22, mitochondrial
AWRIv2 AWRI_2111	ribosomal protein S22, mitochondrial
LAMAP LAMAP2480_4611	interactive domain-containing protein 4B
CBS2499v2 CBS2499_0392	interactive domain-containing protein 4B
AWRIv2 AWRI_3718	chromatin-remodeling complex subunit SWI1
LAMAP LAMAP2480_4613	with methylenetetrahydrofolate reductase (MTHFR) activity in vitro; null mutant has no phenotype and is prototrophic for methionine; MET13 encodes major isozyme of MTHFR
CBS2499v2 CBS2499_0394	with MTHFR activity in vitro; null mutant has no phenotype and is prototrophic for methionine; MET13 encodes major isozyme of methylenetetrahydrofolate reductase (MTHFR)
AWRIv2 AWRI_3715	with MTHFR activity in vitro; null mutant has no phenotype and is prototrophic for methionine; MET13 encodes major isozyme of methylenetetrahydrofolate reductase (MTHFR)
LAMAP LAMAP2480_4615	cytoskeleton-regulatory complex protein END3
CBS2499v2 CBS2499_0395	cytoskeleton-regulatory complex protein END3
AWRIv2 AWRI_3714	cytoskeleton-regulatory complex protein END3
LAMAP LAMAP2480_4617	repair/transcription protein mms19
CBS2499v2 CBS2499_0397	repair/transcription protein mms19
AWRIv2 AWRI_3712	repair/transcription protein MET18/MMS19

LAMAP LAMAP2480_4624	protein of unknown function with strong similarity to alanyl-tRNA synthases from Eubacteria; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YNL040W is not an essential gene
CBS2499v2 CBS2499_0402 AWRIv2 AWRI_3707 LAMAP LAMAP2480_4626 CBS2499v2 CBS2499_0404 AWRIv2 AWRI_3704	protein of unknown function; has strong similarity to alanyl-tRNA synthases from Eubacteria; null mutant displays decreased translation rate and increased readthrough of premature stop codons; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YNL040W is not an essential gene alanyl-tRNA editing protein alaX protein YDR333C quality control complex subunit 1 quality control complex subunit 1
LAMAP LAMAP2480_4639	protein containing three calcium and lipid binding domains; non-tagged protein localizes to mitochondria and GFP-fusion protein localizes to the cell periphery; C-termini of Tcb1p, Tcb2p and Tcb3p interact ER protein involved in ER-plasma membrane tethering; one of 6 proteins (Ist2p, Scs2p, Scs22p, Tcb1p, Tcb2p, Tcb3p) that connect ER to plasma membrane and regulate PI4P levels by controlling access of Sac1p phosphatase to its substrate PI4P in PM; contains 3 calcium and lipid binding domains; non-tagged protein also localizes to mitochondria; C-termini of Tcb1p, Tcb2p and Tcb3p interact; TCB1 has a paralog, TCB2, that arose from the whole genome duplication
CBS2499v2 CBS2499_0416 AWRIv2 AWRI_4036 LAMAP LAMAP2480_4644 CBS2499v2 CBS2499_0422 AWRIv2 AWRI_4039 LAMAP LAMAP2480_4681 CBS2499v2 CBS2499_0298 AWRIv2 AWRI_1986 LAMAP LAMAP2480_4696 CBS2499v2 CBS2499_3885 AWRIv2 AWRI_1877	complex component SEC10 complex component SEC10 complex component SEC10 complex subunit DAD2 complex subunit DAD2 complex subunit DAD2 protein _2245 protein _2245 protein _2245
LAMAP LAMAP2480_4720	synthase, introduces pseudouridines at position 38 or 39 in tRNA, important for maintenance of translation efficiency and normal cell growth, localizes to both the nucleus and cytoplasm; non-essential for viability
CBS2499v2 CBS2499_5027	synthase; introduces pseudouridines at position 38 or 39 in tRNA; also responsible for pseudouracil modification of some mRNAs; important for maintenance of translation efficiency and normal cell growth, localizes to both the nucleus and cytoplasm; non-essential for viability
AWRIv2 AWRI_4141 LAMAP LAMAP2480_4734 CBS2499v2 CBS2499_4818 AWRIv2 AWRI_3393 LAMAP LAMAP2480_4746 CBS2499v2 CBS2499_1971 AWRIv2 AWRI_1599	synthase; introduces pseudouridines at position 38 or 39 in tRNA; also responsible for pseudouracil modification of some mRNAs; important for maintenance of translation efficiency and normal cell growth, localizes to both the nucleus and cytoplasm; non-essential for viability exonuclease C637.09 exonuclease C637.09 exonuclease 1 of RNA polymerase II transcription subunit 8 of RNA polymerase II transcription subunit 8 of RNA polymerase II transcription subunit 8

LAMAP LAMAP2480_4753	thioesterase responsible for depalmitoylation of Gpa1p; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and nucleus and is induced in response to the DNA-damaging agent MMS
CBS2499v2 CBS2499_1964	thioesterase responsible for depalmitoylation of Gpa1p; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and nucleus and is induced in response to the DNA-damaging agent MMS
AWRIv2 AWRI_1606 LAMAP LAMAP2480_4777 CBS2499v2 CBS2499_1937 AWRIv2 AWRI_1624	thioesterase responsible for depalmitoylation of Gpa1p; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and nucleus and is induced in response to the DNA-damaging agent MMS of RNA polymerase II transcription subunit 4 of RNA polymerase II transcription subunit 4 of RNA polymerase II transcription subunit 4
LAMAP LAMAP2480_4778	lysophospholipid acyltransferase, part of MBOAT family of membrane-bound O-acyltransferases; key component of Lands cycle; may have role in fatty acid exchange at sn-2 position of mature glycerophospholipids lysophospholipid acyltransferase; part of MBOAT family of membrane-bound O-acyltransferases; key component of Lands cycle; may have role in fatty acid exchange at sn-2 position of mature glycerophospholipids
CBS2499v2 CBS2499_1936 AWRIv2 AWRI_1625 LAMAP LAMAP2480_4792 CBS2499v2 CBS2499_0793 AWRIv2 AWRI_0064 LAMAP LAMAP2480_4794 CBS2499v2 CBS2499_0795 AWRIv2 AWRI_0062	acyltransferase fungal zinc cluster transcription factor fungal zinc cluster transcription factor fungal zinc cluster transcription factor protein _0074 protein _0074 protein _0074
LAMAP LAMAP2480_4795	helicase with limited sequence similarity to human Rb protein; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YLR419W is not an essential gene
CBS2499v2 CBS2499_0702	helicase with limited sequence similarity to human Rb protein; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YLR419W is not an essential gene
AWRIv2 AWRI_0138 LAMAP LAMAP2480_4796 CBS2499v2 CBS2499_0701 AWRIv2 AWRI_0139 LAMAP LAMAP2480_4797 CBS2499v2 CBS2499_0700 AWRIv2 AWRI_0140 LAMAP LAMAP2480_4801 CBS2499v2 CBS2499_0696 AWRIv2 AWRI_0145	helicase with limited sequence similarity to human Rb protein; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; YLR419W is not an essential gene complex subunit 2 complex subunit 2 complex subunit 2 protein 2 protein 2 protein 2 fusion protein MON1 fusion protein MON1 fusion protein MON1

LAMAP LAMAP2480_4804	ser/thr kinase required for vesicle formation in autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; structurally required for phagophore assembly site formation; during autophagy forms a complex with Atg13p and Atg17p
CBS2499v2 CBS2499_0693	kinase ATG1
AWRIv2 AWRI_0147	kinase ATG1
LAMAP LAMAP2480_4806	threonine-protein kinase atg1
CBS2499v2 CBS2499_0691	threonine-protein kinase atg1
AWRIv2 AWRI_0149	threonine-protein kinase atg1
LAMAP LAMAP2480_4810	regulatory protein RXT2
CBS2499v2 CBS2499_0772	regulatory protein RXT2
AWRIv2 AWRI_0085	regulatory protein RXT2
LAMAP LAMAP2480_4816	protein YFR016C
CBS2499v2 CBS2499_0778	protein YFR016C
AWRIv2 AWRI_0078	protein _0091
LAMAP LAMAP2480_4817	universal archaeal KH domain protein
CBS2499v2 CBS2499_0779	universal archaeal KH domain protein
AWRIv2 AWRI_0077	universal archaeal KH domain protein
LAMAP LAMAP2480_4826	protein 20
CBS2499v2 CBS2499_0562	protein 20
AWRIv2 AWRI_2374	protein 20
LAMAP LAMAP2480_4828	
CBS2499v2 CBS2499_0567	
AWRIv2 AWRI_2371	
LAMAP LAMAP2480_4832	oxidoreductase, mitochondrial
CBS2499v2 CBS2499_0572	oxidoreductase, mitochondrial
AWRIv2 AWRI_2368	oxidoreductase, mitochondrial
LAMAP LAMAP2480_4834	import and degradation protein 27
CBS2499v2 CBS2499_0574	import and degradation protein 27
AWRIv2 AWRI_2365	import and degradation protein 27
LAMAP LAMAP2480_4838	and cobalt transport protein CorA
CBS2499v2 CBS2499_0581	and cobalt transport protein CorA
AWRIv2 AWRI_2361	and cobalt transport protein CorA
LAMAP LAMAP2480_4850	kinase GIN4
CBS2499v2 CBS2499_0594	kinase GIN4
AWRIv2 AWRI_3440	kinase GIN4
LAMAP LAMAP2480_4856	of the Ssh1 translocon complex; Sec61p homolog involved in co-translational pathway of protein translocation; not essential
CBS2499v2 CBS2499_0600	of the Ssh1 translocon complex; Sec61p homolog involved in co-translational pathway of protein translocation; not essential
AWRIv2 AWRI_3437	sixty-one protein homolog
LAMAP LAMAP2480_4870	recombination centers protein 22
CBS2499v2 CBS2499_0620	recombination centers protein 22
AWRIv2 AWRI_4171	recombination centers protein 22
LAMAP LAMAP2480_4879	carboxypeptidase yscS; expression is induced under low-nitrogen conditions

CBS2499v2 CBS2499_3620 AWRIv2 AWRI_2689	carboxypeptidase S; expression is induced under low-nitrogen conditions carboxypeptidase S; expression is induced under low-nitrogen conditions
LAMAP LAMAP2480_4882	FAD transporter; required for uptake of FAD into endoplasmic reticulum; involved in cell wall maintenance
CBS2499v2 CBS2499_3619	FAD transporter; required for uptake of FAD into endoplasmic reticulum; involved in cell wall maintenance; FLC1 has a paralog, FLC3, that arose from the whole genome duplication
AWRIv2 AWRI_2690 LAMAP LAMAP2480_4883	FAD transporter; required for uptake of FAD into endoplasmic reticulum; involved in cell wall maintenance; FLC1 has a paralog, FLC3, that arose from the whole genome duplication ERP1
CBS2499v2 CBS2499_3618 AWRIv2 AWRI_2691	of the p24 family involved in ER to Golgi transport; role in misfolded protein quality control; forms heterotrimeric complex with Erp2p, Emp24p, and Erv25p; localized to COPII-coated vesicles; ERP1 has a paralog, ERP6, that arose from the whole genome duplication with similarity to Emp24p and Erv25p; member of the p24 family involved in ER to Golgi transport
LAMAP LAMAP2480_4884	of the COMPASS (Set1C) complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres; WD40 beta propeller superfamily member with similarity to mammalian Rbbp7
CBS2499v2 CBS2499_3617	of the COMPASS (Set1C) complex; COMPASS methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres; WD40 beta propeller superfamily member with similarity to mammalian Rbbp7
AWRIv2 AWRI_2692 LAMAP LAMAP2480_4890 CBS2499v2 CBS2499_3610 AWRIv2 AWRI_2698	of the COMPASS (Set1C) complex; COMPASS methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres; WD40 beta propeller superfamily member with similarity to mammalian Rbbp7 transporter ESBP6 transporter ESBP6 transporter ESBP6
LAMAP LAMAP2480_4898 CBS2499v2 CBS2499_3602	U3 snoRNP protein involved in maturation of pre-18S rRNA, based on computational analysis of large-scale protein-protein interaction data small nucleolar RNA-associated protein 22
AWRIv2 AWRI_2703 LAMAP LAMAP2480_4900 CBS2499v2 CBS2499_3600 AWRIv2 AWRI_2705	of the small-subunit processome; required for nuclear export of tRNAs; may facilitate binding of Utp8p to aminoacylated tRNAs and their delivery to Los1p for export; conserved from yeast to mammals factor cwf19 factor cwf19 factor cwf19
LAMAP LAMAP2480_4902	component of the Translocase of the Inner Mitochondrial membrane (TIM23 complex); tethers the import motor and regulatory factors (PAM complex) to the translocation channel (Tim23p-Tim17p core complex)
CBS2499v2 CBS2499_3598	component of the TIM23 complex; tethers the import motor and regulatory factors (PAM complex) to the translocation channel (Tim23p-Tim17p core complex); TIM23 complex is short for the translocase of the inner mitochondrial membrane
AWRIv2 AWRI_2706 LAMAP LAMAP2480_4904	component of the TIM23 complex; tethers the import motor and regulatory factors (PAM complex) to the translocation channel (Tim23p-Tim17p core complex); TIM23 complex is short for the translocase of the inner mitochondrial membrane domain

CBS2499v2 CBS2499_3596	subunit of a complex (rvs161p-rvs167p)
AWRIv2 AWRI_2709	subunit of a complex (rvs161p-rvs167p)
LAMAP LAMAP2480_4909	kinetochore protein
CBS2499v2 CBS2499_3591	kinetochore protein
AWRIv2 AWRI_2715	kinetochore protein
LAMAP LAMAP2480_4916	protein _4183
CBS2499v2 CBS2499_3390	protein _4183
AWRIv2 AWRI_3484	protein _4183
LAMAP LAMAP2480_4917	of RNA polymerase II transcription subunit 7
CBS2499v2 CBS2499_3388	of RNA polymerase II transcription subunit 7
AWRIv2 AWRI_3482	of RNA polymerase II transcription subunit 7
LAMAP LAMAP2480_4919	conserved protein with a role in maintaining cell wall integrity; contains six TPR (tetratricopeptide repeat) domains clustered in the C-terminal region; conditional mutant is suppressed by overexpression of GFA1
CBS2499v2 CBS2499_3386	conserved protein with a role in cell wall integrity; contains six TPR (tetratricopeptide repeat) domains clustered in the C-terminal region; conditional mutant is suppressed by overexpression of GFA1; protein abundance increases in response to DNA replication stress
AWRIv2 AWRI_3480	conserved protein with a role in cell wall integrity; contains six TPR (tetratricopeptide repeat) domains clustered in the C-terminal region; conditional mutant is suppressed by overexpression of GFA1; protein abundance increases in response to DNA replication stress
LAMAP LAMAP2480_4923	domain-containing protein YPR097W
CBS2499v2 CBS2499_3383	domain-containing protein YPR097W
AWRIv2 AWRI_3477	domain-containing protein YPR097W
LAMAP LAMAP2480_4924	transporter in the major facilitator superfamily (DHA1 family) of multidrug resistance transporters; mutations in membrane-spanning domains permit cation and histidinol uptake
CBS2499v2 CBS2499_3382	transporter in the major facilitator superfamily; member of the 12-spanner drug:H(+) antiporter DHA1 family; mutations in membrane-spanning domains permit cation and histidinol uptake
AWRIv2 AWRI_3999	transporter in the major facilitator superfamily; member of the 12-spanner drug:H(+) antiporter DHA1 family; mutations in membrane-spanning domains permit cation and histidinol uptake
LAMAP LAMAP2480_4927	sulfonate/alpha-ketoglutarate dioxygenase, involved in sulfonate catabolism for use as a sulfur source; contains sequence that resembles a J domain (typified by the E. coli DnaJ protein); induced by sulphur starvation
CBS2499v2 CBS2499_3381	sulfonate/alpha-ketoglutarate dioxygenase; involved in sulfonate catabolism for use as a sulfur source; contains sequence that resembles a J domain (typified by the E. coli DnaJ protein); induced by sulphur starvation
AWRIv2 AWRI_4000	sulfonate/alpha-ketoglutarate dioxygenase; involved in sulfonate catabolism for use as a sulfur source; contains sequence that resembles a J domain (typified by the E. coli DnaJ protein); induced by sulphur starvation
LAMAP LAMAP2480_4929	protein 4
CBS2499v2 CBS2499_3375	protein 4
AWRIv2 AWRI_4006	protein 4
LAMAP LAMAP2480_4938	MLP1
CBS2499v2 CBS2499_3366	MLP1 homolog
AWRIv2 AWRI_4018	MLP1 homolog

LAMAP|LAMAP2480_4945
CBS2499v2|CBS2499_2984
AWRIv2|AWRI_3871

transcription factor
transcription factor
transcription factor

LAMAP|LAMAP2480_4947
CBS2499v2|CBS2499_2982
AWRIv2|AWRI_3873

involved in synthesis of long-chain dolichols (19-22 isoprene units; as opposed to Rer2p which synthesizes shorter-chain dolichols); localizes to lipid bodies; transcription is induced during stationary phase synthase (geranylgeranyl-diphosphate specific)

LAMAP|LAMAP2480_4987
CBS2499v2|CBS2499_1845
AWRIv2|AWRI_2278

translation initiation factor 3 subunit E
translation initiation factor 3 subunit E
translation initiation factor 3 subunit E

LAMAP|LAMAP2480_5005
CBS2499v2|CBS2499_3441
AWRIv2|AWRI_3361

protein _4035
protein _4035
protein HPODL_00351

LAMAP|LAMAP2480_5006
CBS2499v2|CBS2499_3442
AWRIv2|AWRI_3360

protein _4034
protein _4034
protein _4034

LAMAP|LAMAP2480_5011
CBS2499v2|CBS2499_3446
AWRIv2|AWRI_3354

transport protein yif1
transport protein yif1
transport protein yif1

LAMAP|LAMAP2480_5021
CBS2499v2|CBS2499_3455
AWRIv2|AWRI_4020

cyclin-2
cyclin-2
cyclin-1

LAMAP|LAMAP2480_5022

membrane antiporter with Ca²⁺/H⁺ and K⁺/H⁺ exchange activity, involved in control of cytosolic Ca²⁺ and K⁺ concentrations; has similarity to sodium/calcium exchangers, including the bovine Na⁺/Ca²⁺,K⁺ antiporter

CBS2499v2|CBS2499_3461

membrane antiporter with Ca²⁺/H⁺ and K⁺/H⁺ exchange activity; involved in control of cytosolic Ca²⁺ and K⁺ concentrations; has similarity to sodium/calcium exchangers, including the bovine Na⁺/Ca²⁺,K⁺ antiporter

AWRIv2|AWRI_4021
LAMAP|LAMAP2480_5031
CBS2499v2|CBS2499_3472

membrane antiporter with Ca²⁺/H⁺ and K⁺/H⁺ exchange activity; involved in control of cytosolic Ca²⁺ and K⁺ concentrations; has similarity to sodium/calcium exchangers, including the bovine Na⁺/Ca²⁺,K⁺ antiporter

AWRIv2|AWRI_4027
LAMAP|LAMAP2480_5032
CBS2499v2|CBS2499_3473

specific transcription factor domain
resistance regulator 1
resistance regulator 1

AWRIv2|AWRI_4028
LAMAP|LAMAP2480_5050
CBS2499v2|CBS2499_4555

protein HPODL_02518
protein JL09_g3408
protein YKL077W

AWRIv2|AWRI_1064
LAMAP|LAMAP2480_5137
CBS2499v2|CBS2499_0448

recognition particle 72 kDa protein
recognition particle subunit SRP72
recognition particle subunit SRP72

AWRIv2|AWRI_3917

kinase kinase PBS2
kinase kinase PBS2
kinase kinase PBS2

LAMAP LAMAP2480_5139	segregation protein BFR1
CBS2499v2 CBS2499_0450	segregation protein BFR1
AWRiv2 AWRI_3915	segregation protein BFR1
LAMAP LAMAP2480_5143	YIM1-2
CBS2499v2 CBS2499_0454	YIM1-2
AWRiv2 AWRI_3022	YIM1-2
LAMAP LAMAP2480_5144	antiporter 1
CBS2499v2 CBS2499_0455	antiporter 1
AWRiv2 AWRI_3023	antiporter 1
LAMAP LAMAP2480_5150	protein C1709.03
CBS2499v2 CBS2499_0461	endoplasmic reticulum membrane protein C1709.03
AWRiv2 AWRI_3026	endoplasmic reticulum membrane protein C1709.03
LAMAP LAMAP2480_5152	catalyzes the second step of the pentose phosphate pathway; weak multicopy suppressor of los1-1 mutation; homologous to Sol2p and Sol1p
CBS2499v2 CBS2499_0462	catalyzes the second step of the pentose phosphate pathway; weak multicopy suppressor of los1-1 mutation; homologous to Sol2p and Sol1p; SOL3 has a paralog, SOL4, that arose from the whole genome duplication
AWRiv2 AWRI_3027	catalyzes the second step of the pentose phosphate pathway; weak multicopy suppressor of los1-1 mutation; homologous to Sol2p and Sol1p; SOL3 has a paralog, SOL4, that arose from the whole genome duplication
LAMAP LAMAP2480_5162	osmolarity signaling protein SHO1
CBS2499v2 CBS2499_0467	osmolarity signaling protein SHO1
AWRiv2 AWRI_3029	protein _3620
LAMAP LAMAP2480_5191	protein with a possible role in sequestering heavy metals; has similarity to the type V P-type ATPase Spf1p; homolog of human ATP13A2 (PARK9), mutations in which are associated with Parkinson disease and Kufor-Rakeb syndrome
CBS2499v2 CBS2499_3867	protein with a possible role in sequestering heavy metals; has similarity to the type V P-type ATPase Spf1p; homolog of human ATP13A2 (PARK9), mutations in which are associated with Parkinson disease and Kufor-Rakeb syndrome
AWRiv2 AWRI_1859	ATPase of unknown pump specificity (type V)
LAMAP LAMAP2480_5201	up-regulated gene 80 protein
CBS2499v2 CBS2499_1229	cyclin CLG1
AWRiv2 AWRI_1702	up-regulated gene 80 protein
LAMAP LAMAP2480_5205	that converts nicotinamide to nicotinic acid as part of the NAD(+) salvage pathway, required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span
CBS2499v2 CBS2499_1231	that converts nicotinamide to nicotinic acid; part of the NAD(+) salvage pathway; required for life span extension by calorie restriction; PNC1 expression responds to all known stimuli that extend replicative life span; protein increases in abundance and relative distribution to cytoplasmic foci decreases upon DNA replication stress
AWRiv2 AWRI_1701	and diacylglycerol lipase
LAMAP LAMAP2480_5216	lipase YJR107W
CBS2499v2 CBS2499_1240	lipase YJR107W
AWRiv2 AWRI_1699	lipase YJR107W

LAMAP LAMAP2480_5225	subunit of the core complex of translation initiation factor 3 (eIF3), essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes
CBS2499v2 CBS2499_1250	subunit of the eukaryotic translation initiation factor 3 (eIF3); subunit of the core complex of eIF3; essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes
AWRiv2 AWRI_1691	subunit of the eukaryotic translation initiation factor 3 (eIF3); subunit of the core complex of eIF3; essential for translation; part of a subcomplex (Prt1p-Rpg1p-Nip1p) that stimulates binding of mRNA and tRNA(i)Met to ribosomes
LAMAP LAMAP2480_5232	membrane protein
CBS2499v2 CBS2499_4661	membrane protein
AWRiv2 AWRI_1721	membrane protein
LAMAP LAMAP2480_5239	kinase dsk1
CBS2499v2 CBS2499_4646	kinase SKY1
AWRiv2 AWRI_1731	kinase SKY1
LAMAP LAMAP2480_5262	PH domain-containing protein C637.13c
CBS2499v2 CBS2499_4614	signaling protein slm1
AWRiv2 AWRI_1752	signaling protein slm1
LAMAP LAMAP2480_5292	complex protein 5
CBS2499v2 CBS2499_3085	complex protein 5
AWRiv2 AWRI_1219	of elongator which is required for modification of wobble nucleosides in trna
LAMAP LAMAP2480_5295	excision repair protein (rad2)
CBS2499v2 CBS2499_3082	excision repair protein (rad2)
AWRiv2 AWRI_1223	excision repair protein (rad2)
LAMAP LAMAP2480_5300	protein _1468
CBS2499v2 CBS2499_3076	protein _1468
AWRiv2 AWRI_1226	protein _1468
LAMAP LAMAP2480_5305	protein beta subunit, forms a dimer with Ste18p to activate the mating signaling pathway, forms a heterotrimer with Gpa1p and Ste18p to dampen signaling; may recruit Rho1p to the polarized growth site during mating; contains WD40 repeats
CBS2499v2 CBS2499_3072	protein beta subunit; forms a dimer with Ste18p to activate the mating signaling pathway, forms a heterotrimer with Gpa1p and Ste18p to dampen signaling; may recruit Rho1p to the polarized growth site during mating; contains WD40 repeats
AWRiv2 AWRI_1229	protein beta subunit; forms a dimer with Ste18p to activate the mating signaling pathway, forms a heterotrimer with Gpa1p and Ste18p to dampen signaling; may recruit Rho1p to the polarized growth site during mating; contains WD40 repeats
LAMAP LAMAP2480_5310	protein SWI4
CBS2499v2 CBS2499_2300	factor MBP1
AWRiv2 AWRI_1387	factor MBP1
LAMAP LAMAP2480_5311	NSG2
CBS2499v2 CBS2499_2301	NSG2
AWRiv2 AWRI_1386	biosynthesis regulatory
LAMAP LAMAP2480_5314	SIP5
CBS2499v2 CBS2499_2305	SIP5
AWRiv2 AWRI_1384	SIP5

LAMAP LAMAP2480_5317	export factor MEX67
CBS2499v2 CBS2499_2307	binding protein involved in nuclear mRNA export; component of the nuclear pore; ortholog of human TAP
AWRIv2 AWRI_1382	export factor MEX67
LAMAP LAMAP2480_5318	small nucleolar RNA-associated protein 10
CBS2499v2 CBS2499_2308	small nucleolar RNA-associated protein 10
AWRIv2 AWRI_1380	small nucleolar RNA-associated protein 10
LAMAP LAMAP2480_5342	acid phosphohydrolase 1
CBS2499v2 CBS2499_2346	acid phosphohydrolase 1
AWRIv2 AWRI_1350	acid phosphohydrolase 1
LAMAP LAMAP2480_5347	protein _2222
CBS2499v2 CBS2499_3866	protein _2222
AWRIv2 AWRI_1858	protein _2222
LAMAP LAMAP2480_5366	RNA polymerase III subunit RPC9
CBS2499v2 CBS2499_3846	RNA polymerase III subunit RPC9
AWRIv2 AWRI_1837	RNA polymerase III subunit rpc9
	metal ion transporter involved in manganese homeostasis; has broad specificity for di-valent and tri-valent metals; post-translationally regulated by levels of metal ions; member of the Nramp family of metal transport proteins
LAMAP LAMAP2480_5372	divalent metal ion transporter involved in iron homeostasis; transcriptionally regulated by metal ions; member of the Nramp family of metal transport proteins; protein abundance increases in response to DNA replication stress
CBS2499v2 CBS2499_3840	divalent metal ion transporter involved in iron homeostasis; transcriptionally regulated by metal ions; member of the Nramp family of metal transport proteins; protein abundance increases in response to DNA replication stress
AWRIv2 AWRI_1830	hydrolase YJU3
LAMAP LAMAP2480_5417	lipase
CBS2499v2 CBS2499_0491	lipase
AWRIv2 AWRI_3047	complex subunit DAM1
LAMAP LAMAP2480_5423	complex subunit DAM1
CBS2499v2 CBS2499_0484	complex subunit DAM1
AWRIv2 AWRI_3041	protein _3625
LAMAP LAMAP2480_5432	protein _3625
CBS2499v2 CBS2499_0474	protein _3625
AWRIv2 AWRI_3034	protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
LAMAP LAMAP2480_5433	
	epimerase; catalyzes isomerization of (R)- and (S)-NADHX; homologous to AIBP in mammals and the N-terminal domain of YjeF in E.coli; enzyme is widespread in eukaryotes, prokaryotes and archaea; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
CBS2499v2 CBS2499_0472	
	epimerase; catalyzes isomerization of (R)- and (S)-NADHX; homologous to AIBP in mammals and the N-terminal domain of YjeF in E.coli; enzyme is widespread in eukaryotes, prokaryotes and archaea; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies
AWRIv2 AWRI_3033	

LAMAP LAMAP2480_5458	affinity sulfate permease of the SulP anion transporter family; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates
CBS2499v2 CBS2499_4478	affinity sulfate permease of the SulP anion transporter family; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates
AWRlv2 AWRI_3138	affinity sulfate permease of the SulP anion transporter family; sulfate uptake is mediated by specific sulfate transporters Sul1p and Sul2p, which control the concentration of endogenous activated sulfate intermediates
LAMAP LAMAP2480_5488	protein _2144
CBS2499v2 CBS2499_3674	protein _2144
AWRlv2 AWRI_1795	protein _2144
LAMAP LAMAP2480_5494	RMD9-like, mitochondrial
CBS2499v2 CBS2499_3670	RMD9, mitochondrial
AWRlv2 AWRI_1791	RMD9-like, mitochondrial
LAMAP LAMAP2480_5501	small nucleolar ribonucleoprotein
CBS2499v2 CBS2499_3666	small nucleolar ribonucleoprotein protein LCP5
AWRlv2 AWRI_1787	small nucleolar ribonucleoprotein protein LCP5
LAMAP LAMAP2480_5539	protein particle complex II-specific subunit 130
CBS2499v2 CBS2499_3172	protein particle complex II-specific subunit 130
AWRlv2 AWRI_1888	of 10 subunits of the transport protein particle complex of the cis-golgi
LAMAP LAMAP2480_5548	membrane protein YJL163C
CBS2499v2 CBS2499_3178	membrane protein YJL163C
AWRlv2 AWRI_1896	membrane protein YJL163C
LAMAP LAMAP2480_5557	of glycerol defect protein 1
CBS2499v2 CBS2499_3190	of glycerol defect protein 1
AWRlv2 AWRI_1906	of glycerol defect protein 1
LAMAP LAMAP2480_5568	factor srp1
CBS2499v2 CBS2499_3199	factor srp1
AWRlv2 AWRI_1918	factor srp1
LAMAP LAMAP2480_5584	spindle elongation protein 1
CBS2499v2 CBS2499_3998	spindle elongation protein 1
AWRlv2 AWRI_0283	spindle elongation protein 1
LAMAP LAMAP2480_5610	structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions
CBS2499v2 CBS2499_2007	structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions
AWRlv2 AWRI_0995	structural protein involved in cell polarization, endocytosis, and other cytoskeletal functions
LAMAP LAMAP2480_5611	transcription factor HCM1
CBS2499v2 CBS2499_2008	transcription factor HCM1
AWRlv2 AWRI_0994	transcription factor HCM1
LAMAP LAMAP2480_5612	E3 ubiquitin-protein ligase HUL4
CBS2499v2 CBS2499_2009	E3 ubiquitin-protein ligase HUL4
AWRlv2 AWRI_0993	E3 ubiquitin-protein ligase HUL4
LAMAP LAMAP2480_5621	factor SKN7
CBS2499v2 CBS2499_2020	factor SKN7

AWRIv2 AWRI_0985	factor SKN7
LAMAP LAMAP2480_5626	DNA polymerase alpha-associated DNA helicase A involved in lagging strand DNA synthesis; contains single-stranded DNA stimulated ATPase and dATPase activities; replication protein A stimulates helicase and ATPase activities
CBS2499v2 CBS2499_2025	DNA polymerase alpha-associated DNA helicase A; involved in lagging strand DNA synthesis; contains single-stranded DNA stimulated ATPase and dATPase activities; replication protein A stimulates helicase and ATPase activities
AWRIv2 AWRI_0981	DNA polymerase alpha-associated DNA helicase A; involved in lagging strand DNA synthesis; contains single-stranded DNA stimulated ATPase and dATPase activities; replication protein A stimulates helicase and ATPase activities
LAMAP LAMAP2480_5639	Fe(II) transporter of the plasma membrane
CBS2499v2 CBS2499_2036	Fe(II) transporter of the plasma membrane
AWRIv2 AWRI_0970	Fe(2+) transport protein
LAMAP LAMAP2480_5651	wall mannoprotein PST1
CBS2499v2 CBS2499_0820	wall mannoprotein PST1
AWRIv2 AWRI_0046	wall mannoprotein PST1
LAMAP LAMAP2480_5653	translation initiation factor 3 subunit A
CBS2499v2 CBS2499_0818	translation initiation factor 3 subunit A
AWRIv2 AWRI_0048	translation initiation factor 3 subunit A
LAMAP LAMAP2480_5664	H
CBS2499v2 CBS2499_0808	H1
AWRIv2 AWRI_0054	H
LAMAP LAMAP2480_5670	protein _0066
CBS2499v2 CBS2499_0801	protein _0066
AWRIv2 AWRI_0057	protein _0066
LAMAP LAMAP2480_5705	N-acetyltransferase C550.08
CBS2499v2 CBS2499_3938	N-acetyltransferase C550.08
AWRIv2 AWRI_0227	N-acetyltransferase C550.08
LAMAP LAMAP2480_5720	protein YKR096W
CBS2499v2 CBS2499_1513	protein 1
AWRIv2 AWRI_3930	protein 1
LAMAP LAMAP2480_5724	budding pattern protein 2
CBS2499v2 CBS2499_1517	budding pattern protein 2
AWRIv2 AWRI_3933	budding pattern protein 2
LAMAP LAMAP2480_5726	affinity polyamine permease, preferentially uses spermidine over putrescine; expression is down-regulated by osmotic stress; plasma membrane carnitine transporter, also functions as a low-affinity amino acid permease
CBS2499v2 CBS2499_1519	membrane regulator of polyamine and carnitine transport; has similarity to transporters but lacks transport activity; may act as a sensor that transduces environmental signals; has a positive or negative regulatory effect on transcription of many transporter genes
AWRIv2 AWRI_3935	membrane regulator of polyamine and carnitine transport; has similarity to transporters but lacks transport activity; may act as a sensor that transduces environmental signals; has a positive or negative regulatory effect on transcription of many transporter genes
LAMAP LAMAP2480_5732	protein

CBS2499v2 CBS2499_1525	protein
AWRiv2 AWRI_3941	protein
LAMAP LAMAP2480_5794	transporter, sugar porter (SP) family
CBS2499v2 CBS2499_4594	transporter, sugar porter (SP) family
AWRiv2 AWRI_1095	transporter, sugar porter (SP) family
LAMAP LAMAP2480_5803	superoxide dismutase (SODC)
CBS2499v2 CBS2499_1448	surface superoxide dismutase [Cu-Zn] 6
AWRiv2 AWRI_3777	surface superoxide dismutase [Cu-Zn] 6
LAMAP LAMAP2480_5814	deoxyribonuclease YMR262W
CBS2499v2 CBS2499_1465	deoxyribonuclease YMR262W
AWRiv2 AWRI_3763	protein scn1
LAMAP LAMAP2480_5832	amino acid decarboxylase
CBS2499v2 CBS2499_4161	amino acid decarboxylase
AWRiv2 AWRI_4058	amino acid decarboxylase
	E Vps protein of the ESCRT-III complex, required for sorting of integral membrane proteins into luminal vesicles of multivesicular bodies, and for delivery of newly synthesized vacuolar enzymes to the vacuole, involved in endocytosis
LAMAP LAMAP2480_5855	E Vps protein of the ESCRT-III complex; required for sorting of integral membrane proteins into luminal vesicles of multivesicular bodies, and for delivery of newly synthesized vacuolar enzymes to the vacuole, involved in endocytosis
	E Vps protein of the ESCRT-III complex; required for sorting of integral membrane proteins into luminal vesicles of multivesicular bodies, and for delivery of newly synthesized vacuolar enzymes to the vacuole, involved in endocytosis
CBS2499v2 CBS2499_3280	E Vps protein of the ESCRT-III complex; required for sorting of integral membrane proteins into luminal vesicles of multivesicular bodies, and for delivery of newly synthesized vacuolar enzymes to the vacuole, involved in endocytosis
	involved in endocytosis
AWRiv2 AWRI_2328	kinase PTK2/STK2
LAMAP LAMAP2480_5856	kinase PTK2/STK2
CBS2499v2 CBS2499_3281	kinase PTK2/STK2
AWRiv2 AWRI_2327	kinase PTK2/STK2
LAMAP LAMAP2480_5860	factor PRP9
CBS2499v2 CBS2499_3285	factor PRP9
AWRiv2 AWRI_2323	factor PRP9
	protein of unknown function, likely exists as tetramer, may be regulated by the binding of small-molecule ligands (possibly sulfate ions), may have a role in yeast cell-wall biogenesis
LAMAP LAMAP2480_5866	protein of unknown function; likely exists as tetramer, may be regulated by the binding of small-molecule ligands (possibly sulfate ions), may have a role in yeast cell-wall biogenesis
	protein of unknown function; likely exists as tetramer, may be regulated by the binding of small-molecule ligands (possibly sulfate ions), may have a role in yeast cell-wall biogenesis
CBS2499v2 CBS2499_3291	protein of unknown function; likely exists as tetramer, may be regulated by the binding of small-molecule ligands (possibly sulfate ions), may have a role in yeast cell-wall biogenesis
	ligands (possibly sulfate ions), may have a role in yeast cell-wall biogenesis
AWRiv2 AWRI_2318	component protein SHR3
LAMAP LAMAP2480_5873	component protein SHR3
CBS2499v2 CBS2499_3301	component protein SHR3
AWRiv2 AWRI_2313	component protein SHR3
LAMAP LAMAP2480_5875	coatomer subunit gamma
CBS2499v2 CBS2499_4774	coatomer subunit gamma
	subunit of coatomer; coatomer is a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo
AWRiv2 AWRI_0764	
LAMAP LAMAP2480_5893	
CBS2499v2 CBS2499_0017	

AWRIv2 AWRI_0786	
LAMAP LAMAP2480_5900	import protein MOG1
CBS2499v2 CBS2499_0020	import protein MOG1
AWRIv2 AWRI_0789	import protein MOG1
LAMAP LAMAP2480_5904	oligomeric Golgi complex subunit 8
CBS2499v2 CBS2499_2956	oligomeric Golgi complex subunit 8
AWRIv2 AWRI_3789	oligomeric Golgi complex subunit 8
LAMAP LAMAP2480_5909	protein T10 in DGCR region
CBS2499v2 CBS2499_2961	protein YGR127W
AWRIv2 AWRI_3782	and Golgi organization protein 2 homolog
LAMAP LAMAP2480_5946	O-acetyltransferase YAT2
CBS2499v2 CBS2499_2585	O-acetyltransferase YAT2
AWRIv2 AWRI_0594	O-acetyltransferase YAT2
LAMAP LAMAP2480_5957	B
CBS2499v2 CBS2499_2188	B
AWRIv2 AWRI_3620	B
LAMAP LAMAP2480_5966	symporter
CBS2499v2 CBS2499_1594	symporter
AWRIv2 AWRI_3613	symporter
LAMAP LAMAP2480_5977	complex protein LRP1
CBS2499v2 CBS2499_1604	complex protein LRP1
AWRIv2 AWRI_3606	
	co-chaperone; binds both Hsp82p (Hsp90) and Ssa1p (Hsp70) and stimulates the ATPase activity of SSA1, ts mutants reduce Hsp82p function while over expression suppresses the phenotypes of an HSP82 ts allele and a cpr7 deletion
LAMAP LAMAP2480_5980	
	co-chaperone; binds both Hsp82p (Hsp90) and Ssa1p (Hsp70) and stimulates the ATPase activity of SSA1, ts mutants reduce Hsp82p function while over expression suppresses the phenotypes of an HSP82 ts allele and a cpr7 deletion
CBS2499v2 CBS2499_2003	
	co-chaperone; binds both Hsp82p (Hsp90) and Ssa1p (Hsp70) and stimulates the ATPase activity of SSA1, ts mutants reduce Hsp82p function while over expression suppresses the phenotypes of an HSP82 ts allele and a cpr7 deletion
AWRIv2 AWRI_1002	
	ATP-dependent RNA helicase, nucleolar protein required for synthesis of 60S ribosomal subunits at a late step in the pathway; sediments with 66S pre-ribosomes in sucrose gradients
LAMAP LAMAP2480_6051	
	ATP-dependent RNA helicase; nucleolar protein required for synthesis of 60S ribosomal subunits at a late step in the pathway; sediments with 66S pre-ribosomes in sucrose gradients
CBS2499v2 CBS2499_5026	
	ATP-dependent RNA helicase; nucleolar protein required for synthesis of 60S ribosomal subunits at a late step in the pathway; sediments with 66S pre-ribosomes in sucrose gradients
AWRIv2 AWRI_4140	EMP47
LAMAP LAMAP2480_6053	EMP47
CBS2499v2 CBS2499_1588	EMP47
AWRIv2 AWRI_2868	
LAMAP LAMAP2480_6062	repeat-containing protein PET309, mitochondrial
CBS2499v2 CBS2499_1577	repeat-containing protein PET309, mitochondrial
AWRIv2 AWRI_2627	repeat-containing protein PET309, mitochondrial
LAMAP LAMAP2480_6069	cell-cycle arrest protein 5

CBS2499v2|CBS2499_1569
AWRIv2|AWRI_2635
LAMAP|LAMAP2480_6096
CBS2499v2|CBS2499_4791
AWRIv2|AWRI_1008
LAMAP|LAMAP2480_6102
CBS2499v2|CBS2499_2749
AWRIv2|AWRI_0364

LAMAP|LAMAP2480_6106
CBS2499v2|CBS2499_2754
AWRIv2|AWRI_0358
LAMAP|LAMAP2480_6113
CBS2499v2|CBS2499_2766
AWRIv2|AWRI_0347
LAMAP|LAMAP2480_6116
CBS2499v2|CBS2499_2772
AWRIv2|AWRI_0341
LAMAP|LAMAP2480_6121
CBS2499v2|CBS2499_2776
AWRIv2|AWRI_0337
LAMAP|LAMAP2480_6146
CBS2499v2|CBS2499_4733
AWRIv2|AWRI_2443
LAMAP|LAMAP2480_6153
CBS2499v2|CBS2499_4728
AWRIv2|AWRI_2440
LAMAP|LAMAP2480_6154
CBS2499v2|CBS2499_4727
AWRIv2|AWRI_2439
LAMAP|LAMAP2480_6173
CBS2499v2|CBS2499_3153
AWRIv2|AWRI_3555

LAMAP|LAMAP2480_6176

CBS2499v2|CBS2499_3150

AWRIv2|AWRI_3548
LAMAP|LAMAP2480_6178
CBS2499v2|CBS2499_3143

cell-cycle arrest protein 5
cell-cycle arrest protein 5
switch two complex protein 1
switch two complex protein 1
switch two complex protein 1
kinase ksp1
serine/threonine-protein kinase FMP48
protein kinase 8

sulfate permease; physically interacts with Hsp82p; green fluorescent protein (GFP)-fusion protein localizes to the ER; YPR003C is not an essential gene

sulfate transporter YPR003C
sulfate transporter YPR003C
utilization trans-activator
transcriptional regulatory protein C3C7.04
utilization trans-activator
DNA helicase ii, 70 kDa subunit (ku70)
DNA helicase ii, 70 kDa subunit (ku70)
DNA helicase ii, 70 kDa subunit (ku70)
chaperone D
chaperone D
chaperone D
protein Mb0912
protein Mb0912
protein Mb0912
chitinase 2

B
phosphatase superfamily (branch 1)
protein _2926
protein _2926
SOV1, mitochondrial
SOV1, mitochondrial
SOV1, mitochondrial

of a heterodimeric nuclear SUMO activating enzyme (E1) with Uba2p; activates Smt3p (SUMO) before its conjugation to proteins (sumoylation), which may play a role in protein targeting; essential for viability

of heterodimeric nuclear SUMO activating enzyme E1 with Uba2p; activates Smt3p (SUMO) before its conjugation to proteins (sumoylation), which may play a role in protein targeting; essential for viability; relocalizes to the cytosol in response to hypoxia

of heterodimeric nuclear SUMO activating enzyme E1 with Uba2p; activates Smt3p (SUMO) before its conjugation to proteins (sumoylation), which may play a role in protein targeting; essential for viability; relocalizes to the cytosol in response to hypoxia

transporter
of stop codon protein 6

AWRIv2 AWRI_3543	efflux
LAMAP LAMAP2480_6212	protein sorting-associated protein 41
CBS2499v2 CBS2499_0962	protein sorting-associated protein 41
AWRIv2 AWRI_0734	protein sorting-associated protein 41
LAMAP LAMAP2480_6215	protein
CBS2499v2 CBS2499_0965	protein
AWRIv2 AWRI_0731	protein
LAMAP LAMAP2480_6219	protein 1
CBS2499v2 CBS2499_0969	protein 1
AWRIv2 AWRI_0725	protein 1
LAMAP LAMAP2480_6252	protein _2766
CBS2499v2 CBS2499_3303	protein _2766
AWRIv2 AWRI_2311	protein _2766
LAMAP LAMAP2480_6303	b5
CBS2499v2 CBS2499_1221	b5
AWRIv2 AWRI_1708	b5
	base subunit of the 19S regulatory particle (RP) of the 26S proteasome; N-terminus plays a role in maintaining the structural integrity of the RP; binds selectively to polyubiquitin chains; homolog of the mammalian S5a protein
LAMAP LAMAP2480_6307	base subunit of the 19S RP of the 26S proteasome; N-terminus plays a role in maintaining the structural integrity of the regulatory particle (RP); binds selectively to polyubiquitin chains; homolog of the mammalian S5a protein
CBS2499v2 CBS2499_1218	proteasome regulatory subunit rpn10
AWRIv2 AWRI_2547	LAS1
LAMAP LAMAP2480_6317	LAS1
CBS2499v2 CBS2499_1209	LAS1
AWRIv2 AWRI_2551	protein YDL063C
LAMAP LAMAP2480_6321	import protein 1
CBS2499v2 CBS2499_1206	import protein 1
AWRIv2 AWRI_2553	protein of unknown function, transcription is activated by paralogous transcription factors Yrm1p and Yrr1p and genes involved in pleiotropic drug resistance (PDR); expression is induced in cells treated with the mycotoxin patulin
LAMAP LAMAP2480_6351	protein of unknown function; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p and genes involved in pleiotropic drug resistance (PDR); expression is induced in cells treated with the mycotoxin patulin
CBS2499v2 CBS2499_2357	protein of unknown function; transcription is activated by paralogous transcription factors Yrm1p and Yrr1p and genes involved in pleiotropic drug resistance (PDR); expression is induced in cells treated with the mycotoxin patulin
AWRIv2 AWRI_1342	initiation factor IIE subunit beta
LAMAP LAMAP2480_6354	initiation factor IIE subunit beta
CBS2499v2 CBS2499_2351	initiation factor IIE subunit beta
AWRIv2 AWRI_1344	RNA polymerase I subunit RPA34
LAMAP LAMAP2480_6355	RNA polymerase I subunit RPA34
CBS2499v2 CBS2499_2350	RNA polymerase I subunit RPA34
AWRIv2 AWRI_1345	RNA polymerase I subunit RPA34

LAMAP LAMAP2480_6362	ribosomal protein mitochondrial
CBS2499v2 CBS2499_0956	ribosomal protein mitochondrial
AWRiv2 AWRI_0740	ribosomal protein mitochondrial
LAMAP LAMAP2480_6367	domain-containing protein 2
CBS2499v2 CBS2499_0951	domain-containing protein 2
AWRiv2 AWRI_0745	domain
LAMAP LAMAP2480_6368	protein 3
CBS2499v2 CBS2499_0950	protein 3
AWRiv2 AWRI_0746	protein 3
LAMAP LAMAP2480_6369	factor, CC1-like family
CBS2499v2 CBS2499_0948	factor, CC1-like family
AWRiv2 AWRI_0748	factor, CC1-like family
LAMAP LAMAP2480_6371	t-SNARE syntaxin required for vesicular transport between the ER and the Golgi complex; binds at least 9 SNARE proteins
CBS2499v2 CBS2499_0946	t-SNARE syntaxin; required for vesicular transport between the ER and the Golgi complex; binds at least 9 SNARE proteins
AWRiv2 AWRI_0750	t-SNARE syntaxin; required for vesicular transport between the ER and the Golgi complex; binds at least 9 SNARE proteins
LAMAP LAMAP2480_6373	of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins
CBS2499v2 CBS2499_0944	of the TOM (translocase of outer membrane) complex; involved in the recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; TOM70 has a paralog, TOM71, that arose from the whole genome duplication
AWRiv2 AWRI_0752	of the TOM (translocase of outer membrane) complex; involved in the recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins; TOM70 has a paralog, TOM71, that arose from the whole genome duplication
LAMAP LAMAP2480_6374	cardiolipin-specific phospholipase; functions upstream of Taz1p to generate monolyso-cardiolipin; transcription increases upon genotoxic stress; involved in restricting Ty1 transposition; has homology to mammalian CGI-58
CBS2499v2 CBS2499_0943	cardiolipin-specific phospholipase; functions upstream of Taz1p to generate monolyso-cardiolipin; transcription increases upon genotoxic stress; involved in restricting Ty1 transposition; has homology to mammalian CGI-58
AWRiv2 AWRI_2489	cardiolipin-specific deacylase, mitochondrial
LAMAP LAMAP2480_6378	protein 9
CBS2499v2 CBS2499_0939	protein 9
AWRiv2 AWRI_2491	protein 9
LAMAP LAMAP2480_6414	factor STP2
CBS2499v2 CBS2499_3495	factor STP2
AWRiv2 AWRI_3530	factor STP2
LAMAP LAMAP2480_6444	family
CBS2499v2 CBS2499_4890	family
AWRiv2 AWRI_3966	family
LAMAP LAMAP2480_6445	carboxypeptidase yscS; expression is induced under low-nitrogen conditions
CBS2499v2 CBS2499_4889	carboxypeptidase S; expression is induced under low-nitrogen conditions

AWRIv2|AWRI_3964
LAMAP|LAMAP2480_6448
CBS2499v2|CBS2499_4886
AWRIv2|AWRI_3961
LAMAP|LAMAP2480_6452
CBS2499v2|CBS2499_4882
AWRIv2|AWRI_4132
LAMAP|LAMAP2480_6462
CBS2499v2|CBS2499_2745
AWRIv2|AWRI_0368
LAMAP|LAMAP2480_6471
CBS2499v2|CBS2499_2734

AWRIv2|AWRI_0380
LAMAP|LAMAP2480_6480
CBS2499v2|CBS2499_2722
AWRIv2|AWRI_0393
LAMAP|LAMAP2480_6485
CBS2499v2|CBS2499_4714
AWRIv2|AWRI_2423
LAMAP|LAMAP2480_6490
CBS2499v2|CBS2499_4709
AWRIv2|AWRI_2418
LAMAP|LAMAP2480_6499
CBS2499v2|CBS2499_1923
AWRIv2|AWRI_1641
LAMAP|LAMAP2480_6500
CBS2499v2|CBS2499_1922
AWRIv2|AWRI_1642
LAMAP|LAMAP2480_6502
CBS2499v2|CBS2499_1919
AWRIv2|AWRI_1645
LAMAP|LAMAP2480_6503
CBS2499v2|CBS2499_1918
AWRIv2|AWRI_1646
LAMAP|LAMAP2480_6504
CBS2499v2|CBS2499_1917
AWRIv2|AWRI_1647

LAMAP|LAMAP2480_6505

CBS2499v2|CBS2499_1916

carboxypeptidase S; expression is induced under low-nitrogen conditions

transporter C757.13

transporter C757.13

transporter C757.13

protein HPODL_05036

protein HPODL_05036

transcription factor

protein YOR296W

protein YOR296W

protein YOR296W

aminopeptidase, overproduction stimulates glycogen accumulation

N

amino peptidase; overproduction stimulates glycogen accumulation; AAP1 has a paralog, APE2, that arose from the whole genome duplication

biogenesis protein ALB1

biogenesis protein ALB1

biogenesis protein ALB1

protein HPODL_01186

protein HPODL_01186

n-methyltransferase

5'-phosphate oxidase C1952.08c homolog

5'-phosphate oxidase YLR456W homolog

5'-phosphate oxidase C1952.08c homolog

protein C922.05c

protein C922.05c

protein C922.05c

kinase 1

kinase 1

transcriptional regulatory protein YJL206C

transcriptional regulatory protein YJL206C

transcriptional regulatory protein YJL206C

transcriptional regulatory protein C417.09c

transcriptional regulatory protein C417.09c

transcriptional regulatory protein C417.09c

nucleoside transporter family

nucleoside transporter family

nucleoside transporter family

permease, transports maltose, maltotriose, alpha-methylglucoside, and turanose; identical to Mph3p; encoded in a subtelomeric position in a region likely to have undergone duplication

permease; transports maltose, maltotriose, alpha-methylglucoside, and turanose; identical to Mph3p; encoded in a subtelomeric position in a region likely to have undergone duplication

AWRIv2 AWRI_1648	permease; transports maltose, maltotriose, alpha-methylglucoside, and turanose; identical to Mph3p; encoded in a subtelomeric position in a region likely to have undergone duplication
LAMAP LAMAP2480_6506	invertase
CBS2499v2 CBS2499_1915	invertase
AWRIv2 AWRI_1649	invertase
LAMAP LAMAP2480_6507	transporter, sugar porter (SP) family
CBS2499v2 CBS2499_1914	transporter, sugar porter (SP) family
AWRIv2 AWRI_1650	transporter, sugar porter (SP) family
LAMAP LAMAP2480_6528	protein HPODL_03877
CBS2499v2 CBS2499_3562	protein HPODL_03877
AWRIv2 AWRI_3906	protein HPODL_03877
LAMAP LAMAP2480_6530	domain containing protein
CBS2499v2 CBS2499_3564	domain containing protein
AWRIv2 AWRI_3907	domain containing protein
LAMAP LAMAP2480_6537	regulatory protein ASH1
CBS2499v2 CBS2499_0901	regulatory protein ASH1
AWRIv2 AWRI_2520	regulatory protein ASH1
LAMAP LAMAP2480_6538	protein product
CBS2499v2 CBS2499_0898	ECM7
AWRIv2 AWRI_2522	ECM7
LAMAP LAMAP2480_6543	protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; periodically expressed during the metabolic cycle; weak similarity to bacterial cation transport protein
CBS2499v2 CBS2499_0887	cyclotransferase; cleaves the gamma-glutamyl bond of glutathione to yield 5-oxoproline and a Cys-Gly dipeptide; similar to mammalian pro-apoptotic protein ChaC1; expression of mouse ChaC1 in yeast increases apoptosis; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; periodically expressed during the metabolic cycle
AWRIv2 AWRI_2533	cyclotransferase; cleaves the gamma-glutamyl bond of glutathione to yield 5-oxoproline and a Cys-Gly dipeptide; similar to mammalian pro-apoptotic protein ChaC1; expression of mouse ChaC1 in yeast increases apoptosis; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm and nucleus; periodically expressed during the metabolic cycle
LAMAP LAMAP2480_6546	repair protein rad4
CBS2499v2 CBS2499_0884	repair protein rad4
AWRIv2 AWRI_2535	repair protein RAD4
LAMAP LAMAP2480_6563	malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; phosphorylated
CBS2499v2 CBS2499_4506	malate dehydrogenase; catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; phosphorylated
AWRIv2 AWRI_1028	malate dehydrogenase; catalyzes interconversion of malate and oxaloacetate; involved in the tricarboxylic acid (TCA) cycle; phosphorylated
LAMAP LAMAP2480_6588	transport protein SEC31
CBS2499v2 CBS2499_4090	transport protein SEC31
AWRIv2 AWRI_2734	transport protein SEC31
LAMAP LAMAP2480_6595	protein

CBS2499v2 CBS2499_4082	protein
AWRIv2 AWRI_2729	protein
LAMAP LAMAP2480_6606	ATPase
CBS2499v2 CBS2499_3247	2-reductase
AWRIv2 AWRI_2360	2-reductase
LAMAP LAMAP2480_6607	CASP
CBS2499v2 CBS2499_3248	CASP
AWRIv2 AWRI_2359	CASP
LAMAP LAMAP2480_6613	binding domain of Hap4 for binding to Hap2/3/5
CBS2499v2 CBS2499_3255	binding domain of Hap4 for binding to Hap2/3/5
AWRIv2 AWRI_2356	binding domain of Hap4 for binding to Hap2/3/5
LAMAP LAMAP2480_6622	class I and II
CBS2499v2 CBS2499_3264	protein _2807
AWRIv2 AWRI_2345	protein _2807
LAMAP LAMAP2480_6636	protein YMR074C
CBS2499v2 CBS2499_1865	protein MK1619
AWRIv2 AWRI_2290	protein YMR074C
LAMAP LAMAP2480_6660	initiation factor (eIF) 2A; associates specifically with both 40S subunits and 80 S ribosomes, and interacts genetically with both eIF5b and eIF4E; homologous to mammalian eIF2A
CBS2499v2 CBS2499_2230	initiation factor (eIF) 2A; associates specifically with both 40S subunits and 80 S ribosomes, and interacts genetically with both eIF5b and eIF4E; homologous to mammalian eIF2A
AWRIv2 AWRI_2832	translation initiation factor 2A
LAMAP LAMAP2480_6663	domain-containing protein
CBS2499v2 CBS2499_2227	domain-containing protein
AWRIv2 AWRI_2830	domain-containing protein
LAMAP LAMAP2480_6684	protein _0018
CBS2499v2 CBS2499_0852	protein _0018
AWRIv2 AWRI_0015	protein _0018
LAMAP LAMAP2480_6688	division cycle protein 27 homolog B
CBS2499v2 CBS2499_0849	
AWRIv2 AWRI_0018	bimA
LAMAP LAMAP2480_6691	transport protein SEC20
CBS2499v2 CBS2499_0846	transport protein SEC20
AWRIv2 AWRI_0020	transport protein SEC20
LAMAP LAMAP2480_6693	acetyltransferase type B subunit 2
CBS2499v2 CBS2499_0844	acetyltransferase type B subunit 2
AWRIv2 AWRI_0022	acetyltransferase type B subunit 2
LAMAP LAMAP2480_6696	protein YLR352W
CBS2499v2 CBS2499_0841	protein YLR352W
AWRIv2 AWRI_0025	protein YLR352W
LAMAP LAMAP2480_6701	protein _4892
CBS2499v2 CBS2499_1800	protein _4892
AWRIv2 AWRI_4121	protein _4892
LAMAP LAMAP2480_6704	complex subunit 5
CBS2499v2 CBS2499_1804	complex subunit 5

AWRIv2 AWRI_4116	complex subunit 5
LAMAP LAMAP2480_6717	PUN1
CBS2499v2 CBS2499_1824	PUN1
AWRIv2 AWRI_2264	PUN1
LAMAP LAMAP2480_6718	mitochondrial outer membrane protein YPR098C
CBS2499v2 CBS2499_1825	mitochondrial outer membrane protein YPR098C
AWRIv2 AWRI_2265	mitochondrial outer membrane protein YPR098C
	(R,R)-butanediol dehydrogenase, catalyzes oxidation of (R,R)-2,3-butanediol to (3R)-acetoin, oxidation of meso-butanediol to (3S)-acetoin, and reduction of acetoin; enhances use of 2,3-butanediol as an aerobic carbon source
LAMAP LAMAP2480_6719	(R,R)-butanediol dehydrogenase; catalyzes oxidation of (R,R)-2,3-butanediol to (3R)-acetoin, oxidation of meso-butanediol to (3S)-acetoin, and reduction of acetoin; enhances use of 2,3-butanediol as an aerobic carbon source
	(R,R)-butanediol dehydrogenase; catalyzes oxidation of (R,R)-2,3-butanediol to (3R)-acetoin, oxidation of meso-butanediol to (3S)-acetoin, and reduction of acetoin; enhances use of 2,3-butanediol as an aerobic carbon source
CBS2499v2 CBS2499_1830	(R,R)-butanediol dehydrogenase; catalyzes oxidation of (R,R)-2,3-butanediol to (3R)-acetoin, oxidation of meso-butanediol to (3S)-acetoin, and reduction of acetoin; enhances use of 2,3-butanediol as an aerobic carbon source
	acid phosphatase
AWRIv2 AWRI_2268	acid phosphatase
LAMAP LAMAP2480_6728	acid phosphatase
CBS2499v2 CBS2499_4460	acid phosphatase
AWRIv2 AWRI_3150	acid phosphatase
	ATP-dependent RNA helicase of the DEAD-box family involved in ribosomal biogenesis; essential for growth under anaerobic conditions
LAMAP LAMAP2480_6732	ATP-dependent RNA helicase of the DEAD-box family; involved in ribosomal biogenesis; required at post-transcriptional step for efficient retrotransposition; essential for growth under anaerobic conditions
	ATP-dependent RNA helicase of the DEAD-box family; involved in ribosomal biogenesis; required at post-transcriptional step for efficient retrotransposition; essential for growth under anaerobic conditions
CBS2499v2 CBS2499_4465	ATP-dependent RNA helicase of the DEAD-box family; involved in ribosomal biogenesis; required at post-transcriptional step for efficient retrotransposition; essential for growth under anaerobic conditions
	ATP-dependent RNA helicase of the DEAD-box family; involved in ribosomal biogenesis; required at post-transcriptional step for efficient retrotransposition; essential for growth under anaerobic conditions
AWRIv2 AWRI_3149	assembly factor, functions with other V-ATPase assembly factors in the ER to efficiently assemble the V-ATPase membrane sector (V0)
LAMAP LAMAP2480_6753	assembly factor; functions with other V-ATPase assembly factors in the ER to efficiently assemble the V-ATPase membrane sector (V0); protein abundance increases in response to DNA replication stress
	assembly factor; functions with other V-ATPase assembly factors in the ER to efficiently assemble the V-ATPase membrane sector (V0); protein abundance increases in response to DNA replication stress
CBS2499v2 CBS2499_3729	assembly factor; functions with other V-ATPase assembly factors in the ER to efficiently assemble the V-ATPase membrane sector (V0); protein abundance increases in response to DNA replication stress
	assembly factor; functions with other V-ATPase assembly factors in the ER to efficiently assemble the V-ATPase membrane sector (V0); protein abundance increases in response to DNA replication stress
AWRIv2 AWRI_1160	polyadenylated RNA-binding protein NAB2
LAMAP LAMAP2480_6782	polyadenylated RNA-binding protein NAB2
CBS2499v2 CBS2499_2159	polyadenylated RNA-binding protein NAB2
AWRIv2 AWRI_2890	polyadenylated RNA-binding protein NAB2
LAMAP LAMAP2480_6792	ALG9
CBS2499v2 CBS2499_2139	alg9
AWRIv2 AWRI_2906	ALG9
LAMAP LAMAP2480_6797	serine/threonine-protein kinase HAL5-like
CBS2499v2 CBS2499_2275	kinase hal4
AWRIv2 AWRI_3829	serine/threonine-protein kinase HAL5-like

LAMAP LAMAP2480_6800	protein _4573
CBS2499v2 CBS2499_2278	protein _4573
AWRIv2 AWRI_3833	protein _4573
LAMAP LAMAP2480_6813	BOB1
CBS2499v2 CBS2499_2296	BOB1
AWRIv2 AWRI_3850	BOB1
	membrane riboflavin transporter; facilitates the uptake of vitamin B2; required for FAD-dependent processes; sequence similarity to mammalian monocarboxylate permeases, however mutants are not deficient in monocarboxylate transport
LAMAP LAMAP2480_6814	membrane riboflavin transporter; facilitates the uptake of vitamin B2; required for FAD-dependent processes; sequence similarity to mammalian monocarboxylate permeases, however mutants are not deficient in monocarboxylate transport
CBS2499v2 CBS2499_4208	transporter MCH4
AWRIv2 AWRI_3063	subunit of Sec63 complex (Sec63p, Sec62p, Sec66p and Sec72p); with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-dependent and post-translational SRP-independent protein targeting and import into the ER
LAMAP LAMAP2480_6816	subunit of Sec63 complex; with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-dependent and post-translational SRP-independent protein targeting and import into the ER; other members are Sec63p, Sec62p, and Sec72p
CBS2499v2 CBS2499_4210	subunit of Sec63 complex; with Sec61 complex, Kar2p/BiP and Lhs1p forms a channel competent for SRP-dependent and post-translational SRP-independent protein targeting and import into the ER; other members are Sec63p, Sec62p, and Sec72p
AWRIv2 AWRI_3060	transcription complex subunit 3
LAMAP LAMAP2480_6824	negative regulator of transcription subunit 3
CBS2499v2 CBS2499_4217	negative regulator of transcription subunit 3
AWRIv2 AWRI_3054	
LAMAP LAMAP2480_6826	of TFIIH and nucleotide excision repair factor 3 complexes, involved in transcription initiation, required for nucleotide excision repair; ring finger protein similar to mammalian CAK and TFIIH subunit
CBS2499v2 CBS2499_4218	of TFIIH and nucleotide excision repair factor 3 complexes; involved in transcription initiation, required for nucleotide excision repair; ring finger protein similar to mammalian CAK and TFIIH subunit
AWRIv2 AWRI_3053	of TFIIH and nucleotide excision repair factor 3 complexes; involved in transcription initiation, required for nucleotide excision repair; ring finger protein similar to mammalian CAK and TFIIH subunit
LAMAP LAMAP2480_6842	complex subunit mu
CBS2499v2 CBS2499_3814	complex subunit mu
AWRIv2 AWRI_4087	complex subunit mu
LAMAP LAMAP2480_6849	synthetase, synthesizes PRPP, which is required for nucleotide, histidine, and tryptophan biosynthesis; one of five related enzymes, which are active as heteromultimeric complexes
CBS2499v2 CBS2499_3809	synthetase; synthesizes PRPP, which is required for nucleotide, histidine, and tryptophan biosynthesis; one of five related enzymes, which are active as heteromultimeric complexes; forms cytoplasmic foci upon DNA replication stress

AWRIv2 AWRI_4091	synthetase; synthesizes PRPP, which is required for nucleotide, histidine, and tryptophan biosynthesis; one of five related enzymes, which are active as heteromultimeric complexes; forms cytoplasmic foci upon DNA replication stress
LAMAP LAMAP2480_6855	protein _2952
CBS2499v2 CBS2499_1162	protein _2952
AWRIv2 AWRI_2451	protein _2952
	subunit of the Hat1p-Hat2p histone acetyltransferase complex that uses the cofactor acetyl coenzyme A, to acetylate free nuclear and cytoplasmic histone H4; involved in telomeric silencing and DNA double-strand break repair
LAMAP LAMAP2480_6879	subunit of the Hat1p-Hat2p histone acetyltransferase complex; uses the cofactor acetyl coenzyme A to acetylate free nuclear and cytoplasmic histone H4; involved in telomeric silencing and DNA double-strand break repair
	subunit of the Hat1p-Hat2p histone acetyltransferase complex; uses the cofactor acetyl coenzyme A to acetylate free nuclear and cytoplasmic histone H4; involved in telomeric silencing and DNA double-strand break repair
CBS2499v2 CBS2499_3675	subunit of the Hat1p-Hat2p histone acetyltransferase complex; uses the cofactor acetyl coenzyme A to acetylate free nuclear and cytoplasmic histone H4; involved in telomeric silencing and DNA double-strand break repair
	subunit of the Hat1p-Hat2p histone acetyltransferase complex; uses the cofactor acetyl coenzyme A to acetylate free nuclear and cytoplasmic histone H4; involved in telomeric silencing and DNA double-strand break repair
AWRIv2 AWRI_1796	OPI10
LAMAP LAMAP2480_6904	OPI10
CBS2499v2 CBS2499_0636	OPI10
AWRIv2 AWRI_3636	OPI10
LAMAP LAMAP2480_6911	cis-trans isomerase B
CBS2499v2 CBS2499_0624	cis-trans isomerase B
AWRIv2 AWRI_4149	cis-trans isomerase B
LAMAP LAMAP2480_6917	resistance MFS transporter, drug:H⁺ antiporter-2 (14 Spanner) (DHA2) family
CBS2499v2 CBS2499_4891	resistance MFS transporter, drug:H ⁺ antiporter-2 (14 Spanner) (DHA2) family
AWRIv2 AWRI_3967	resistance protein fnx1
	catalyzes the interconversion of UDP-galactose and UDP-D-glucose in galactose metabolism; also catalyzes the conversion of alpha-D-glucose or alpha-D-galactose to their beta-anomers
LAMAP LAMAP2480_6921	catalyzes the interconversion of UDP-galactose and UDP-D-glucose in galactose metabolism; also catalyzes the conversion of alpha-D-glucose or alpha-D-galactose to their beta-anomers
	catalyzes the interconversion of UDP-galactose and UDP-D-glucose in galactose metabolism; also catalyzes the conversion of alpha-D-glucose or alpha-D-galactose to their beta-anomers
CBS2499v2 CBS2499_4898	catalyzes the interconversion of UDP-galactose and UDP-D-glucose in galactose metabolism; also catalyzes the conversion of alpha-D-glucose or alpha-D-galactose to their beta-anomers
	catalyzes the interconversion of UDP-galactose and UDP-D-glucose in galactose metabolism; also catalyzes the conversion of alpha-D-glucose or alpha-D-galactose to their beta-anomers
AWRIv2 AWRI_3972	4,6-dehydratase
LAMAP LAMAP2480_6922	4,6-dehydratase
CBS2499v2 CBS2499_4899	4,6-dehydratase
AWRIv2 AWRI_3973	4,6-dehydratase
LAMAP LAMAP2480_6926	transporter, sugar porter (SP) family
CBS2499v2 CBS2499_4904	permease
AWRIv2 AWRI_3977	transporter, sugar porter (SP) family
LAMAP LAMAP2480_6944	carboxyl-terminal hydrolase 16
CBS2499v2 CBS2499_1546	carboxyl-terminal hydrolase 16
AWRIv2 AWRI_2659	enzyme anchored to the outer mitochondrial membrane
LAMAP LAMAP2480_6947	ubiquitin-protein ligase BRE1
CBS2499v2 CBS2499_1543	ubiquitin-protein ligase BRE1
AWRIv2 AWRI_2664	ubiquitin-protein ligase BRE1
LAMAP LAMAP2480_6972	translation initiation factor 3 subunit J
CBS2499v2 CBS2499_4206	translation initiation factor 3 subunit J

AWRlv2 AWRI_3065	translation initiation factor 3 subunit J
LAMAP LAMAP2480_6979	organelle assembly protein TopJ
CBS2499v2 CBS2499_4196	initiation factor TFIID subunit 9
AWRlv2 AWRI_3069	organelle assembly protein TopJ
LAMAP LAMAP2480_6984	methyltransferase C1347.09
CBS2499v2 CBS2499_4192	methyltransferase C1347.09
AWRlv2 AWRI_3475	methyltransferase C1347.09
LAMAP LAMAP2480_7013	protein pof9
CBS2499v2 CBS2499_3497	protein pof9
AWRlv2 AWRI_3532	factor 1
LAMAP LAMAP2480_7014	of telomere capping protein 1
CBS2499v2 CBS2499_0984	of telomere capping protein 1
AWRlv2 AWRI_0709	of telomere capping protein 1
LAMAP LAMAP2480_7020	protein _0880
CBS2499v2 CBS2499_0973	protein _0880
AWRlv2 AWRI_0721	protein _0880
LAMAP LAMAP2480_7028	PBN1
CBS2499v2 CBS2499_0966	PBN1
AWRlv2 AWRI_0730	pbn1
LAMAP LAMAP2480_7029	oligomeric Golgi complex subunit 3
CBS2499v2 CBS2499_0963	oligomeric Golgi complex subunit 3
AWRlv2 AWRI_0732	oligomeric Golgi complex subunit 3
LAMAP LAMAP2480_7044	of unknown function, component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A
CBS2499v2 CBS2499_0721	of the SWR1 complex; complex exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A; protein abundance increases in response to DNA replication stress; relocalizes to the cytosol in response to hypoxia
AWRlv2 AWRI_0118	of the SWR1 complex; complex exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A; protein abundance increases in response to DNA replication stress; relocalizes to the cytosol in response to hypoxia
LAMAP LAMAP2480_7045	polymerase V
CBS2499v2 CBS2499_0720	polymerase V
AWRlv2 AWRI_0119	polymerase V
LAMAP LAMAP2480_7057	structural protein of SCF complexes (which also contain Skp1p, Cdc34p, Hrt1p and an F-box protein) involved in ubiquitination; SCF promotes the G1-S transition by targeting G1 cyclins and the Cln-CDK inhibitor Sic1p for degradation
CBS2499v2 CBS2499_1695	structural protein of SCF complexes (which also contain Skp1p, Cdc34p, Hrt1p and an F-box protein) involved in ubiquitination; SCF promotes the G1-S transition by targeting G1 cyclins and the Cln-CDK inhibitor Sic1p for degradation
AWRlv2 AWRI_1401	structural protein of SCF complexes (which also contain Skp1p, Cdc34p, Hrt1p and an F-box protein) involved in ubiquitination; SCF promotes the G1-S transition by targeting G1 cyclins and the Cln-CDK inhibitor Sic1p for degradation
LAMAP LAMAP2480_7062	utilization trans-activator
CBS2499v2 CBS2499_0752	utilization trans-activator

AWRIv2 AWRI_0096	utilization trans-activator
LAMAP LAMAP2480_7063	protein _0115
CBS2499v2 CBS2499_0751	protein _0115
AWRIv2 AWRI_0097	protein _0115
LAMAP LAMAP2480_7105	protein _0308
CBS2499v2 CBS2499_3960	protein _0308
AWRIv2 AWRI_0248	protein _0308
LAMAP LAMAP2480_7106	I inositol-1,4,5-trisphosphate 5-phosphatase 1
CBS2499v2 CBS2499_3961	I inositol polyphosphate 5-phosphatase 1
AWRIv2 AWRI_0249	protein HPODL_04556
LAMAP LAMAP2480_7112	protein
CBS2499v2 CBS2499_3969	protein
AWRIv2 AWRI_0257	protein _0319
LAMAP LAMAP2480_7122	protein 11
CBS2499v2 CBS2499_2682	protein 11
AWRIv2 AWRI_0436	protein 11
LAMAP LAMAP2480_7124	distribution protein nudE homolog 1
CBS2499v2 CBS2499_2680	distribution protein nudE homolog 1
AWRIv2 AWRI_0438	distribution protein nudE homolog 1
LAMAP LAMAP2480_7125	MFS-type transporter C1683.03c
CBS2499v2 CBS2499_2678	MFS-type transporter C1683.03c
AWRIv2 AWRI_0440	MFS-type transporter C1683.03c
LAMAP LAMAP2480_7126	protein _0537
CBS2499v2 CBS2499_2675	protein _0537
AWRIv2 AWRI_0442	protein _0537
	protein required for assembly of alpha and beta subunits into the F1 sector of mitochondrial F1F0 ATP synthase; mutation of human ATP12 reduces active ATP synthase levels and is associated with the disorder ATPAF2 deficiency
LAMAP LAMAP2480_7130	
	factor for the F1 sector of mitochondrial F1F0 ATP synthase; conserved protein; required for the assembly of alpha and beta subunits into the F1 sector of the mitochondrial F1F0 ATP synthase; mutation of human ATP12 reduces active ATP synthase levels and is associated with the disorder ATPAF2 deficiency
CBS2499v2 CBS2499_3774	
	factor for the F1 sector of mitochondrial F1F0 ATP synthase; conserved protein; required for the assembly of alpha and beta subunits into the F1 sector of the mitochondrial F1F0 ATP synthase; mutation of human ATP12 reduces active ATP synthase levels and is associated with the disorder ATPAF2 deficiency
AWRIv2 AWRI_1131	O-mannosyltransferase, transfers mannose from dolichyl phosphate-D-mannose to protein serine/threonine residues of secretory proteins; reaction is essential for cell wall rigidity; member of a family of mannosyltransferases
LAMAP LAMAP2480_7146	O-mannosyltransferase; transfers mannose from dolichyl phosphate-D-mannose to protein serine/threonine residues of secretory proteins; reaction is essential for cell wall rigidity; member of a family of mannosyltransferases
CBS2499v2 CBS2499_2812	

AWRIv2 AWRI_2774	O-mannosyltransferase; transfers mannose from dolichyl phosphate-D-mannose to protein serine/threonine residues of secretory proteins; reaction is essential for cell wall rigidity; member of a family of
LAMAP LAMAP2480_7151	mannosyltransferases
CBS2499v2 CBS2499_2808	transport protein CTR1
AWRIv2 AWRI_2778	transport protein CTR1
LAMAP LAMAP2480_7154	transport protein CTR1
CBS2499v2 CBS2499_2802	ste16
AWRIv2 AWRI_2783	ste16
LAMAP LAMAP2480_7159	ste16
CBS2499v2 CBS2499_0828	involved in the transcription of 35s rna genes by rna polymerase i
AWRIv2 AWRI_0036	involved in the transcription of 35s rna genes by rna polymerase i
LAMAP LAMAP2480_7165	involved in the transcription of 35s rna genes by rna polymerase i
CBS2499v2 CBS2499_0823	protein
AWRIv2 AWRI_0040	protein
LAMAP LAMAP2480_7174	protein
CBS2499v2 CBS2499_4863	cis-trans isomerase (cyclophilin) of the endoplasmic reticulum, catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; transcriptionally induced in response to unfolded proteins in the ER
AWRIv2 AWRI_3669	cis-trans isomerase (cyclophilin) of the ER; catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; transcriptionally induced in response to unfolded proteins in the ER; CPR5 has a paralog, CPR2, that arose from the whole genome duplication
LAMAP LAMAP2480_7176	cis-trans isomerase (cyclophilin) of the ER; catalyzes the cis-trans isomerization of peptide bonds N-terminal to proline residues; transcriptionally induced in response to unfolded proteins in the ER; CPR5 has a paralog, CPR2, that arose from the whole genome duplication
CBS2499v2 CBS2499_4858	protein _4374
AWRIv2 AWRI_3664	protein _4374
LAMAP LAMAP2480_7177	protein _4374
CBS2499v2 CBS2499_4857	subunit of the COMPASS (Set1C) complex, which methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres; WD40 beta propeller superfamily member and ortholog of mammalian WDR5
AWRIv2 AWRI_3663	subunit of the COMPASS (Set1C) complex; COMPASS methylates histone H3 on lysine 4 and is required in transcriptional silencing near telomeres; WD40 beta propeller superfamily member and ortholog of mammalian WDR5
LAMAP LAMAP2480_7197	repeat-containing protein 5
CBS2499v2 CBS2499_3426	intermembrane space cysteine motif-containing protein MIC17
AWRIv2 AWRI_3373	intermembrane space cysteine motif-containing protein MIX17
LAMAP LAMAP2480_7199	intermembrane space cysteine motif-containing protein MIX17
CBS2499v2 CBS2499_3427	WD repeat-containing protein C2A9.03
AWRIv2 AWRI_3372	WD repeat-containing protein C2A9.03
LAMAP LAMAP2480_7203	WD repeat-containing protein C2A9.03
CBS2499v2 CBS2499_3436	protein HPODL_01905
AWRIv2 AWRI_3367	protein JL09_g2106
LAMAP LAMAP2480_7204	protein _4041
	gis3

CBS2499v2 CBS2499_3439	gis3
AWRIv2 AWRI_3363	gis3
LAMAP LAMAP2480_7208	regulatory protein GLN3
CBS2499v2 CBS2499_2306	regulatory protein GLN3
AWRIv2 AWRI_1383	regulatory protein GLN3
LAMAP LAMAP2480_7218	required for export of the ribosomal subunits; associates with the RNA components of the pre-ribosomes; has a role in nuclear import in association with Pse1p; contains HEAT-repeats
CBS2499v2 CBS2499_1558	required for export of the ribosomal subunits; associates with the RNA components of the pre-ribosomes; has a role in nuclear import in association with Pse1p; also plays a role in the cell cycle and the DNA damage response; contains HEAT-repeats
AWRIv2 AWRI_2647	required for export of the ribosomal subunits; associates with the RNA components of the pre-ribosomes; has a role in nuclear import in association with Pse1p; also plays a role in the cell cycle and the DNA damage response; contains HEAT-repeats
LAMAP LAMAP2480_7219	initiation factor TFIID subunit 3
CBS2499v2 CBS2499_1557	initiation factor TFIID subunit 3
AWRIv2 AWRI_2649	protein _3190
LAMAP LAMAP2480_7238	targeting signal receptor
CBS2499v2 CBS2499_0390	PEP-CTERM system TPR-repeat lipoprotein
AWRIv2 AWRI_3720	targeting signal receptor
LAMAP LAMAP2480_7248	membrane protein PER10
CBS2499v2 CBS2499_1161	membrane protein PER10
AWRIv2 AWRI_2452	membrane protein PER10
LAMAP LAMAP2480_7275	protein kinase that phosphorylates and downregulates flippase activator Fpk1p; mutations affect receptor-mediated endocytosis and sphingolipid-mediated and cell integrity signaling pathways; homolog of mammalian kinase SGK
CBS2499v2 CBS2499_4381	protein kinase; phosphorylates and downregulates flippase activator Fpk1p; inactivates Orm1p and Orm2p (inhibitors of serine:palmitoyl-coenzyme A transferase) by phosphorylation in response to compromised sphingolipid synthesis; mutations affect receptor-mediated endocytosis and sphingolipid-mediated and cell integrity signaling pathways; homolog of mammalian kinase SGK; YPK1 has a paralog, YPK2, that arose from the whole genome duplication
AWRIv2 AWRI_4070	protein kinase; phosphorylates and downregulates flippase activator Fpk1p; inactivates Orm1p and Orm2p (inhibitors of serine:palmitoyl-coenzyme A transferase) by phosphorylation in response to compromised sphingolipid synthesis; mutations affect receptor-mediated endocytosis and sphingolipid-mediated and cell integrity signaling pathways; homolog of mammalian kinase SGK; YPK1 has a paralog, YPK2, that arose from the whole genome duplication
LAMAP LAMAP2480_7326	protein YML020W
CBS2499v2 CBS2499_3651	protein YML020W
AWRIv2 AWRI_1775	protein YML020W
LAMAP LAMAP2480_7338	segregation in meiosis protein 3
CBS2499v2 CBS2499_2708	segregation in meiosis protein 3
AWRIv2 AWRI_0408	segregation in meiosis protein 3
LAMAP LAMAP2480_7344	protein that inhibits replication of Brome mosaic virus in <i>S. cerevisiae</i> , which is a model system for studying replication of positive-strand RNA viruses in their natural hosts; deletion increases stop codon readthrough

CBS2499v2 CBS2499_2628 AWRIv2 AWRI_0487	of translation termination 1 of translation termination 1
LAMAP LAMAP2480_7345	uroporphyrinogen III transmethylase; involved in the biosynthesis of siroheme, a prosthetic group used by sulfite reductase; required for sulfate assimilation and methionine biosynthesis
CBS2499v2 CBS2499_2627	uroporphyrinogen III transmethylase; involved in the biosynthesis of siroheme, a prosthetic group used by sulfite reductase; required for sulfate assimilation and methionine biosynthesis
AWRIv2 AWRI_0488	uroporphyrinogen III transmethylase; involved in the biosynthesis of siroheme, a prosthetic group used by sulfite reductase; required for sulfate assimilation and methionine biosynthesis
LAMAP LAMAP2480_7346	protein subunit of the glycosylphosphatidylinositol transamidase complex that adds GPIs to newly synthesized proteins; human PIG-Sp homolog
CBS2499v2 CBS2499_2624	transamidase component GPI17
AWRIv2 AWRI_0491	transamidase component GPI17
LAMAP LAMAP2480_7349	repeat-containing protein At3g06920
CBS2499v2 CBS2499_2621	repeat-containing protein At1g09900
AWRIv2 AWRI_0494	repeat-containing protein At4g31850, chloroplastic
LAMAP LAMAP2480_7374	intracellular esterase that can function as an S-formylglutathione hydrolase; may be involved in the detoxification of formaldehyde, which can be metabolized to S-formylglutathione; similar to human esterase D
CBS2499v2 CBS2499_2477	that can function as an S-formylglutathione hydrolase; non-essential intracellular esterase; may be involved in the detoxification of formaldehyde, which can be metabolized to S-formylglutathione; similar to human esterase D
AWRIv2 AWRI_0515	esterase D
LAMAP LAMAP2480_7388	protein 2
CBS2499v2 CBS2499_0678	3-phosphate-binding protein 2
AWRIv2 AWRI_0162	3-phosphate-binding protein 2
LAMAP LAMAP2480_7389	acid permease
CBS2499v2 CBS2499_0677	acid permease
AWRIv2 AWRI_0163	acid permease
LAMAP LAMAP2480_7394	protein _0202
CBS2499v2 CBS2499_0671	protein _0202
AWRIv2 AWRI_0170	protein _0202
LAMAP LAMAP2480_7399	decay protein 4
CBS2499v2 CBS2499_1124	decay protein 4
AWRIv2 AWRI_2482	decay protein 4
LAMAP LAMAP2480_7419	
CBS2499v2 CBS2499_4598	
AWRIv2 AWRI_1098	
LAMAP LAMAP2480_7420	nucleoside transporter family
CBS2499v2 CBS2499_4599	nucleoside transporter family
AWRIv2 AWRI_1099	nucleoside transporter family
LAMAP LAMAP2480_7421	beta-glucosidase I
CBS2499v2 CBS2499_4600	beta-glucosidase I

AWRIv2|AWRI_1100
LAMAP|LAMAP2480_7422
CBS2499v2|CBS2499_4601
AWRIv2|AWRI_1101
LAMAP|LAMAP2480_7425
CBS2499v2|CBS2499_2834
AWRIv2|AWRI_2911
LAMAP|LAMAP2480_7427
CBS2499v2|CBS2499_2837
AWRIv2|AWRI_2913

LAMAP|LAMAP2480_7429

CBS2499v2|CBS2499_2839

AWRIv2|AWRI_2915
LAMAP|LAMAP2480_7446
CBS2499v2|CBS2499_2426
AWRIv2|AWRI_3303
LAMAP|LAMAP2480_7452
CBS2499v2|CBS2499_3040
AWRIv2|AWRI_1262
LAMAP|LAMAP2480_7464
CBS2499v2|CBS2499_2449
AWRIv2|AWRI_0502
LAMAP|LAMAP2480_7477
CBS2499v2|CBS2499_2753
AWRIv2|AWRI_0359
LAMAP|LAMAP2480_7482
CBS2499v2|CBS2499_2748
AWRIv2|AWRI_0365
LAMAP|LAMAP2480_7502
CBS2499v2|CBS2499_1135
AWRIv2|AWRI_2473

LAMAP|LAMAP2480_7504

CBS2499v2|CBS2499_1132

beta-glucosidase I

transporter C36.03c

transporter C36.03c

transporter C36.03c

factor, CC1-like family

factor, CC1-like family

factor, CC1-like family

protein PRP40

protein PRP40

protein PRP40

protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm;

YIR007W is a non-essential gene

glycosidase; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YIR007W is a non-essential gene

glycosidase; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YIR007W is a non-essential gene

MUM2

MUM2

protein _3963

trans-sulfuration enzyme YHR112C

trans-sulfuration enzyme YHR112C

trans-sulfuration enzyme YHR112C

endopeptidase ctsD

endopeptidase ctsD

aspartic-type endopeptidase CTSD (Fragment)

protein YNL144C

protein YNL144C

protein YNL144C

and cobalt transport protein CorA

and cobalt transport protein CorA

and cobalt transport protein CorA

protein 4

protein 4

membrane zinc transporter, transports zinc from the cytosol into the vacuole for storage; also has a role in resistance to zinc shock resulting from a sudden influx of zinc into the cytoplasm

membrane zinc transporter; transports zinc from cytosol to vacuole for storage; also has role in resistance to zinc shock resulting from sudden influx of zinc into cytoplasm; human ortholog SLC30A10 functions as a Mn transporter and mutations in SLC30A10 cause neurotoxic accumulation of Mn in liver and brain; ZRC1 has a paralog, COT1, that arose from the whole genome duplication

AWRIv2 AWRI_2475	membrane zinc transporter; transports zinc from cytosol to vacuole for storage; also has role in resistance to zinc shock resulting from sudden influx of zinc into cytoplasm; human ortholog SLC30A10 functions as a Mn transporter and mutations in SLC30A10 cause neurotoxic accumulation of Mn in liver and brain; ZRC1 has a paralog, COT1, that arose from the whole genome duplication
LAMAP LAMAP2480_7523	peroxisomal protein POX18
CBS2499v2 CBS2499_3400	peroxisomal protein POX18
AWRIv2 AWRI_3494	peroxisomal protein POX18
LAMAP LAMAP2480_7526	domain-containing protein 2 homolog A
CBS2499v2 CBS2499_3406	domain-containing protein 2 homolog A
AWRIv2 AWRI_3500	domain-containing protein 2 homolog A
LAMAP LAMAP2480_7527	protein _4202
CBS2499v2 CBS2499_3408	protein _4202
AWRIv2 AWRI_3502	protein _4202
LAMAP LAMAP2480_7542	UFE1
CBS2499v2 CBS2499_3515	UFE1
AWRIv2 AWRI_3327	required for er membrane fusion and vesicular traffic
LAMAP LAMAP2480_7546	protein sepH
CBS2499v2 CBS2499_3879	division control protein 7
AWRIv2 AWRI_1870	division control protein 7
LAMAP LAMAP2480_7547	protein PP7435_Chr4-0240
CBS2499v2 CBS2499_3878	protein JL09_g2862
AWRIv2 AWRI_1869	protein
LAMAP LAMAP2480_7550	midA homolog, mitochondrial
CBS2499v2 CBS2499_3875	dehydrogenase [ubiquinone] complex I, assembly factor 7
AWRIv2 AWRI_1867	protein JL09_g2894
	metal ion transporter involved in manganese homeostasis; has broad specificity for di-valent and tri-valent metals; post-translationally regulated by levels of metal ions; member of the Nramp family of metal transport proteins
LAMAP LAMAP2480_7551	metal ion transporter involved in manganese homeostasis; has broad specificity for di-valent and tri-valent metals; post-translationally regulated by levels of metal ions; member of the Nramp family of metal transport proteins
CBS2499v2 CBS2499_3874	metal ion transporter involved in manganese homeostasis; has broad specificity for di-valent and tri-valent metals; post-translationally regulated by levels of metal ions; member of the Nramp family of metal transport proteins
AWRIv2 AWRI_1866	histone deacetylase SIR2
LAMAP LAMAP2480_7553	histone deacetylase HST4
CBS2499v2 CBS2499_3871	histone deacetylase HST4
AWRIv2 AWRI_1864	histone deacetylase HST4
LAMAP LAMAP2480_7565	of Elongator complex, which is required for modification of wobble nucleosides in tRNA; target of Kluyveromyces lactis zymocin
CBS2499v2 CBS2499_1243	of Elongator complex; Elongator is required for modification of wobble nucleosides in tRNA; target of Kluyveromyces lactis zymocin
AWRIv2 AWRI_1698	of Elongator complex; Elongator is required for modification of wobble nucleosides in tRNA; target of Kluyveromyces lactis zymocin

LAMAP LAMAP2480_7570	protein YOR389W
CBS2499v2 CBS2499_2672	protein YOR389W
AWRIv2 AWRI_0445	protein YOR389W
LAMAP LAMAP2480_7611	complex component SEC15
CBS2499v2 CBS2499_0924	complex component SEC15
AWRIv2 AWRI_2502	complex component SEC15
LAMAP LAMAP2480_7613	protein C1259.12c
CBS2499v2 CBS2499_0926	protein C1259.12c
AWRIv2 AWRI_2500	protein C1259.12c
LAMAP LAMAP2480_7631	to ER traffic protein 2
CBS2499v2 CBS2499_2165	to ER traffic protein 2
AWRIv2 AWRI_2884	to er traffic protein 2
LAMAP LAMAP2480_7634	monophosphate (dCMP) deaminase required for dCTP and dTTP synthesis; expression is NOT cell cycle regulated
CBS2499v2 CBS2499_2173	monophosphate (dCMP) deaminase; involved in dUMP and dTMP biosynthesis; expression is NOT cell cycle regulated
AWRIv2 AWRI_2876	monophosphate (dCMP) deaminase; involved in dUMP and dTMP biosynthesis; expression is NOT cell cycle regulated
LAMAP LAMAP2480_7637	carboxyl-terminal hydrolase 3
CBS2499v2 CBS2499_2179	carboxyl-terminal hydrolase 3
AWRIv2 AWRI_2872	carboxyl-terminal hydrolase 3
LAMAP LAMAP2480_7640	protein _0464
CBS2499v2 CBS2499_2735	protein _0464
AWRIv2 AWRI_0379	protein _0464
LAMAP LAMAP2480_7645	glycosylase
CBS2499v2 CBS2499_2740	glycosylase
AWRIv2 AWRI_0373	glycosylase
LAMAP LAMAP2480_7646	N-acetyltransferase 1
CBS2499v2 CBS2499_2741	N-acetyltransferase 1
AWRIv2 AWRI_0372	N-acetyltransferase 1
LAMAP LAMAP2480_7659	protein that binds nucleosomes; a component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A
CBS2499v2 CBS2499_0709	protein that binds nucleosomes; a component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A
AWRIv2 AWRI_0131	protein ARP6
LAMAP LAMAP2480_7674	ABC transporter
CBS2499v2 CBS2499_3031	ABC transporter
AWRIv2 AWRI_1271	ABC transporter
LAMAP LAMAP2480_7703	ribosomal protein of the large subunit
CBS2499v2 CBS2499_4547	ribosomal protein of the large subunit
AWRIv2 AWRI_1057	ribosomal protein of the large subunit
LAMAP LAMAP2480_7705	synthase, catalyzes the synthesis of phosphatidylglycerolphosphate from CDP-diacylglycerol and sn-glycerol 3-phosphate in the first committed and rate-limiting step of cardiolipin biosynthesis

CBS2499v2 CBS2499_4550	synthase; catalyzes the synthesis of phosphatidylglycerolphosphate from CDP-diacylglycerol and sn-glycerol 3-phosphate in the first committed and rate-limiting step of cardiolipin biosynthesis
AWRIv2 AWRI_1060	synthase; catalyzes the synthesis of phosphatidylglycerolphosphate from CDP-diacylglycerol and sn-glycerol 3-phosphate in the first committed and rate-limiting step of cardiolipin biosynthesis
LAMAP LAMAP2480_7706	long chain fatty acyl-CoA synthetase and long chain fatty acid transporter; activates imported fatty acids with a preference for very long lengths (C20-C26); has a separate function in the transport of long chain fatty acids
CBS2499v2 CBS2499_4552	long chain fatty acyl-CoA synthetase and fatty acid transporter; activates imported fatty acids with a preference for very long lengths (C20-C26); has a separate function in the transport of long chain fatty acids
AWRIv2 AWRI_1062	long chain fatty acyl-CoA synthetase and fatty acid transporter; activates imported fatty acids with a preference for very long lengths (C20-C26); has a separate function in the transport of long chain fatty acids
LAMAP LAMAP2480_7752	alpha glucosidase I, ER type II integral membrane N-glycoprotein involved in assembly of cell wall beta 1,6 glucan and asparagine-linked protein glycosylation; also involved in ER protein quality control and sensing of ER stress
CBS2499v2 CBS2499_0829	alpha glucosidase I; ER type II integral membrane N-glycoprotein involved in assembly of cell wall beta 1,6 glucan and asparagine-linked protein glycosylation; also involved in ER protein quality control and sensing of ER stress
AWRIv2 AWRI_0035	alpha glucosidase I; ER type II integral membrane N-glycoprotein involved in assembly of cell wall beta 1,6 glucan and asparagine-linked protein glycosylation; also involved in ER protein quality control and sensing of ER stress
LAMAP LAMAP2480_7764	serine/threonine protein kinase involved in mating; phosphoactivated by Ste7p; substrates include Ste12p, Far1p, Bni1p, Sst2p; inhibits invasive growth during mating by phosphorylating Tec1p, promoting its degradation
CBS2499v2 CBS2499_4844	serine/threonine protein kinase involved in mating; phosphoactivated by Ste7p; substrates include Ste12p, Far1p, Bni1p, Sst2p; inhibits invasive growth during mating by phosphorylating Tec1p, promoting its; inhibits recruitment of Ste5p, Cdc42p-mediated asymmetry and mating morphogenesis
AWRIv2 AWRI_3412	serine/threonine protein kinase involved in mating; phosphoactivated by Ste7p; substrates include Ste12p, Far1p, Bni1p, Sst2p; inhibits invasive growth during mating by phosphorylating Tec1p, promoting its; inhibits recruitment of Ste5p, Cdc42p-mediated asymmetry and mating morphogenesis
LAMAP LAMAP2480_7770	diffusion facilitator family transporter
CBS2499v2 CBS2499_0433	diffusion facilitator family transporter
AWRIv2 AWRI_3926	diffusion facilitator family transporter
LAMAP LAMAP2480_7794	endo-beta-N-acetylglucosaminidase
CBS2499v2 CBS2499_2790	endo-beta-N-acetylglucosaminidase
AWRIv2 AWRI_2799	endo-beta-N-acetylglucosaminidase
LAMAP LAMAP2480_7795	translation initiation factor 3 subunit C
CBS2499v2 CBS2499_2793	translation initiation factor 3 subunit C
AWRIv2 AWRI_2796	translation initiation factor 3 subunit C
LAMAP LAMAP2480_7796	ribosomal protein RSM18, mitochondrial
CBS2499v2 CBS2499_2796	protein S18

AWRIv2 AWRI_2791	protein S18
LAMAP LAMAP2480_7798	domain-containing histone demethylation protein 1
CBS2499v2 CBS2499_2795	domain-containing histone demethylation protein 1
AWRIv2 AWRI_2793	domain-containing histone demethylation protein 1
LAMAP LAMAP2480_7813	protein
CBS2499v2 CBS2499_2492	protein
AWRIv2 AWRI_0521	protein
LAMAP LAMAP2480_7816	
CBS2499v2 CBS2499_2653	derlin-2 homolog
AWRIv2 AWRI_0463	derlin-2 homolog
LAMAP LAMAP2480_7820	uptake protein, Trk family
CBS2499v2 CBS2499_2662	uptake protein, Trk family
AWRIv2 AWRI_0454	uptake protein, Trk family
LAMAP LAMAP2480_7821	factor, CC1-like family
CBS2499v2 CBS2499_2664	factor, CC1-like family
AWRIv2 AWRI_0452	factor, CC1-like family
	subunit of the mitochondrial processing protease (MPP), essential processing enzyme that cleaves the N-terminal targeting sequences from mitochondrially imported proteins
LAMAP LAMAP2480_7826	subunit of the mitochondrial processing protease (MPP); essential processing enzyme that cleaves the N-terminal targeting sequences from mitochondrially imported proteins
	subunit of the mitochondrial processing protease (MPP); essential processing enzyme that cleaves the N-terminal targeting sequences from mitochondrially imported proteins
CBS2499v2 CBS2499_2831	subunit of the mitochondrial processing protease (MPP); essential processing enzyme that cleaves the N-terminal targeting sequences from mitochondrially imported proteins
	zinc finger-like
AWRIv2 AWRI_2753	zinc finger-like
LAMAP LAMAP2480_7828	zinc finger-like
CBS2499v2 CBS2499_2829	O-acyltransferase 2
AWRIv2 AWRI_2755	O-acyltransferase 2
LAMAP LAMAP2480_7832	O-acyltransferase 2
CBS2499v2 CBS2499_2824	protein C12C2.05c
AWRIv2 AWRI_2761	BZZ1
LAMAP LAMAP2480_7879	BZZ1
CBS2499v2 CBS2499_3525	inducer phosphatase
AWRIv2 AWRI_3338	inducer phosphatase
LAMAP LAMAP2480_7888	inducer phosphatase
CBS2499v2 CBS2499_2629	protein _0627, partial
AWRIv2 AWRI_0486	protein _0627, partial
LAMAP LAMAP2480_7901	protein _0627, partial
CBS2499v2 CBS2499_2483	NUP49/NSP49
AWRIv2 AWRI_0519	NUP49/NSP49
LAMAP LAMAP2480_7919	NUP49/NSP49
CBS2499v2 CBS2499_4417	endonuclease subunit Sen34
AWRIv2 AWRI_2090	intron endonuclease
LAMAP LAMAP2480_7924	intron endonuclease
CBS2499v2 CBS2499_4125	
AWRIv2 AWRI_4102	

LAMAP LAMAP2480_7932	required for mismatch repair in mitosis and meiosis as well as crossing over during meiosis; forms a complex with Pms1p and Msh2p-Msh3p during mismatch repair; human homolog is associated with hereditary non-polyposis colon cancer
CBS2499v2 CBS2499_4880	required for mismatch repair in mitosis and meiosis; also required for crossing over during meiosis; forms a complex with Pms1p and Msh2p-Msh3p during mismatch repair; human homolog is associated with hereditary non-polyposis colon cancer
AWRIv2 AWRI_4131	required for mismatch repair in mitosis and meiosis; also required for crossing over during meiosis; forms a complex with Pms1p and Msh2p-Msh3p during mismatch repair; human homolog is associated with hereditary non-polyposis colon cancer
LAMAP LAMAP2480_7944	reticulum transmembrane protein 1
CBS2499v2 CBS2499_2632	reticulum transmembrane protein 1
AWRIv2 AWRI_0483	protein
LAMAP LAMAP2480_8006	of 66S pre-ribosomal particles, involved in 60S ribosomal subunit biogenesis
CBS2499v2 CBS2499_2833	of 66S pre-ribosomal particles; involved in 60S ribosomal subunit biogenesis
AWRIv2 AWRI_2751	of 66S pre-ribosomal particles; involved in 60S ribosomal subunit biogenesis
LAMAP LAMAP2480_8042	transcriptional regulatory protein YLR278C
CBS2499v2 CBS2499_5034	transcriptional regulatory protein YLR278C
AWRIv2 AWRI_4186	transcriptional regulatory protein YLR278C
LAMAP LAMAP2480_8054	CoA binding protein
CBS2499v2 CBS2499_0681	protein 2
AWRIv2 AWRI_0158	protein 37
LAMAP LAMAP2480_8057	ADP-ribosylation factor GTPase-activating protein AGD5
CBS2499v2 CBS2499_0694	ADP-ribosylation factor GTPase-activating protein AGD5
AWRIv2 AWRI_0146	GTS1
LAMAP LAMAP2480_8061	converts D-xylulose and ATP to xylulose 5-phosphate and ADP; rate limiting step in fermentation of xylulose; required for xylose fermentation by recombinant S. cerevisiae strains
CBS2499v2 CBS2499_2856	converts D-xylulose and ATP to xylulose 5-phosphate and ADP; rate limiting step in fermentation of xylulose; required for xylose fermentation by recombinant S. cerevisiae strains
AWRIv2 AWRI_2926	converts D-xylulose and ATP to xylulose 5-phosphate and ADP; rate limiting step in fermentation of xylulose; required for xylose fermentation by recombinant S. cerevisiae strains
LAMAP LAMAP2480_8076	protein sorting-associated protein 27
CBS2499v2 CBS2499_3024	protein sorting-associated protein 27
AWRIv2 AWRI_1276	protein sorting-associated protein 27
LAMAP LAMAP2480_8097	mismatch repair protein HSM3
CBS2499v2 CBS2499_2175	mismatch repair protein HSM3
AWRIv2 AWRI_2874	mismatch repair protein HSM3
LAMAP LAMAP2480_8103	involved in cis-Golgi membrane traffic; v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p; required for multiple vacuolar sorting pathways
CBS2499v2 CBS2499_2821	involved in cis-Golgi membrane traffic; v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p; required for multiple vacuolar sorting pathways
AWRIv2 AWRI_2764	involved in cis-Golgi membrane traffic; v-SNARE that interacts with two t-SNARES, Sed5p and Pep12p; required for multiple vacuolar sorting pathways
LAMAP LAMAP2480_8106	finger protein

CBS2499v2 CBS2499_2817	finger protein 264
AWRIv2 AWRI_2768	finger protein 467
LAMAP LAMAP2480_8109	protein 3 homolog
CBS2499v2 CBS2499_1049	protein 3 homolog
AWRIv2 AWRI_0641	site selection protein 6
LAMAP LAMAP2480_8135	integral membrane protein required for efflux of amino acids during autophagic body breakdown in the vacuole; null mutation causes a gradual loss of viability during starvation
CBS2499v2 CBS2499_4691	integral membrane protein required for efflux of amino acids; required for efflux of amino acids during autophagic body breakdown in the vacuole; null mutation causes a gradual loss of viability during starvation
AWRIv2 AWRI_2407	integral membrane protein required for efflux of amino acids; required for efflux of amino acids during autophagic body breakdown in the vacuole; null mutation causes a gradual loss of viability during starvation
LAMAP LAMAP2480_8161	N-methyltransferase, H3 lysine-79 specific
CBS2499v2 CBS2499_4363	N-methyltransferase, H3 lysine-79 specific
AWRIv2 AWRI_1187	N-methyltransferase, H3 lysine-79 specific
LAMAP LAMAP2480_8217	family
CBS2499v2 CBS2499_4132	family
AWRIv2 AWRI_3456	exonuclease phosphatase family protein
LAMAP LAMAP2480_8224	arginine N-methyltransferase skb1
CBS2499v2 CBS2499_3273	arginine N-methyltransferase HSL7
AWRIv2 AWRI_2336	arginine N-methyltransferase HSL7
LAMAP LAMAP2480_8225	of the cytosolic iron-sulfur (FeS) protein assembly machinery, required for maturation of cytosolic and nuclear FeS proteins and for normal resistance to oxidative stress; homologous to human Narf
CBS2499v2 CBS2499_0810	of the cytosolic iron-sulfur (FeS) protein assembly machinery; required for maturation of cytosolic and nuclear FeS proteins and for normal resistance to oxidative stress; deficiency results in shortened lifespan and sensitivity to paraquat; homologous to human Narf
AWRIv2 AWRI_0052	Fe-S cluster assembly factor NAR1
LAMAP LAMAP2480_8238	utilization protein A
CBS2499v2 CBS2499_2906	utilization protein A
AWRIv2 AWRI_2979	utilization protein A
LAMAP LAMAP2480_8249	protein subunit of the glycosylphosphatidylinositol transamidase complex that adds GPIs to newly synthesized proteins; human PIG-Tp homolog
CBS2499v2 CBS2499_3032	of the glycosylphosphatidylinositol transamidase complex; transmembrane protein; adds GPIs to newly synthesized proteins; human PIG-Tp homolog
AWRIv2 AWRI_1270	of the glycosylphosphatidylinositol transamidase complex; transmembrane protein; adds GPIs to newly synthesized proteins; human PIG-Tp homolog
LAMAP LAMAP2480_8260	that binds to Hsp82p and activates its ATPase activity; similar to Hch1p; expression is regulated by stresses such as heat shock
CBS2499v2 CBS2499_3836	that binds Hsp82p and activates its ATPase activity; plays a role in determining prion variants; similar to Hch1p; expression is regulated by stresses such as heat shock; protein abundance increases in response to DNA replication stress
AWRIv2 AWRI_1825	protein C1711.08

LAMAP LAMAP2480_8266	9 superfamily member 3
CBS2499v2 CBS2499_3799	9 superfamily member 3
AWRIv2 AWRI_1108	9 superfamily member 3
LAMAP LAMAP2480_8267	monooxygenase [N-oxide-forming] 2
CBS2499v2 CBS2499_3796	monooxygenase [N-oxide-forming] 2
AWRIv2 AWRI_1111	monooxygenase [N-oxide-forming] 2
LAMAP LAMAP2480_8270	complexes subunit NGG1
CBS2499v2 CBS2499_4377	complexes subunit NGG1
AWRIv2 AWRI_4073	complexes subunit NGG1
LAMAP LAMAP2480_8294	regulator CRZ1
CBS2499v2 CBS2499_2046	regulator CRZ1
AWRIv2 AWRI_0959	regulator CRZ1
LAMAP LAMAP2480_8296	LDB17
CBS2499v2 CBS2499_2798	LDB17
AWRIv2 AWRI_2789	LDB17
	cyclin involved in cell cycle progression; activates Cdc28p to promote the G2/M transition; may be involved in DNA replication and spindle assembly; accumulates during S phase and G2, then targeted for ubiquitin-mediated degradation
LAMAP LAMAP2480_8300	
	cyclin involved in cell cycle progression; activates Cdc28p to promote the G2/M transition; may be involved in DNA replication and spindle assembly; accumulates during S phase and G2, then targeted for ubiquitin-mediated degradation; CLB4 has a paralog, CLB3, that arose from the whole genome duplication
CBS2499v2 CBS2499_2715	
	cyclin involved in cell cycle progression; activates Cdc28p to promote the G2/M transition; may be involved in DNA replication and spindle assembly; accumulates during S phase and G2, then targeted for ubiquitin-mediated degradation; CLB4 has a paralog, CLB3, that arose from the whole genome duplication
AWRIv2 AWRI_0400	complex component SEC8
LAMAP LAMAP2480_8308	complex component SEC8
CBS2499v2 CBS2499_2947	complex component SEC8
AWRIv2 AWRI_3798	complex component SEC8
	dehydrogenase, oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane
LAMAP LAMAP2480_8309	dehydrogenase; oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane
CBS2499v2 CBS2499_2948	dehydrogenase; oxidizes D-lactate to pyruvate, transcription is heme-dependent, repressed by glucose, and derepressed in ethanol or lactate; located in the mitochondrial inner membrane
AWRIv2 AWRI_3797	desaturase
LAMAP LAMAP2480_8310	desaturase
CBS2499v2 CBS2499_2949	fatty acid desaturase; required for monounsaturated fatty acid synthesis and for normal distribution of mitochondria
	fatty acid desaturase; required for monounsaturated fatty acid synthesis and for normal distribution of mitochondria
AWRIv2 AWRI_3796	membrane protein YLR326W
LAMAP LAMAP2480_8331	membrane protein YLR326W
CBS2499v2 CBS2499_0799	membrane protein YLR326W
AWRIv2 AWRI_0059	membrane protein YLR326W

LAMAP LAMAP2480_8363	protein _2160
CBS2499v2 CBS2499_5103	protein _2160
AWRiv2 AWRI_1806	protein _2160
LAMAP LAMAP2480_8380	protein of unknown function, member of the multi-drug and toxin extrusion (MATE) family of the multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) exporter superfamily
CBS2499v2 CBS2499_3025	protein of unknown function; member of the multi-drug and toxin extrusion (MATE) family of the multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) exporter superfamily
AWRiv2 AWRI_1275	efflux family protein
LAMAP LAMAP2480_8422	repeat protein required for ubiquitin-mediated protein degradation, forms complex with Cdc48p, plays a role in controlling cellular ubiquitin concentration; also promotes efficient NHEJ in postdiauxic/stationary phase
 	repeat protein required for ubiquitin-mediated protein degradation; forms a complex with Cdc48p; plays a role in controlling cellular ubiquitin concentration; also promotes efficient NHEJ in postdiauxic/stationary phase; facilitates N-terminus-dependent proteolysis of centromeric histone H3 (Cse4p) for faithful chromosome segregation; protein increases in abundance and relocalizes from nucleus to nuclear periphery upon DNA replication stress
CBS2499v2 CBS2499_0407	DOA1
AWRiv2 AWRI_3702	protein kinase; may play a role in stress response, many CA⁺⁺/calmodulan dependent phosphorylation substrates demonstrated in vitro, amino acid sequence similar to Cmk1p and mammalian Cam Kinase II
LAMAP LAMAP2480_8438	protein kinase; may play a role in stress response, many CA ⁺⁺ /calmodulan dependent phosphorylation substrates demonstrated in vitro, amino acid sequence similar to mammalian Cam Kinase II; CMK2 has a paralog, CMK1, that arose from the whole genome duplication
CBS2499v2 CBS2499_0501	protein kinase II
AWRiv2 AWRI_3856	beta SMX1
LAMAP LAMAP2480_8470	beta SMX1
CBS2499v2 CBS2499_4641	beta SMX1
AWRiv2 AWRI_1734	beta SMX1
LAMAP LAMAP2480_8487	MSS2, mitochondrial
CBS2499v2 CBS2499_1667	MSS2, mitochondrial
AWRiv2 AWRI_2177	bound inner membrane protein of the mitochondrial matrix
LAMAP LAMAP2480_8489	protein PB17E12.11
CBS2499v2 CBS2499_1669	glycosyltransferase subunit 3
AWRiv2 AWRI_2178	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 3
LAMAP LAMAP2480_8497	synthetase
CBS2499v2 CBS2499_1464	synthetase
AWRiv2 AWRI_3764	synthetase
LAMAP LAMAP2480_8505	protein _2117
CBS2499v2 CBS2499_3655	protein _2117
AWRiv2 AWRI_1778	protein
LAMAP LAMAP2480_8513	amidase C869.01
CBS2499v2 CBS2499_5041	amidase C869.01
AWRiv2 AWRI_4194	amidase C869.01
LAMAP LAMAP2480_8535	modification-related protein YNG2

CBS2499v2 CBS2499_3474	modification-related protein YNG2
AWRIv2 AWRI_4029	modification-related protein png1
LAMAP LAMAP2480_8547	protein _4537
CBS2499v2 CBS2499_2945	protein _4537
AWRIv2 AWRI_3800	protein _4537
LAMAP LAMAP2480_8553	threonine protein kinase
CBS2499v2 CBS2499_3373	kinase PKH2
AWRIv2 AWRI_4008	kinase PKH2
LAMAP LAMAP2480_8595	RING finger protein C6B12.07c
CBS2499v2 CBS2499_0411	RING finger protein C6B12.07c
AWRIv2 AWRI_3699	regulator of yeast form adherence 3
LAMAP LAMAP2480_8596	enzyme E1
CBS2499v2 CBS2499_0412	enzyme E1
AWRIv2 AWRI_3698	enzyme E1
LAMAP LAMAP2480_8609	exo-1,3-beta-glucanase; contributes to ascospore thermoresistance
CBS2499v2 CBS2499_1028	exo-1,3-beta-glucanase; contributes to ascospore thermoresistance; SPR1 has a paralog, EXG1, that arose from the whole genome duplication
AWRIv2 AWRI_0662	exo-1,3-beta-glucanase of the cell wall; involved in cell wall beta-glucan assembly; exists as three differentially glycosylated isoenzymes; EXG1 has a paralog, SPR1, that arose from the whole genome duplication
LAMAP LAMAP2480_8631	kinase par-1
CBS2499v2 CBS2499_2519	kinase par-1
AWRIv2 AWRI_0542	kinase MARK1
LAMAP LAMAP2480_8642	synthetase, catalyzes the ATP-dependent synthesis of glutathione (GSH) from gamma-glutamylcysteine and glycine; induced by oxidative stress and heat shock
CBS2499v2 CBS2499_1482	synthetase; catalyzes the ATP-dependent synthesis of glutathione (GSH) from gamma-glutamylcysteine and glycine; induced by oxidative stress and heat shock
AWRIv2 AWRI_3679	synthetase; catalyzes the ATP-dependent synthesis of glutathione (GSH) from gamma-glutamylcysteine and glycine; induced by oxidative stress and heat shock
LAMAP LAMAP2480_8656	protein L4 of the large (60S) ribosomal subunit, nearly identical to Rpl8Ap and has similarity to rat L7a ribosomal protein; mutation results in decreased amounts of free 60S subunits
CBS2499v2 CBS2499_0830	60S subunit protein L8B; required for processing of 27SA3 pre-rRNA to 27SB pre-rRNA during assembly of large ribosomal subunit; depletion leads to a turnover of pre-rRNA; L8 binds to Domain I of 25S and 5.8 S rRNAs; mutation results in decreased amounts of free 60S subunits; homologous to mammalian ribosomal protein L7A, no bacterial homolog; RPL8B has a paralog, RPL8A, that arose from the whole genome duplication
AWRIv2 AWRI_0034	60S subunit protein L8B; required for processing of 27SA3 pre-rRNA to 27SB pre-rRNA during assembly of large ribosomal subunit; depletion leads to a turnover of pre-rRNA; L8 binds to Domain I of 25S and 5.8 S rRNAs; mutation results in decreased amounts of free 60S subunits; homologous to mammalian ribosomal protein L7A, no bacterial homolog; RPL8B has a paralog, RPL8A, that arose from the whole genome duplication
LAMAP LAMAP2480_8658	proliferation transcriptional regulator
CBS2499v2 CBS2499_1933	resistance regulator 1
AWRIv2 AWRI_1628	resistance regulator 1

AWRIv2 AWRI_1605	protein _1889
LAMAP LAMAP2480_8926	protein HPODL_04743
CBS2499v2 CBS2499_2951	protein HPODL_04743
AWRIv2 AWRI_3794	protein HPODL_04743
LAMAP LAMAP2480_8927	atpase v1 domain subunit g
CBS2499v2 CBS2499_2950	ATPase, G subunit
AWRIv2 AWRI_3795	proton ATPase subunit G
LAMAP LAMAP2480_8934	protein HPODL_04360
CBS2499v2 CBS2499_4129	protein HPODL_04360
AWRIv2 AWRI_3453	beta- -n- contains wsc domain-containing protein
LAMAP LAMAP2480_8950	decarboxylase, catalyzes decarboxylation of phenylpyruvate to phenylacetaldehyde, which is the first specific step in the Ehrlich pathway
CBS2499v2 CBS2499_3061	decarboxylase; catalyzes decarboxylation of phenylpyruvate to phenylacetaldehyde, which is the first specific step in the Ehrlich pathway; involved in protein N-terminal Met and Ala catabolism
AWRIv2 AWRI_1241	decarboxylase; catalyzes decarboxylation of phenylpyruvate to phenylacetaldehyde, which is the first specific step in the Ehrlich pathway; involved in protein N-terminal Met and Ala catabolism
LAMAP LAMAP2480_9015	protein particle complex subunit 6B
CBS2499v2 CBS2499_1145	protein particle complex subunit 6B
AWRIv2 AWRI_2468	protein particle complex subunit 6A
LAMAP LAMAP2480_9038	2-dehydropantoate 2-reductase
CBS2499v2 CBS2499_1768	2-dehydropantoate 2-reductase
AWRIv2 AWRI_1456	2-reductase
LAMAP LAMAP2480_9042	MGA2
CBS2499v2 CBS2499_3200	MGA2
AWRIv2 AWRI_1919	SPT23
LAMAP LAMAP2480_9065	resistance MFS transporter, drug:H+ antiporter-2 (14 Spanner) (DHA2) family
CBS2499v2 CBS2499_4596	resistance MFS transporter, drug:H+ antiporter-2 (14 Spanner) (DHA2) family
AWRIv2 AWRI_1096	resistance MFS transporter, drug:H+ antiporter-2 (14 Spanner) (DHA2) family
LAMAP LAMAP2480_9083	and RING finger domain-containing protein C126.07c
CBS2499v2 CBS2499_3397	protein 36
AWRIv2 AWRI_3491	protein 36
LAMAP LAMAP2480_9100	transporter, sugar porter (SP) family
CBS2499v2 CBS2499_4900	transporter, sugar porter (SP) family
AWRIv2 AWRI_3974	transporter, sugar porter (SP) family
LAMAP LAMAP2480_9105	protein _3449
CBS2499v2 CBS2499_1589	protein _3449
AWRIv2 AWRI_2869	protein _3449
LAMAP LAMAP2480_9116	N-acetyltransferase 1
CBS2499v2 CBS2499_1013	N-acetyltransferase 1
AWRIv2 AWRI_0672	N-acetyltransferase 1
LAMAP LAMAP2480_9120	ribosomal protein L3, mitochondrial

CBS2499v2 CBS2499_2886	ribosomal protein of the large subunit; located in close proximity to the polypeptide exit channel of the ribosome; mutations in human homolog MRPL44 cause childhood cardiomyopathy; human MRPL44 deficiency results in inefficient assembly of the mitochondrial ribosome, and in tissue-specific respiratory chain deficiency, manifesting as either Complex I+Complex IV or Complex IV deficiency, depending on a cell type
AWRlv2 AWRI_2956	ribosomal protein of the large subunit; located in close proximity to the polypeptide exit channel of the ribosome; mutations in human homolog MRPL44 cause childhood cardiomyopathy; human MRPL44 deficiency results in inefficient assembly of the mitochondrial ribosome, and in tissue-specific respiratory chain deficiency, manifesting as either Complex I+Complex IV or Complex IV deficiency, depending on a cell type
LAMAP LAMAP2480_9123	MFS-type transporter C1271.10c
CBS2499v2 CBS2499_4684	MFS-type transporter C1271.10c
AWRlv2 AWRI_4196	MFS-type transporter C1271.10c
LAMAP LAMAP2480_9167	exchange factor SIL1
CBS2499v2 CBS2499_3023	exchange factor SIL1
AWRlv2 AWRI_1277	exchange factor SIL1
LAMAP LAMAP2480_9172	KRI1 homolog
CBS2499v2 CBS2499_4996	kri1
AWRlv2 AWRI_1477	KRI1
LAMAP LAMAP2480_9174	export protein BRR6
CBS2499v2 CBS2499_1991	export protein BRR6
AWRlv2 AWRI_1580	export protein BRR6
LAMAP LAMAP2480_9178	protein SEC72
CBS2499v2 CBS2499_2500	protein SEC72
AWRlv2 AWRI_0527	protein SEC72
LAMAP LAMAP2480_9182	protein _2243
CBS2499v2 CBS2499_3883	protein _2243
AWRlv2 AWRI_1875	protein _2243
LAMAP LAMAP2480_9187	oxidase, converts spermine to spermidine, which is required for the essential hypusination modification of translation factor eIF-5A; also involved in pantothenic acid biosynthesis
CBS2499v2 CBS2499_2269	oxidase; converts spermine to spermidine, which is required for the essential hypusination modification of translation factor eIF-5A; also involved in pantothenic acid biosynthesis
AWRlv2 AWRI_2855	protein
LAMAP LAMAP2480_9221	transport protein SEC9
CBS2499v2 CBS2499_3421	transport protein SEC9
AWRlv2 AWRI_3378	transport protein SEC9
LAMAP LAMAP2480_9223	IVY1
CBS2499v2 CBS2499_1149	IVY1
AWRlv2 AWRI_2465	IVY1
LAMAP LAMAP2480_9249	protein _3065
CBS2499v2 CBS2499_1216	protein _3065
AWRlv2 AWRI_2548	protein _3065
LAMAP LAMAP2480_9258	repeat-containing protein LWD1
CBS2499v2 CBS2499_3422	repeat-containing protein YPL247C

AWRlv2|AWRI_3377

LAMAP|LAMAP2480_9273

CBS2499v2|CBS2499_3258

AWRlv2|AWRI_2352

LAMAP|LAMAP2480_9277

CBS2499v2|CBS2499_2604

AWRlv2|AWRI_3953

LAMAP|LAMAP2480_9321

CBS2499v2|CBS2499_4219

AWRlv2|AWRI_3052

LAMAP|LAMAP2480_9334

CBS2499v2|CBS2499_4894

AWRlv2|AWRI_3968

LAMAP|LAMAP2480_9341

CBS2499v2|CBS2499_2943

AWRlv2|AWRI_3018

LAMAP|LAMAP2480_9360

CBS2499v2|CBS2499_2813

AWRlv2|AWRI_2773

LAMAP|LAMAP2480_9387

CBS2499v2|CBS2499_3043

AWRlv2|AWRI_1257

LAMAP|LAMAP2480_9397

CBS2499v2|CBS2499_3798

AWRlv2|AWRI_1109

LAMAP|LAMAP2480_9427

CBS2499v2|CBS2499_2212

AWRlv2|AWRI_2821

LAMAP|LAMAP2480_9435

CBS2499v2|CBS2499_0835

AWRlv2|AWRI_0029

LAMAP|LAMAP2480_9455

CBS2499v2|CBS2499_3037

AWRlv2|AWRI_1265

LAMAP|LAMAP2480_9513

CBS2499v2|CBS2499_0933

and CUL4-associated factor 7

RNA helicase, component of the mitochondrial degradosome along with the RNase Dss1p; the degradosome associates with the ribosome and mediates RNA turnover; also required during splicing of the COX1 A15_beta intron

RNA helicase; component of the mitochondrial degradosome along with the RNase Dss1p; the degradosome associates with the ribosome and mediates RNA turnover; also required during splicing of the COX1 A15_beta intron

RNA helicase; component of the mitochondrial degradosome along with the RNase Dss1p; the degradosome associates with the ribosome and mediates RNA turnover; also required during splicing of the COX1 A15_beta intron

protein _4704

protein _4704

protein _4704

protein _3652

protein _3652

protein _3652

MFS-type transporter C947.06c

MFS-type transporter C947.06c

MFS-type transporter C947.06c

actin-related protein involved in chromatin remodeling, component of chromatin-remodeling enzyme complexes

actin-related protein involved in chromatin remodeling; component of chromatin-remodeling enzyme complexes

protein 4

protein PIN4

protein PIN4

protein PIN4

suppression protein

suppression protein

factor

phosphatase-like protein OCA2

phosphatase-like protein OCA2

phosphatase-like protein OCA2

thioesterase 1

thioesterase 1

thioesterase-dolichyl pyrophosphate phosphatase fusion 1

protein HPODL_02291

protein HPODL_02291

protein HPODL_02291

polymerase-associated protein LEO1

polymerase-associated protein LEO1

polymerase-associated protein LEO1

binding protein

protein HPODL_02920

AWRIv2 AWRI_2494	binding protein
LAMAP LAMAP2480_9529	decarboxylase/phosphopantothenate--cysteine ligase
CBS2499v2 CBS2499_3410	decarboxylase/phosphopantothenate--cysteine ligase
AWRIv2 AWRI_3506	decarboxylase/phosphopantothenate--cysteine ligase
LAMAP LAMAP2480_9549	secreted protein
CBS2499v2 CBS2499_0821	secreted protein
AWRIv2 AWRI_0045	protein
LAMAP LAMAP2480_9566	maintenance of chromosomes protein 3
	of the multiprotein cohesin complex; required for sister chromatid cohesion in mitotic cells; also required, with Rec8p, for cohesion and recombination during meiosis; phylogenetically conserved SMC chromosomal ATPase family member
CBS2499v2 CBS2499_4036	segregation protein sudA
AWRIv2 AWRI_0309	NADPH oxidoreductase containing flavin mononucleotide (FMN), homologous to Oye3p with different ligand binding and catalytic properties; may be involved in sterol metabolism, oxidative stress response, and programmed cell death
LAMAP LAMAP2480_9577	NADPH oxidoreductase containing flavin mononucleotide (FMN); responsible for geraniol reduction into citronellol during fermentation; homologous to Oye3p with different ligand binding and catalytic properties; may be involved in sterol metabolism, oxidative stress response, and programmed cell death; protein abundance increases in response to DNA replication stress
CBS2499v2 CBS2499_4679	NADPH oxidoreductase containing flavin mononucleotide (FMN); responsible for geraniol reduction into citronellol during fermentation; homologous to Oye3p with different ligand binding and catalytic properties; may be involved in sterol metabolism, oxidative stress response, and programmed cell death; protein abundance increases in response to DNA replication stress
AWRIv2 AWRI_3177	repeat-containing protein 26
LAMAP LAMAP2480_9583	degradation protein 7
CBS2499v2 CBS2499_4690	WD repeat-containing protein C343.04c
AWRIv2 AWRI_2408	pore complex subunit
LAMAP LAMAP2480_9601	pore complex subunit
CBS2499v2 CBS2499_3412	pore complex subunit
AWRIv2 AWRI_3508	protein sorting-associated protein 17
LAMAP LAMAP2480_9606	protein sorting-associated protein 17
CBS2499v2 CBS2499_2343	protein sorting-associated protein 17
AWRIv2 AWRI_1353	protein PB24D3.06c
LAMAP LAMAP2480_9612	protein PB24D3.06c
CBS2499v2 CBS2499_3476	protein PB24D3.06c
AWRIv2 AWRI_4031	protein YEL023C
LAMAP LAMAP2480_9630	protein YEL023C
CBS2499v2 CBS2499_4995	protein YEL023C
AWRIv2 AWRI_1476	transporter PTR2
LAMAP LAMAP2480_9676	transporter PTR2
CBS2499v2 CBS2499_2913	transporter PTR2
AWRIv2 AWRI_2988	protein _0110
LAMAP LAMAP2480_9681	protein _0110
CBS2499v2 CBS2499_0758	protein
AWRIv2 AWRI_0093	

LAMAP|LAMAP2480_9797

CBS2499v2|CBS2499_3380

AWRiv2|AWRI_4001

LAMAP|LAMAP2480_9803

CBS2499v2|CBS2499_1851

AWRiv2|AWRI_2283

LAMAP|LAMAP2480_9807

CBS2499v2|CBS2499_4020

AWRiv2|AWRI_0299

LAMAP|LAMAP2480_9822

CBS2499v2|CBS2499_4019

AWRiv2|AWRI_0298

LAMAP|LAMAP2480_9845

CBS2499v2|CBS2499_0633

AWRiv2|AWRI_3633

LAMAP|LAMAP2480_9883

CBS2499v2|CBS2499_2954

AWRiv2|AWRI_3791

LAMAP|LAMAP2480_9906

CBS2499v2|CBS2499_2805

AWRiv2|AWRI_2781

LAMAP|LAMAP2480_9909

CBS2499v2|CBS2499_4015

AWRiv2|AWRI_0296

LAMAP|LAMAP2480_9943

CBS2499v2|CBS2499_3148

AWRiv2|AWRI_3546

LAMAP|LAMAP2480_9999

CBS2499v2|CBS2499_2079

AWRiv2|AWRI_0925

LAMAP|LAMAP2480_10006

CBS2499v2|CBS2499_3203

AWRiv2|AWRI_1923

LAMAP|LAMAP2480_10012

CBS2499v2|CBS2499_2879

AWRiv2|AWRI_2948

LAMAP|LAMAP2480_10061

amino acid permease, may act to supply the cell with amino acids as nitrogen source in nitrogen-poor conditions; transcription is induced under conditions of sulfur limitation; plays a role in regulating Ty1 transposition

amino acid permease; may act to supply the cell with amino acids as nitrogen source in nitrogen-poor conditions; transcription is induced under conditions of sulfur limitation; plays a role in regulating Ty1 transposition

amino acid permease; may act to supply the cell with amino acids as nitrogen source in nitrogen-poor conditions; transcription is induced under conditions of sulfur limitation; plays a role in regulating Ty1 transposition

protein _2735

protein JL09_g3762

protein _2735

fatty acid ethyl ester synthase/esterase 2

fatty acid ethyl ester synthase/esterase 2

fatty acid ethyl ester synthase/esterase 1

transporter required for normal sporulation; phosphorylated in mitochondria

transporter required for normal sporulation; phosphorylated in mitochondria; ADY2 has a paralog, ATO2, that arose from the whole genome duplication

transport outward protein 2

membrane protein PEX13

membrane protein PEX13

membrane protein PEX13

regulator protein palF/RIM8

regulator protein palF/RIM8

regulator protein palF/RIM8

ribosomal protein of the small subunit

ribosomal protein of the small subunit

ribosomal protein of the small subunit

protein _4245

protein _4245

protein _4245

protein YBR271W

N-methyltransferase EFM2

N-methyltransferase EFM2

transporter ESBP6

transporter ESBP6

transporter ESBP6

protein _3533

protein _3533

protein _3533

factor, CC1-like family

CBS2499v2 CBS2499_0736	factor, CC1-like family
AWRIv2 AWRI_0105	HRB1
LAMAP LAMAP2480_10082	MFS-type transporter C3E7.06c
CBS2499v2 CBS2499_2937	resistance MFS transporter, drug:H ⁺ antiporter-2 (14 Spanner) (DHA2) family
AWRIv2 AWRI_3010	resistance protein fnx1
LAMAP LAMAP2480_10085	domain-containing protein C19F8.03c
CBS2499v2 CBS2499_1595	domain-containing protein C19F8.03c
AWRIv2 AWRI_3612	domain-containing protein C19F8.03c
LAMAP LAMAP2480_10145	protein
CBS2499v2 CBS2499_4250	protein _1801
AWRIv2 AWRI_1523	protein _1801
LAMAP LAMAP2480_10163	ribonuclease POP2
CBS2499v2 CBS2499_1584	ribonuclease POP2
AWRIv2 AWRI_2860	ribonuclease POP2
LAMAP LAMAP2480_10165	protein _4061
CBS2499v2 CBS2499_3415	protein _4061
AWRIv2 AWRI_3384	protein _4061
LAMAP LAMAP2480_10264	biogenesis
CBS2499v2 CBS2499_2631	biogenesis
AWRIv2 AWRI_0484	biogenesis
LAMAP LAMAP2480_10338	enzyme E2-34 kDa
CBS2499v2 CBS2499_0717	enzyme E2-34 kDa
AWRIv2 AWRI_0122	enzyme E2-34 kDa
LAMAP LAMAP2480_10354	acetate-hydrolyzing esterase
CBS2499v2 CBS2499_4592	acetate-hydrolyzing esterase
AWRIv2 AWRI_1094	acetate-hydrolyzing esterase
LAMAP LAMAP2480_10358	acetate-hydrolyzing esterase, required in balance with alcohol acetyltransferase to maintain optimal amounts of isoamyl acetate, which is particularly important in sake brewing
CBS2499v2 CBS2499_4354	acetate-hydrolyzing esterase; required in balance with alcohol acetyltransferase to maintain optimal amounts of isoamyl acetate, which is particularly important in sake brewing
AWRIv2 AWRI_2582	acetate-hydrolyzing esterase; required in balance with alcohol acetyltransferase to maintain optimal amounts of isoamyl acetate, which is particularly important in sake brewing
LAMAP LAMAP2480_10376	phosphatase, phosphatase domain
CBS2499v2 CBS2499_1504	acid phosphatase
AWRIv2 AWRI_3693	acid phosphatase
LAMAP LAMAP2480_10381	repair protein rad21
CBS2499v2 CBS2499_2811	subunit rad21
AWRIv2 AWRI_2775	subunit rad21
LAMAP LAMAP2480_10435	N-lysine methyltransferase 3
CBS2499v2 CBS2499_2941	protein C16C6.01c
AWRIv2 AWRI_3015	protein
LAMAP LAMAP2480_10452	protein _0236
CBS2499v2 CBS2499_3344	protein MIG1
AWRIv2 AWRI_0193	protein _0236

LAMAP LAMAP2480_10465	RNA-processing protein 14
CBS2499v2 CBS2499_2732	RNA-processing protein 14
AWRIv2 AWRI_0382	of pre-ribosomal ribosomal biogenesis
LAMAP LAMAP2480_10475	protein HPODL_03882
CBS2499v2 CBS2499_3555	protein HPODL_03882
AWRIv2 AWRI_3902	protein _4647
	protein of unknown function; sequence similarity to bacterial and human gluconokinase; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; upregulated by deletion of the RNAP-II associated factor, PAF1
LAMAP LAMAP2480_10482	
CBS2499v2 CBS2499_3249	gluconokinase; sequence similarity to bacterial and human gluconokinase; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; upregulated by deletion of the RNAP-II associated factor, PAF1
AWRIv2 AWRI_2358	gluconokinase; sequence similarity to bacterial and human gluconokinase; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; upregulated by deletion of the RNAP-II associated factor, PAF1
LAMAP LAMAP2480_10525	to glucose repression protein 1
CBS2499v2 CBS2499_2453	to glucose repression protein 1
AWRIv2 AWRI_0506	protein _0604
LAMAP LAMAP2480_10536	URE2
CBS2499v2 CBS2499_2916	S-transferase 1
AWRIv2 AWRI_2994	S-transferase 1
LAMAP LAMAP2480_10581	protein PIG2
CBS2499v2 CBS2499_2692	phosphatase 1 regulatory subunit 3C
AWRIv2 AWRI_0424	phosphatase 1 regulatory subunit 3C
LAMAP LAMAP2480_10613	initiation factor IIA large subunit
CBS2499v2 CBS2499_0445	initiation factor IIA large subunit
AWRIv2 AWRI_3920	initiation factor IIA large subunit
LAMAP LAMAP2480_10671	methyltransferase EFM1
	methyltransferase; involved in the monomethylation of eEF1A (Tef1p/Tef2p); SET-domain family member; predicted involvement in ribosome biogenesis; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm
CBS2499v2 CBS2499_3582	N-methyltransferase EFM1
AWRIv2 AWRI_4153	phosphatase regulatory subunit
LAMAP LAMAP2480_10700	phosphatase 1 regulatory subunit 3C
CBS2499v2 CBS2499_4078	phosphatase 1 regulatory subunit 3C
AWRIv2 AWRI_2726	phosphatase 1 regulatory subunit 3C
LAMAP LAMAP2480_10719	of the Golgi involved in protein mannosylation
CBS2499v2 CBS2499_2623	2-alpha-mannosyltransferase 2
AWRIv2 AWRI_0492	2-alpha-mannosyltransferase 2
LAMAP LAMAP2480_10745	protein
CBS2499v2 CBS2499_4039	protein
AWRIv2 AWRI_0314	protein
LAMAP LAMAP2480_10774	regulatory protein SDS3
CBS2499v2 CBS2499_0634	regulatory protein SDS3
AWRIv2 AWRI_3634	of defective silencing

LAMAP LAMAP2480_10791	domain
CBS2499v2 CBS2499_2643	protein _0569
AWRIv2 AWRI_0472	protein _0569
LAMAP LAMAP2480_10799	protein of unknown function
	membrane protein kinase; negatively regulates membrane fusion; associates with vacuolar membrane through palmitoylation of one or more cysteines in consensus sequence; vacuolar membrane association is essential to its kinase activity; mutant shows defect in CPY processing; ortholog of human serine/threonine kinase 16 (STK16)
CBS2499v2 CBS2499_1627	kinase ENV7
AWRIv2 AWRI_2143	glutamine amidotransferase YLR126C
LAMAP LAMAP2480_10880	glutamine amidotransferase-like protein C13C5.04
CBS2499v2 CBS2499_2934	glutamine amidotransferase YLR126C
AWRIv2 AWRI_3007	carrier protein
LAMAP LAMAP2480_10901	carrier protein
CBS2499v2 CBS2499_1542	carrier protein
AWRIv2 AWRI_2665	protein _0517
LAMAP LAMAP2480_11053	protein _0517
CBS2499v2 CBS2499_2691	protein _0517
AWRIv2 AWRI_0426	protein 16
LAMAP LAMAP2480_11096	protein 16
CBS2499v2 CBS2499_3650	protein 16
AWRIv2 AWRI_1774	protein 16
	reductase, part of the dTTP biosynthetic pathway, involved in folate metabolism, possibly required for mitochondrial function
LAMAP LAMAP2480_11147	reductase involved in tetrahydrofolate biosynthesis; required for respiratory metabolism
CBS2499v2 CBS2499_3234	reductase involved in tetrahydrofolate biosynthesis; required for respiratory metabolism
AWRIv2 AWRI_1949	activator HAC1
LAMAP LAMAP2480_11165	activator HAC1
CBS2499v2 CBS2499_4799	activator HAC1
AWRIv2 AWRI_1012	activator HAC1
LAMAP LAMAP2480_11174	phospholipase C
CBS2499v2 CBS2499_2860	phospholipase C
AWRIv2 AWRI_2930	phospholipase C
LAMAP LAMAP2480_11311	shifted protein
CBS2499v2 CBS2499_3409	shifted protein
AWRIv2 AWRI_3503	shifted protein
LAMAP LAMAP2480_11318	deacetylase 1
CBS2499v2 CBS2499_4597	deacetylase 1
AWRIv2 AWRI_1097	deacetylase 1
	involved in transcription initiation at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p
LAMAP LAMAP2480_11336	
	involved in transcription initiation; functions at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p; BDF1 has a paralog, BDF2, that arose from the whole genome duplication
CBS2499v2 CBS2499_4126	

AWRlv2 AWRI_4103	involved in transcription initiation; functions at TATA-containing promoters; associates with the basal transcription factor TFIID; contains two bromodomains; corresponds to the C-terminal region of mammalian TAF1; redundant with Bdf2p; BDF1 has a paralog, BDF2, that arose from the whole genome duplication
LAMAP LAMAP2480_11457	of the septin ring of the mother-bud neck that is required for cytokinesis; septins recruit proteins to the neck and can act as a barrier to diffusion at the membrane, and they comprise the 10nm filaments seen with EM
CBS2499v2 CBS2499_3119	of the septin ring that is required for cytokinesis; septins are GTP-binding proteins that assemble into rod-like hetero-oligomers that can associate with other rods to form filaments; septin rings at the mother-bud neck act as scaffolds for recruiting cell division factors and as barriers to prevent diffusion of specific proteins between mother and daughter cells
AWRlv2 AWRI_3748	of the septin ring that is required for cytokinesis; septins are GTP-binding proteins that assemble into rod-like hetero-oligomers that can associate with other rods to form filaments; septin rings at the mother-bud neck act as scaffolds for recruiting cell division factors and as barriers to prevent diffusion of specific proteins between mother and daughter cells
LAMAP LAMAP2480_11474	subunit (19 kDa), involved in RNA polymerase II transcription initiation, similar to histone H4 with atypical histone fold motif of Spt3-like transcription factors
CBS2499v2 CBS2499_3161	initiation factor TFIID subunit 13
AWRlv2 AWRI_3561	initiation factor TFIID subunit 13
LAMAP LAMAP2480_11483	protein _1406
CBS2499v2 CBS2499_3714	protein _1406
AWRlv2 AWRI_1173	protein _1406
LAMAP LAMAP2480_11519	protein
CBS2499v2 CBS2499_2654	protein
AWRlv2 AWRI_0462	protein
LAMAP LAMAP2480_11530	of the mitochondrial inner membrane, involved in turnover of membrane-embedded proteins; member of a family of predicted membrane-bound metallopeptidases in prokaryotes and higher eukaryotes
CBS2499v2 CBS2499_1891	metalloendopeptidase OMA1
AWRlv2 AWRI_3992	metalloendopeptidase OMA1
LAMAP LAMAP2480_11598	protein _3253
CBS2499v2 CBS2499_3604	protein _3253
AWRlv2 AWRI_2701	protein _3253
LAMAP LAMAP2480_11611	protein _0863
CBS2499v2 CBS2499_0987	protein _0863
AWRlv2 AWRI_0705	protein _0863
LAMAP LAMAP2480_11649	aminotransferase C660.12c
CBS2499v2 CBS2499_4721	sulfoxide lyase
AWRlv2 AWRI_2431	sulfoxide lyase
LAMAP LAMAP2480_11729	dioxygenase
CBS2499v2 CBS2499_2690	dioxygenase CDG1
AWRlv2 AWRI_0427	dioxygenase CDG1
LAMAP LAMAP2480_11738	methyltransferase subunit
CBS2499v2 CBS2499_2717	methyltransferase subunit

AWRIv2 AWRI_0398	methyltransferase subunit
LAMAP LAMAP2480_11912	up-regulated gene 14 protein
CBS2499v2 CBS2499_2779	up-regulated gene 14 protein
AWRIv2 AWRI_0333	4-epimerase
LAMAP LAMAP2480_11956	acidic ribosomal protein P1-alpha
CBS2499v2 CBS2499_2135	acidic ribosomal protein P1-alpha
AWRIv2 AWRI_0872	acidic ribosomal protein P1-alpha
LAMAP LAMAP2480_11990	(Like Sm) protein; forms heteroheptameric complex (with Lsm2p, Lsm3p, Lsm4p, Lsm5p, Lsm6p, and Lsm7p) involved in degradation of cytoplasmic mRNAs
	(Like Sm) protein; forms heteroheptameric complex (with Lsm2p, Lsm3p, Lsm4p, Lsm5p, Lsm6p, and Lsm7p) involved in degradation of cytoplasmic mRNAs; also enters the nucleus and positively regulates transcription initiation; unlike most Sm-like proteins, Lsm1p requires both its SM-domain and C-terminal domain for RNA- binding; binds to mRNAs under glucose starvation, most often in the 3' UTR; forms cytoplasmic foci upon DNA replication stress
CBS2499v2 CBS2499_2719	(Like Sm) protein; forms heteroheptameric complex (with Lsm2p, Lsm3p, Lsm4p, Lsm5p, Lsm6p, and Lsm7p) involved in degradation of cytoplasmic mRNAs; also enters the nucleus and positively regulates transcription initiation; unlike most Sm-like proteins, Lsm1p requires both its SM-domain and C-terminal domain for RNA- binding; binds to mRNAs under glucose starvation, most often in the 3' UTR; forms cytoplasmic foci upon DNA replication stress
AWRIv2 AWRI_0396	of the TOM (translocase of outer membrane) complex responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins
LAMAP LAMAP2480_12039	of the TOM (translocase of outer membrane) complex; responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins
CBS2499v2 CBS2499_3393	of the TOM (translocase of outer membrane) complex; responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins
AWRIv2 AWRI_3488	of the TOM (translocase of outer membrane) complex; responsible for recognition and initial import steps for all mitochondrially directed proteins; acts as a receptor for incoming precursor proteins