"Reconstruction and Validation of Saccharomyces cerevisiae iND750, a Fully Compartmentalized Genome-scale Metabolic Model"

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Supplementary Material

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ABBREVIATION	REACTION NAME	REACTION Reactions that occur entirely within one compartment have a compartmental abbreviation at the beginning of the equation. Otherwise, metabolite location is noted immediately after its abbreviation. Compartment Abbreviations [c] : cytosol [e] : extracellular [g] : Golgi appratus [m] : mitochondrion [n] : nucleus [r] : endoplasmic reticulum [v] : vacoule [x] : peroxisome	E.C. #	SUBSYSTEM	ORF	PROTEIN
HCO3En	HCO3 equilibrium reaction, nuclear	[n] : co2 + h2o <==> h + hco3		--		
HCO3Em	HCO3 equilibration reaction, mitochondrial	[m] : co2 + h2o <==> h + hco3		--		
HCO3E	HCO3 equilibration reaction	[c] : co2 + h2o <==> h + hco3		--		
HCYSMT	homocysteine S-methyltransferase	[c] : amet + hcys-L --> ahcys + h + met-L	EC-2.1.1.10	Alanine and aspartate metabolism	(YPL273W or YLL062C)	(Sam4) or (Mht1)
CSNATirm	carnitine O-acetyltransferase, reverse direction, mitochondrial	[m] : accoa + crn --> acrn + coa	EC-2.3.1.7	Alanine and aspartate metabolism	YML042W	Cat2-m
CSNATifm	carnitine O-aceyltransferase, forward reaction, mitochondrial	[m] : acrn + coa --> accoa + crn	EC-2.3.1.7	Alanine and aspartate metabolism	YAR035W	Yat1-m
CSNAT	carnitine O-acetyltransferase	[c] : accoa + crn --> acrn + coa	EC-2.3.1.7	Alanine and aspartate metabolism		
ASPTRSm	Aspartyl-tRNA synthetase, mitochondrial	[m] : asp-L + atp + trnaasp --> amp + asptrna + ppi	EC-6.1.1.12	Alanine and aspartate metabolism	YPL104W	Msd1-m
ASPTRS	Aspartyl-tRNA synthetase	[c] : asp-L + atp + trnaasp --> amp + asptrna + ppi	EC-6.1.1.12	Alanine and aspartate metabolism	YLL018C	Dps1
ASPTAp	aspartate transaminase, peroxisomal	[x] : akg + asp-L <==> glu-L + oaa	EC-2.6.1.1	Alanine and aspartate metabolism	YLR027C	Aat2-p
ASPTAm	aspartate transaminase, mitochondrial	[m] : akg + asp-L <==> glu-L + oaa	EC-2.6.1.1	Alanine and aspartate metabolism	YKL106W	Aat1-m
ASPTA	aspartate transaminase	[c] : akg + asp-L <==> glu-L + oaa	EC-2.6.1.1	Alanine and aspartate metabolism	YLR027C	Aat2
ASPKi	aspartate kinase, irreversible	[c] : asp-L + atp --> 4pasp + adp	EC-2.7.2.4	Alanine and aspartate metabolism	YER052C	Hom3
ASNS1	asparagine synthase (glutamine-hydrolysing)	[c] : asp-L + atp + gln-L + h2o --> amp + asn-L + glu-L + h + ppi	EC-6.3.5.4	Alanine and aspartate metabolism	(YGR124W or YPR145W or YML096W)	(Asn2) or (Asn1) or (Asn3)
ASADi	aspartate-semialdehyde dehydrogenase, irreversible	[c] : 4pasp + h + nadph --> aspsa + nadp + pi	EC-1.2.1.11	Alanine and aspartate metabolism	YDR158W	Hom2
ALATRS	Alanyl-tRNA synthetase	[c] : ala-L + atp + trnaala --> alatrna + amp + ppi	EC-6.1.1.7	Alanine and aspartate metabolism	YOR335C	Ala1
ALATA_Lm	L-alanine transaminase, mitochondrial	[m] : akg + ala-L <==> glu-L + pyr	EC-2.6.1.2	Alanine and aspartate metabolism	YLR089C	Alt2-m
ALATA_L	L-alanine transaminase	[c] : akg + ala-L <==> glu-L + pyr	EC-2.6.1.2	Alanine and aspartate metabolism	YDR111C	Alt1
TREHv	alpha,alpha-trehalase, vacuolar	[v] : h2o + tre --> (2) glc-D	EC-3.2.1.28	Alternate Carbon Metabolism	YPR026W	Ath1-v
TREH	alpha,alpha-trehalase	[c] : h2o + tre --> (2) glc-D	EC-3.2.1.28	Alternate Carbon Metabolism	(YDR001C or YBR001C)	(Nth1) or (Nth2)
TRE6PS	alpha,alpha-trehalose-phosphate synthase (UDP-forming)	[c] : g6p + udpg --> h + tre6p + udp	EC-2.4.1.15	Alternate Carbon Metabolism	((YBR126C and YDR074W and YML100W) or (YBR126C and YDR074W and YMR261C))	(Tpsl) or (Tps3)
TRE6PP	trehalose-phosphatase	[c] : h2o + tre6p --> pi + tre	EC-3.1.3.12	Alternate Carbon Metabolism	((YBR126C and YDR074W and YML100W) or (YBR126C and YDR074W and YMR261C))	(Tpsl) or (Tps3)
SUCRe	sucrose hydrolyzing enxyme, extracellular	[e] : h2o + sucr --> fru + glc-D	EC-3.2.1.26	Alternate Carbon Metabolism	YIL162W	Suc2-e
SBTR	D-sorbitol reductase	[c] : glc-D + h + nadph --> nadp + sbt-D	EC-1.1.1.21	Alternate Carbon Metabolism	YHR104W	Gre3
SBTD_L	L-sorbitol dehydrogenase (L-sorbose-producing)	[c] : nad + sbt-L --> h + nadh + srb-L	EC-1.1.1.14	Alternate Carbon Metabolism	YJR159W	Sor1
SBTD_D2	D-sorbitol dehydrogenase (D-fructose producing)	[c] : nad + sbt-D --> fru + h + nadh	EC-1.1.1.14	Alternate Carbon Metabolism	YJR159W	Sor1
LGTHL	lactoylglutathione lyase	[c] : gthrd + mthgxl --> lgt-S	EC-4.4.1.5	Alternate Carbon Metabolism	YML004C	Glo1
L-LACDm	L-Lactate dehydrogenase, mitochondrial	[m] : (2) ficytc + lac-L --> (2) focytc + pyr	EC-1.1.2.3	Alternate Carbon Metabolism	YML054C	Cyb2-m
GLYOXm	hydroxyacylglutathione hydrolase, mitochondrial	[m] : h2o + lgt-S --> gthrd + h + lac-D	EC-3.1.2.6	Alternate Carbon Metabolism	YOR040W	Glo4-m
GLYOX	hydroxyacylglutathione hydrolase	[c] : h2o + lgt-S --> gthrd + h + lac-D	EC-3.1.2.6	Alternate Carbon Metabolism	YDR272W	Glo2
GLYGS	glycogen (starch) synthase	[c] : h2o + udpg --> 14glun + h + udp	EC-2.4.1.11	Alternate Carbon Metabolism	(YFR015C or YLR258W)	(Gsy1) or (Gsy2)
GLCS2	glycogen synthase (UDPGlc)	[c] : udpg --> glycogen + h + udp	EC-2.4.1.11	Alternate Carbon Metabolism	(YFR015C or YLR258W)	(Gsy1) or (Gsy2)
GLCP	glycogen phosphorylase	[c] : glycogen + pi --> g1p	EC-2.4.1.1	Alternate Carbon Metabolism	YPR160W	Gph1
GBEZ	1,4-alpha-glucan branching enzyme	[c] : 14glun --> glycogen + h2o	EC-2.4.1.18	Alternate Carbon Metabolism	YEL011W	Glc3
D-LACDm	D-lactate dehydrogenase, mitochondrial	[m] : (2) ficytc + lac-D --> (2) focytc + pyr	EC-1.1.2.4	Alternate Carbon Metabolism	YDL174C	Dld1-m
13GS	1,3-beta-glucan synthase	[c] : udpg --> 13BDglcn + h + udp	EC-2.4.1.34	Alternate Carbon Metabolism	((YCR034W and YGR032W) or (YCR034W and YLR342W) or (YCR034W and YMR306W))	(Bdgs1) or (Bdgs2) or (Bdgs3)
CHTNDA	chitin deacetylase	[c] : chitin + h2o --> ac + chitos + h	EC-3.5.1.41	Aminosugars Metabolism	(YLR307W or YLR308W)	(Cda1) or (Cda2)
PPCK	phosphoenolpyruvate carboxykinase	[c] : atp + oaa --> adp + co2 + pep	EC-4.1.1.49	Anaplerotic reactions	YKR097W	Pck1
PC	pyruvate carboxylase	[c] : atp + hco3 + pyr --> adp + h + oaa + pi	EC-6.4.1.1	Anaplerotic reactions	(YGL062W or YBR218C)	(Pyc1) or (Pyc2)
ME2m	malic enzyme (NADP), mitochondrial	[m] : mal-L + nadp --> co2 + nadph + pyr	EC-1.1.1.40	Anaplerotic reactions	YKL029C	Mae1-m
ME1m	malic enzyme (NAD), mitochondrial	[m] : mal-L + nad --> co2 + nadh + pyr	EC-1.1.1.38	Anaplerotic reactions	YKL029C	Mae1-m
MCITS	2-methylcitrate synthase	[c] : h2o + oaa + ppcoa --> 2mcit + coa + h	EC-4.1.3.31	Anaplerotic reactions		
MCITLm	methyisocitrate lyase, mitochondrial	[m] : 2mcit --> pyr + succ	EC-4.1.3.30	Anaplerotic reactions	YPR006C	Icl2
MALSp	malate synthase, peroxisomal	[x] : accoa + glx + h2o --> coa + h + mal-L	EC-4.1.3.2	Anaplerotic reactions	(YIR031C or YNL117W)	(Dal7-p) or (Mls1-p)
ICL	Isocitrate lyase	[c] : icit --> glx + succ	EC-4.1.3.1	Anaplerotic reactions	YER065C	Icl1
FBP	fructose-bisphosphatase	[c] : fdp + h2o --> f6p + pi	EC-3.1.3.11	Anaplerotic reactions	YLR377C	Fbp1
ARABR	arabinose reductase	[c] : arab-L + h + nadph --> abt + nadp	EC-1.1.1.21	Arabinose Metabolism	YHR104W	Gre3
ARAB1D2	D-arabinose 1-dehydrogenase (NADP)	[c] : arab-D + nadp --> Dara14lac + h + nadph	EC-	Arabinose Metabolism	YBR149W	Ara1
ARAB1D1	D-arabinose 1-dehydrogenase (NAD)	[c] : arab-D + nad --> Dara14lac + h + nadh	EC-	Arabinose Metabolism	YBR149W	Ara1
SPRMS	spermine synthase	[c] : ametam + spmd --> 5mta + h + sprm	EC-2.5.1.22	Arginine and Proline Metabolism	YLR146C	Spe4
SPMS	spermidine synthase	[c] : ametam + ptrc --> 5mta + h + spmd	EC-2.5.1.16	Arginine and Proline Metabolism	YPR069C	Spe3
PROTRS	Prolyl-tRNA synthetase	[c] : atp + pro-L + trnapro --> amp + ppi + protrna	EC-6.1.1.15	Arginine and Proline Metabolism	(YER087W or YHR020W)	(Prt1) or (Prt2)
PRO1xm	proline oxidase (NAD), mitochondrial	[m] : nad + pro-L --> 1pyr5c + (2) h + nadh		Arginine and Proline Metabolism	YLR142W	Put1-m

PHCHGSm	L-1-Pyrroline-3-hydroxy-5-carboxylate spontaneous conversion to L-4-	[m] : 1p3h5c + h + h2o <==> 4hglusa		Arginine and Proline Metabolism		
PHCDm	L-1-pyrroline-3-hydroxy-5-carboxylate dehydrogenase, mitochondrial	[m] : 1p3h5c + (2) h2o + nad --> e4hglu + h + nadh	EC-1.5.1.12	Arginine and Proline Metabolism	YHR037W	Put2-m
P5CR	pyrroline-5-carboxylate reductase	[c] : 1pyr5c + (2) h + nadph --> nadp + pro-L	EC-1.5.1.2	Arginine and Proline Metabolism	YER023W	Pro3
ORNTACim	ornithine transacetylase, irreversible, mitochondrial	[m] : acorn + glu-L --> acglu + orn	EC-2.3.1.35	Arginine and Proline Metabolism	YMR062C	Ecm40-m
ORNTA	ornithine transaminase	[c] : akg + orn --> glu-L + glu5sa	EC-2.6.1.13	Arginine and Proline Metabolism	YLR438W	Car2
ORNDC	Ornithine Decarboxylase	[c] : h + orn --> co2 + ptrc	EC-4.1.1.17	Arginine and Proline Metabolism	YKL184W	Spe1
OCBTi	ornithine carbamoyltransferase, irreversible	[c] : cbp + orn --> citr-L + h + pi	EC-2.1.3.3	Arginine and Proline Metabolism	YJL088W	Arg3
HPROym	L-hydroxyproline dehydrogenase (NADP), mitochondrial	[m] : 4hpro-LT + nadp --> 1p3h5c + (2) h + nadph	EC-1.5.1.12	Arginine and Proline Metabolism	YHR037W	Put2-m
HPROxm	L-hydroxyproline dehydrogenase (NAD), mitochondrial	[m] : 4hpro-LT + nad --> 1p3h5c + (2) h + nadh	EC-1.5.1.12	Arginine and Proline Metabolism	YHR037W	Put2-m
HPROb	L-hydroxyproline reductase (NADP)	[c] : 1p3h5c + (2) h + nadph --> 4hpro-LT + nadp	EC-1.5.1.2	Arginine and Proline Metabolism	YER023W	Pro3
HPROa	L-hydroxyproline reductase (NAD)	[c] : 1p3h5c + (2) h + nadh --> 4hpro-LT + nad	EC-1.5.1.2	Arginine and Proline Metabolism	YER023W	Pro3
GLU5K	glutamate 5-kinase	[c] : atp + glu-L --> adp + glu5p	EC-2.7.2.11	Arginine and Proline Metabolism	YDR300C	Pro1
G5SD2	glutamate-5-semialdehyde dehydrogenase	[c] : glu5p + h + nadh --> glu5sa + nad + pi	EC-1.2.1.41	Arginine and Proline Metabolism	YOR323C	Pro2
G5SD	glutamate-5-semialdehyde dehydrogenase	[c] : glu5p + h + nadph --> glu5sa + nadp + pi	EC-1.2.1.41	Arginine and Proline Metabolism	YOR323C	Pro2
G5SADrm	L-glutamate 5-semialdehyde dehydratase, reversible, mitochondrial	[m] : glu5sa <==> 1pyr5c + h + h2o		Arginine and Proline Metabolism		
G5SADr	L-glutamate 5-semialdehyde dehydratase, reversible	[c] : glu5sa <==> 1pyr5c + h + h2o		Arginine and Proline Metabolism		
EHGLATp	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase, peroxisomal	[x] : akg + e4hglu --> 4h2oglt + glu-L	EC-2.6.1.1	Arginine and Proline Metabolism	YLR027C	Aat2-p
EHGLATm	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase, mitochondrial	[m] : akg + e4hglu --> 4h2oglt + glu-L	EC-2.6.1.1	Arginine and Proline Metabolism	YKL106W	Aat1-m
EHGLAT	L-erythro-4-Hydroxyglutamate:2-oxoglutarate aminotransferase	[c] : akg + e4hglu --> 4h2oglt + glu-L	EC-2.6.1.1	Arginine and Proline Metabolism	YLR027C	Aat2
DXHPScm	deoxyhypusine synthase, cytosolic/mitochondrial	h2o[c] + q6[m] + spmd[c] --> 13dampp[c] + 4abutn[c] + q6h2[m]	EC-1.5.99.6	Arginine and Proline Metabolism	YHR068W	Dys1
CBPSn	carbamoyl-phosphate synthase (glutamine-hydrolysing), nuclear	[n] : (2) atp + gln-L + h2o + hco3 --> (2) adp + cbp + glu-L + (2) h + pi	EC-6.3.5.5	Arginine and Proline Metabolism	YJL130C	Ura2-n
CBPS	carbamoyl-phosphate synthase (glutamine-hydrolysing)	[c] : (2) atp + gln-L + h2o + hco3 --> (2) adp + cbp + glu-L + (2) h + pi	EC-6.3.5.5	Arginine and Proline Metabolism	(YJR109C and YOR303W)	Cpa
ARGTRSm	Arginyl-tRNA synthetase, mitochondrial	[m] : arg-L + atp + trnaarg --> amp + argtrna + ppi	EC-6.1.1.19	Arginine and Proline Metabolism	YHR091C	Msr1-m
ARGTRS	Arginyl-tRNA synthetase	[c] : arg-L + atp + trnaarg --> amp + argtrna + ppi	EC-6.1.1.19	Arginine and Proline Metabolism	YDR341C	Msr2
ARGSSr	argininosuccinate synthase, reversible	[c] : asp-L + atp + citr-L <==> amp + argsuc + h + ppi	EC-6.3.4.5	Arginine and Proline Metabolism	YOL058W	Arg1
ARGSL	argininosuccinate lyase	[c] : argsuc <==> arg-L + fum	EC-4.3.2.1	Arginine and Proline Metabolism	YHR018C	Arg4
ARGN	arginase	[c] : arg-L + h2o --> orn + urea	EC-3.5.3.1	Arginine and Proline Metabolism	YPL111W	Car1
AMID	amidase	[c] : 4gudbd + h2o --> 4gudbutn + nh4	EC-3.5.1.4	Arginine and Proline Metabolism	(YMR293C or YDR242W)	(Amd4) or (Amd2)
AGPRim	N-acetyl-g-glutamyl-phosphate reductase, irreversible, mitochondrial	[m] : acg5p + h + nadph --> acg5sa + nadp + pi	EC-1.2.1.38	Arginine and Proline Metabolism	YER069W	Arg5-m
ADMDC	adenosylmethionine decarboxylase	[c] : amet + h --> ametam + co2	EC-4.1.1.50	Arginine and Proline Metabolism	YOL052C	Spe2
ACOTAim	acteylornithine transaminase, irreversible, mitochondrial	[m] : acg5sa + glu-L --> acorn + akg	EC-2.6.1.11	Arginine and Proline Metabolism	YOL140W	Arg8-m
ACGSm	N-acteylglutamate synthase, mitochondrial	[m] : accoa + glu-L --> acglu + coa + h	EC-2.3.1.1	Arginine and Proline Metabolism	(YMR062C or YJL071W)	(Ecm40-m) or (Arg2-m)
ACGKm	acetylglutamate kinase, mitochondrial	[m] : acglu + atp --> acg5p + adp	EC-2.7.2.8	Arginine and Proline Metabolism	YER069W	Arg5-m
4HGLSDm	L-4-hydroxyglutamate semialdehyde dehydrogenase, mitochondrial	[m] : 4hglusa + h2o + nad <==> e4hglu + (2) h + nadh	EC-1.5.1.12	Arginine and Proline Metabolism	YHR037W	Put2-m
ASNTRSm	asparaginyl-tRNA synthetase, miotchondrial	[m] : asn-L + atp + trnaasn --> amp + asntrna + ppi	EC-6.1.1.22	Asparagine metabolism	YCR024C	Ded82-m
ASNTRS	Asparaginyl-tRNA synthetase	[c] : asn-L + atp + trnaasn --> amp + asntrna + ppi	EC-6.1.1.22	Asparagine metabolism	YHR019C	Ded81
ASNNe	L-asparaginase, extracellular	[e] : asn-L + h2o --> asp-L + nh4	EC-3.5.1.1	Asparagine metabolism	(YLR160C or YLR158C or YLR157C or YLR155C)	(Asp34-e) or (Asp33-e) or (Asp32-e) or (Asp31-e)
ASNN	L-asparaginase	[c] : asn-L + h2o --> asp-L + nh4	EC-3.5.1.1	Asparagine metabolism	YDR321W	Asp1
SUCOAS1m	Succinate--CoA ligase (ADP-forming), mitochondrial	[m] : atp + coa + succ <==> adp + pi + succoa	EC-6.2.1.4	Citrate Cycle (TCA)	(YGR244C and YOR142W)	Lsc-m
SUCD2_u6m	succinate dehydrogenase (ubiquinone-6), mitochondrial	[m] : q6 + succ <==> fum + q6h2	EC-1.3.5.1	Citrate Cycle (TCA)	((YDR178W and YKL141W and YKL148C and YLL041C) or (YKL141W and YKL148C and YLL041C and YLR164W) or (YDR178W and YKL148C and YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C))	(Sdh-m) or (Sdh2-m) or (Sdh3-m) or (Sdh4-m)
ITCOALm	Itaconate--CoA ligase (ADP-forming), mitochondrial	[m] : atp + coa + itacon <==> adp + itaccoa + pi	EC-6.2.1.5	Citrate Cycle (TCA)	(YGR244C and YOR142W)	Lsc-m
ICDHyp	Isocitrate dehydrogenase (NADP+), peroxisomal	[x] : icit + nadp --> akg + co2 + nadph	EC-1.1.1.42	Citrate Cycle (TCA)	YNL009W	Idp3-p
ICDHym	Isocitrate dehydrogenase (NADP+), mitochondrial	[m] : icit + nadp --> akg + co2 + nadph	EC-1.1.1.42	Citrate Cycle (TCA)	YDL066W	Idp1-m
ICDHy	isocitrate dehydrogenase (NADP)	[c] : icit + nadp --> akg + co2 + nadph	EC-1.1.1.42	Citrate Cycle (TCA)	YLR174W	Idp2
ICDHxm	Isocitrate dehydrogenase (NAD+), mitochondrial	[m] : icit + nad --> akg + co2 + nadh	EC-1.1.1.41	Citrate Cycle (TCA)	(YNL037C and YOR136W)	Idh-m
CSp	citrate synthase, peroxisomal	[x] : accoa + h2o + oaa --> cit + coa + h	EC-4.1.3.7	Citrate Cycle (TCA)	YCR005C	Cit2-p
CSm	citrate synthase, mitochondrial	[m] : accoa + h2o + oaa --> cit + coa + h	EC-4.1.3.7	Citrate Cycle (TCA)	(YNR001C or YPR001W)	(Cit1-m) or (Cit3-m)
AKGDbm	oxoglutarate dehydrogenase (dihydrolipoamide S-succinyltransferase), mitochondrial	[m] : coa + sdhlam --> dhlam + succoa	EC-2.3.1.61	Citrate Cycle (TCA)	(YIL125W and YDR148C and YFL018C)	(Kgd1-m and Kgd2-m and PdE3-m)
AKGDam	oxoglutarate dehydrogenase (lipoamide), mitochondrial	[m] : akg + h + lpam <==> co2 + sdhlam	EC-1.2.4.2	Citrate Cycle (TCA)	(YIL125W and YDR148C and YFL018C)	(Kgd1-m and Kgd2-m and PdE3-m)
ACONTm	Aconitate hydratase, mitochondrial	[m] : cit <==> icit	EC-4.2.1.3	Citrate Cycle (TCA)	(YLR304C or YJL200C)	(Aco1-m) or (Aco2-m)
ACONT	aconitase	[c] : cit <==> icit	EC-4.2.1.3	Citrate Cycle (TCA)	YLR304C	Aco1
SULR	sulfite reductase (NADPH2)	[c] : (3) h2o + h2s + (3) nadp <==> (5) h + (3) nadph + so3	EC-1.8.2.2	Cysteine Metabolism	(YJR137C or YFR030W)	(Ecm17) or (Met10)
SLFAT	sulfate adenylyltransferase (ADP)	[c] : adp + h + so4 <==> aps + pi	EC-2.7.7.5	Cysteine Metabolism	YCL050C	Apa1
SERATi	serine O-acetyltransferase, irreversible	[c] : accoa + ser-L --> acser + coa	EC-2.3.1.30	Cysteine Metabolism		
SADT	sulfate adenylyltransferase	[c] : atp + h + so4 --> aps + ppi	EC-2.7.7.4	Cysteine Metabolism	YJR010W	Met3

PAPSR	phosphoadenylyl-sulfate reductase (thioredoxin)	[c] : paps + trdrd --> (2) h + pap + so3 + trdox	EC-1.8.4.8	Cysteine Metabolism	YPR167C	Met16
CYSTRS	Cysteinyl-tRNA synthetase	[c] : atp + cys-L + trnacys --> amp + cystrna + ppi	EC-6.1.1.16	Cysteine Metabolism	YNL247W	Cyt1
CYSS	cysteine synthase	[c] : acser + h2s --> ac + cys-L + h	EC-4.2.99.8	Cysteine Metabolism	YGR012W	Csy1
BPNT	3',5'-bisphosphate nucleotidase	[c] : h2o + pap --> amp + pi	EC-3.1.3.7	Cysteine Metabolism	YOL064C	Met22
ADSK	adenylyl-sulfate kinase	[c] : aps + atp --> adp + h + paps	EC-2.7.1.25	Cysteine Metabolism	YKL001C	Met14
NMNAT	nicotinamide-nucleotide adenylyltransferase	[c] : atp + h + nmn --> nad + ppi	EC-2.7.7.1	Fatty Acid Biosynthesis	YGR010W	Nma2
NADDPp	NAD diphosphatase, peroxisomal	[x] : h2o + nad --> amp + (2) h + nmn	EC-3.6.1.22	Fatty Acid Biosynthesis	YGL067W	Npy1-p
MCOATAm	Malonyl-CoA-ACO transacylase, mitochondrial	[m] : ACP + malcoa <==> coa + malACP	EC-2.3.1.39	Fatty Acid Biosynthesis	YOR221C	Mct1-m
MCOATA	Malonyl-CoA-ACP transacylase	[c] : ACP + malcoa <==> coa + malACP	EC-2.3.1.39	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
KATp	3-ketoacyl-CoA thiolase, peroxisomal	[x] : 3oacoa + coa --> accoa + acoa	EC-2.3.1.16	Fatty Acid Biosynthesis	YIL160C	Pot1-p
HACDp	3-hydroxyacyl-CoA dehydrogenase, peroxisomal	[x] : 3hacoa + nad <==> 3oacoa + h + nadh	EC-1.1.1.35	Fatty Acid Biosynthesis	YKR009C	Fox2-p
FAS80_L	fatty acid synthase (n-C8:0), lumped reaction	[c] : accoa + (8) h + (3) malcoa + (6) nadph --> (3) co2 + (4) coa + (2) h2o + (6) nadp + octa	EC-2.3.1.85	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FAS80COA_L	fatty acyl-CoA synthase (n-C8:0CoA), lumped reaction	[c] : accoa + (9) h + (3) malcoa + (6) nadph --> (3) co2 + (3) coa + (3) h2o + (6) nadp + occoa	EC-2.3.1.86	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FAS80ACPm_L	fatty acyl-ACP synthase (n-C8:0ACP), mitochondrial, lumped reaction	[m] : acACP + (9) h + (3) malACP + (6) nadph --> (3) ACP + (3) co2 + (3) h2o + (6) nadp + ocACP		Fatty Acid Biosynthesis	(YKL192C and YER061C and YOR221C and YKL055C)	(Acp1-m and Cem1-m and Mct1-m and Oar1-m)
FAS260	fatty acid synthase (n-C26:0)	[c] : (3) h + malcoa + (2) nadph + ttc --> co2 + coa + h2o + hexc + (2) nadp	EC-2.3.1.85	Fatty Acid Biosynthesis	YLR372W	Sur4
FAS240_L	fatty acid synthase (n-C24:0), lumped reaction	[c] : (9) h + (3) malcoa + (6) nadph + ocdca --> (3) co2 + (3) coa + (3) h2o + (6) nadp + ttc	EC-2.3.1.85	Fatty Acid Biosynthesis	YCR034W	Fen1
FAS182ACPm	fatty-acyl-ACP synthase (n-C18:2ACP), mitochondrial	[m] : (5) h + malACP + (4) nadph + (2) o2 + palmACP --> ACP + co2 + (5) h2o + (4) nadp + ocdcyaACP		Fatty Acid Biosynthesis	(YKL192C and YER061C and YOR221C and YKL055C)	(Acp1-m and Cem1-m and Mct1-m and Oar1-m)
FAS181ACPm	fatty-acyl-ACP synthase (n-C18:1ACP), mitochondrial	[m] : (4) h + malACP + (3) nadph + o2 + palmACP --> ACP + co2 + (3) h2o + (3) nadp + octeACP		Fatty Acid Biosynthesis	(YKL192C and YER061C and YOR221C and YKL055C)	(Acp1-m and Cem1-m and Mct1-m and Oar1-m)
FAS180COA	fatty-acyl-CoA synthase (n-C18:0CoA)	[c] : (3) h + malcoa + (2) nadph + pmtcoa --> co2 + coa + h2o + (2) nadp + stcoa	EC-2.3.1.86	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FAS180ACPm	fatty-acyl-ACP synthase (n-C18:0ACP), mitochondrial	[m] : (3) h + malACP + (2) nadph + palmACP --> ACP + co2 + h2o + (2) nadp + ocdcaACP		Fatty Acid Biosynthesis	(YKL192C and YER061C and YOR221C and YKL055C)	(Acp1-m and Cem1-m and Mct1-m and Oar1-m)
FAS180	fatty acid synthase (n-C18:0)	[c] : (3) h + hdca + malcoa + (2) nadph --> co2 + coa + h2o + (2) nadp + ocdca	EC-2.3.1.85	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FAS161ACPm	fatty-acyl-ACP synthase (n-C16:1ACP), mitochondrial	[m] : (4) h + malACP + myrsACP + (3) nadph + o2 --> ACP + co2 + (3) h2o + hdeACP + (3) nadp		Fatty Acid Biosynthesis	(YKL192C and YER061C and YOR221C and YKL055C)	(Acp1-m and Cem1-m and Mct1-m and Oar1-m)
FAS160COA	fatty-acyl-CoA synthase (n-C16:0CoA)	[c] : (3) h + malcoa + (2) nadph + tdcoa --> co2 + coa + h2o + (2) nadp + pmtcoa	EC-2.3.1.86	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FAS160ACPm	fatty-acyl-ACP synthase (n-C16:0ACP), mitochondrial	[m] : (3) h + malACP + myrsACP + (2) nadph --> ACP + co2 + h2o + (2) nadp + palmACP		Fatty Acid Biosynthesis	(YKL192C and YER061C and YOR221C and YKL055C)	(Acp1-m and Cem1-m and Mct1-m and Oar1-m)
FAS160	fatty acid synthase (n-C16:0)	[c] : (3) h + malcoa + (2) nadph + ttdca --> co2 + coa + h2o + hdca + (2) nadp	EC-2.3.1.85	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FAS141ACPm	fatty-acyl-ACP synthase (n-C14:1ACP), mitochondrial	[m] : ddcaACP + (4) h + malACP + (3) nadph + o2 --> ACP + co2 + (3) h2o + (3) nadp + tdeACP		Fatty Acid Biosynthesis	(YKL192C and YER061C and YOR221C and YKL055C)	(Acp1-m and Cem1-m and Mct1-m and Oar1-m)
FAS140COA	fatty-acyl-CoA synthase (n-C14:0CoA)	[c] : ddcacoa + (3) h + malcoa + (2) nadph --> co2 + coa + h2o + (2) nadp + tdcoa	EC-2.3.1.86	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FAS140ACPm	fatty-acyl-ACP synthase (n-C14:0ACP), mitochondrial	[m] : ddcaACP + (3) h + malACP + (2) nadph --> ACP + co2 + h2o + myrsACP + (2) nadp		Fatty Acid Biosynthesis	(YKL192C and YER061C and YOR221C and YKL055C)	(Acp1-m and Cem1-m and Mct1-m and Oar1-m)
FAS140	fatty acid synthase (n-C14:0)	[c] : ddca + (3) h + malcoa + (2) nadph --> co2 + coa + h2o + (2) nadp + ttdca	EC-2.3.1.85	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FAS120COA	fatty-acyl-CoA synthase (n-C12:0CoA)	[c] : dcacoa + (3) h + malcoa + (2) nadph --> co2 + coa + ddcacoa + h2o + (2) nadp	EC-2.3.1.86	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FAS120ACPm	fatty-acyl-ACP synthase (n-C12:0ACP), mitochondrial	[m] : dcaACP + (3) h + malACP + (2) nadph --> ACP + co2 + ddcaACP + h2o + (2) nadp		Fatty Acid Biosynthesis	(YKL192C and YER061C and YOR221C and YKL055C)	(Acp1-m and Cem1-m and Mct1-m and Oar1-m)
FAS120	fatty acid synthase (n-C12:0)	[c] : dca + (3) h + malcoa + (2) nadph --> co2 + coa + ddca + h2o + (2) nadp	EC-2.3.1.85	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)

FAS100COA	fatty acyl-CoA synthase (n-C10:0CoA)	[c] : (3) h + malcoa + (2) nadph + occoa --> co2 + coa + dcacoa + h2o + (2) nadp	EC-2.3.1.86	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FAS100ACPm	fatty-acyl-ACP synthase (n-C10:0ACP), mitochondrial	[m] : (3) h + malACP + (2) nadph + ocACP --> ACP + co2 + dcaACP + h2o + (2) nadp		Fatty Acid Biosynthesis	(YKL192C and YER061C and YOR221C and YKL055C)	(Acp1-m and Cem1-m and Mct1-m and Oar1-m)
FAS100	fatty acid synthase (n-C10:0)	[c] : (3) h + malcoa + (2) nadph + octa --> co2 + coa + dca + h2o + (2) nadp	EC-2.3.1.85	Fatty Acid Biosynthesis	(YGR037C and YNR016C and (YKL182W and YPL231W))	(Acb1 and Acc1 and Fas)
FACOAL80p	fatty-acid--CoA ligase (octanoate), peroxisomal	[x] : atp + coa + octa <==> amp + occoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
FACOAL260p	fatty-acid--CoA ligase (n-C26:0), peroxisomal	[x] : atp + coa + hexc <==> amp + hexccoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	YBR041W	Fat1-p
FACOAL240p	fatty-acid--CoA ligase (n-C24:0), peroxisomal	[x] : atp + coa + ttc <==> amp + ppi + ttccoa	EC-6.2.1.3	Fatty Acid Biosynthesis	YBR041W	Fat1-p
FACOAL182	fatty-acid--CoA ligase (octadecynoate)	[c] : atp + coa + ocdcya <==> amp + ocdycacoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	(YMR246W or YIL009W or YOR317W)	(Faa4) or (Faa3) or (Faa1)
FACOAL181	fatty-acid--CoA ligase (octadecenoate)	[c] : atp + coa + ocdcea <==> amp + odecoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	(YOR317W or YIL009W or YMR246W)	(Faa1) or (Faa3) or (Faa4)
FACOAL180	fatty-acid--CoA ligase (octadecanoate)	[c] : atp + coa + ocdca <==> amp + ppi + stcoa	EC-6.2.1.3	Fatty Acid Biosynthesis	(YOR317W or YIL009W or YMR246W)	(Faa1) or (Faa3) or (Faa4)
FACOAL161p	fatty-acid--CoA ligase (hexadecenoate), peroxisomal	[x] : atp + coa + hdcea <==> amp + hdcoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
FACOAL161	fatty-acid--CoA ligase (hexadecenoate)	[c] : atp + coa + hdcea <==> amp + hdcoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	(YOR317W or YIL009W or YMR246W)	(Faa1) or (Faa3) or (Faa4)
FACOAL160p	fatty-acid--CoA ligase (hexadecanoate), peroxisomal	[x] : atp + coa + hdca <==> amp + pmtcoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
FACOAL160	fatty-acid--CoA ligase (hexadecanoate)	[c] : atp + coa + hdca <==> amp + pmtcoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	(YOR317W or YIL009W or YMR246W)	(Faa1) or (Faa3) or (Faa4)
FACOAL141p	fatty-acid--CoA ligase (tetradecenoate), peroxisomal	[x] : atp + coa + ttdcea <==> amp + ppi + tdecoa	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
FACOAL141	fatty-acid--CoA ligase (tetradecenoate)	[c] : atp + coa + ttdcea <==> amp + ppi + tdecoa	EC-6.2.1.3	Fatty Acid Biosynthesis	(YOR317W or YIL009W or YMR246W)	(Faa1) or (Faa3) or (Faa4)
FACOAL140p	fatty-acid--CoA ligase (tetradecanoate), peroxisomal	[x] : atp + coa + ttdca <==> amp + ppi + tdcoa	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
FACOAL140	fatty-acid--CoA ligase (tetradecanoate)	[c] : atp + coa + ttdca <==> amp + ppi + tdcoa	EC-6.2.1.3	Fatty Acid Biosynthesis	(YOR317W or YIL009W or YMR246W)	(Faa1) or (Faa3) or (Faa4)
FACOAL120p	fatty-acid--CoA ligase (dodecanoate), peroxisomal	[x] : atp + coa + ddca <==> amp + ddcacoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
FACOAL100p	fatty-acid--CoA ligase (decanoate), peroxisomal	[x] : atp + coa + dca <==> amp + dcacoa + ppi	EC-6.2.1.3	Fatty Acid Biosynthesis	YER015W	Faa2-p
FA182ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + ocdcyaACP <==> ACP + h + ocdcya	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA181ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + octeACP <==> ACP + h + ocdcea	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA180ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + ocdcaACP <==> ACP + h + ocdca	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA161ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + hdeACP <==> ACP + h + hdcea	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA160ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + palmACP <==> ACP + h + hdca	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA141ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + tdeACP <==> ACP + h + ttdcea	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA140ACPH	fatty-acyl-ACP hydrolase	[c] : h2o + myrsACP <==> ACP + h + ttdca	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
FA120ACPH	fatty-acyl-ACP hydrolase	[c] : ddcaACP + h2o <==> ACP + ddca + h	EC-3.1.2.14	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
DESAT18_2	Oleoyl-CoA desaturase (n-C18:1CoA -> n-C18:2CoA)	[c] : h + nadph + o2 + odecoa --> (2) h2o + nadp + ocdycacoa	EC-	Fatty Acid Biosynthesis		
DESAT18	stearoyl-CoA desaturase (n-C18:0CoA -> n-C18:1CoA)	[c] : h + nadph + o2 + stcoa --> (2) h2o + nadp + odecoa	EC-	Fatty Acid Biosynthesis	YGL055W	Ole1
DESAT16	Palmitoyl-CoA desaturase (n-C16:0CoA -> n-C16:1CoA)	[c] : h + nadph + o2 + pmtcoa --> (2) h2o + hdcoa + nadp	EC-	Fatty Acid Biosynthesis	YGL055W	Ole1
DESAT14	Myristicoyl-CoA desaturase (n-C14:0CoA -> n-C14:1CoA)	[c] : h + nadph + o2 + tdcoa --> (2) h2o + nadp + tdecoa	EC-	Fatty Acid Biosynthesis		
ACOATAm	Acetyl-CoA ACP transacylase, mitochondrial	[m] : ACP + accoa <==> acACP + coa	EC-2.3.1.41	Fatty Acid Biosynthesis	YER061C	Cem1-m
ACOATA	Acetyl-CoA ACP transacylase	[c] : ACP + accoa <==> acACP + coa	EC-2.3.1.38	Fatty Acid Biosynthesis	(YKL182W and YPL231W	Fas
ACCOACr	acetyl-CoA carboxylate, reversible reaction	[c] : accoa + atp + hco3 <==> adp + h + malcoa + pi	EC-6.4.1.2	Fatty Acid Biosynthesis	YNR016C	Acc1
ACACT1m	acetyl-CoA C-acetyltransferase, mitochondrial	[m] : (2) accoa --> aacoa + coa	EC-2.3.1.9	Fatty Acid Biosynthesis	YPL028W	Erg10-m
ACACT1	acetyl-CoA C-acetyltransferase	[c] : (2) accoa --> aacoa + coa	EC-2.3.1.9	Fatty Acid Biosynthesis	YPL028W	Erg10
HACD8p	3-hydroxyacyl-CoA dehydrogenase (3-oxooctadecanoyl-CoA), peroxisomal	[x] : 3ohodcoa + h + nadh <==> 3hodcoa + nad	EC-1.1.1.35	Fatty Acid Degradation	YKR009C	Fox2-p
HACD7p	3-hydroxyacyl-CoA dehydrogenase (3-oxohexadecanoyl-CoA), peroxisomal	[x] : 3ohdcoa + h + nadh <==> 3hhdcoa + nad	EC-1.1.1.35	Fatty Acid Degradation	YKR009C	Fox2-p
HACD6p	3-Hydroxyacyl-CoA dehydrogenase (3-oxotetradecanoyl-CoA), peroxisomal	[x] : 3otdcoa + h + nadh <==> 3htdcoa + nad	EC-1.1.1.35	Fatty Acid Degradation	YKR009C	Fox2-p
HACD5p	3-hydroxyacyl-CoA dehydrogenase (3-oxodecanoyl-CoA), peroxisomal	[x] : 3oddcoa + h + nadh <==> 3hddcoa + nad	EC-1.1.1.35	Fatty Acid Degradation	YKR009C	Fox2-p
HACD4p	3-hydroxyacyl-CoA dehydrogenase (3-oxodecanoyl-CoA), peroxisomal	[x] : 3odcoa + h + nadh <==> 3hdcoa + nad	EC-1.1.1.35	Fatty Acid Degradation	YKR009C	Fox2-p
HACD10p	3-hydroxyacyl-CoA dehydrogenase (3-oxohexacosyl-CoA), peroxisomal	[x] : 3hxccoa + nad <==> 3ohxccoa + h + nadh	EC-1.1.1.35	Fatty Acid Degradation	YKR009C	Fox2-p
FAO80p	fatty acid oxidation (octanoyl-CoA), peroxisomal	[x] : (3) coa + (3) h2o + (3) nad + (3) o2 + occoa --> (4) accoa + (3) h + (3) h2o2 + (3) nadh		Fatty Acid Degradation		
FAO240p	fatty acid oxidation (tetradecansoyl-CoA), peroxisomal	[x] : (3) coa + (3) h2o + (3) nad + (3) o2 + ttccoa --> (3) accoa + (3) h + (3) h2o2 + (3) nadh + stcoa		Fatty Acid Degradation		
FAO182p_odd/odd	Fatty acid oxidation (double bonds on odd num. carbon), peroxisomal	[x] : (8) coa + (8) h2o + (8) nad + (6) o2 + ocdycacoa --> (9) accoa + (8) h + (6) h2o2 + (8) nadh		Fatty Acid Degradation		
FAO182p_even/odd	Fatty acid oxidation (double bond on even and odd num. carbon), peroxisomal	[x] : (8) coa + (8) h2o + (8) nad + nadph + (7) o2 + ocdycacoa --> (9) accoa + (7) h + (7) h2o2 + (8) nadh + nadp		Fatty Acid Degradation		
FAO182p_even/even	Fatty acid oxidation (double bonds on even num. carbon), peroxisomal	[x] : (8) coa + (8) h2o + (8) nad + (2) nadph + (8) o2 + ocdycacoa --> (9) accoa + (6) h + (8) h2o2 + (8) nadh + (2) nadp		Fatty Acid Degradation		
FAO181p_odd	Fatty acid oxidation (double bond on odd num. carbon), peroxisomal	[x] : (8) coa + (8) h2o + (8) nad + (7) o2 + odecoa --> (9) accoa + (8) h + (7) h2o2 + (8) nadh		Fatty Acid Degradation		
FAO181p_even	Fatty acid oxidation (double bond on even num. carbon), peroxisomal	[x] : (8) coa + (8) h2o + (8) nad + nadph + (8) o2 + odecoa --> (9) accoa + (7) h + (8) h2o2 + (8) nadh + nadp		Fatty Acid Degradation		
FAO161p_odd	Fatty acid oxidation (double bond on odd num. carbon), peroxisomal	[x] : (7) coa + (7) h2o + hdcoa + (7) nad + (6) o2 --> (8) accoa + (7) h + (6) h2o2 + (7) nadh		Fatty Acid Degradation		
FAO161p_even	Fatty acid oxidation (double bond on even num. carbon), peroxisomal	[x] : (7) coa + (7) h2o + hdcoa + (7) nad + nadph + (7) o2 --> (8) accoa + (6) h + (7) h2o2 + (7) nadh + nadp		Fatty Acid Degradation		
FAO141p_odd	Fatty acid oxidation (double bond on odd num. carbon), peroxisomal	[x] : (6) coa + (6) h2o + (6) nad + (5) o2 + tdecoa --> (7) accoa + (6) h + (5) h2o2 + (6) nadh		Fatty Acid Degradation		
FAO141p_even	fatty acid oxidation (double bonds on even num. carbon), peroxisomal	[x] : (6) coa + (6) h2o + (6) nad + nadph + (6) o2 + tdecoa --> (7) accoa + (5) h + (6) h2o2 + (6) nadh + nadp		Fatty Acid Degradation		
ECOAH8p	3-hydroxyacyl-CoA dehydratase (3-hydroxyoctadecanoyl-CoA), peroxisomal	[x] : 3hodcoa <==> h2o + od2coa	EC-4.2.1.17	Fatty Acid Degradation	YKR009C	Fox2-p
ECOAH7p	3-hydroxyacyl-CoA dehydratase (3-hydroxyhexadecanoyl-CoA), peroxisomal	[x] : 3hhdcoa <==> h2o + hdd2coa	EC-4.2.1.17	Fatty Acid Degradation	YKR009C	Fox2-p
ECOAH6p	3-hydroxyacyl-CoA dehydratase (3-hydroxytetradecanoyl-CoA), peroxisomal	[x] : 3htdcoa <==> h2o + td2coa	EC-4.2.1.17	Fatty Acid Degradation	YKR009C	Fox2-p

ECOAH5p	3-hydroxyacyl-CoA dehydratase (3-hydroxydodecanoyl-CoA), peroxisomal	[x] : 3hddcoa <==> dd2coa + h2o	EC-4.2.1.17	Fatty Acid Degradation	YKR009C	Fox2-p
ECOAH4p	3-hydroxyacyl-CoA dehydratase (3-hydroxydecanoyl-CoA), peroxisomal	[x] : 3hdcoa <==> dc2coa + h2o	EC-4.2.1.17	Fatty Acid Degradation	YKR009C	Fox2-p
ECOAH11p	3-hydroxyacyl-CoA dehydratase (3-hydroxyhexacosyl-CoA), peroxisomal	[x] : h2o + hxc2coa <==> 3hxccoa	EC-4.2.1.17	Fatty Acid Degradation	YKR009C	Fox2-p
ACOAO9p	acyl-CoA oxidase (hexacanoyl-CoA), peroxisomal	[x] : hexccoa + o2 --> h2o2 + hxc2coa	EC-1.3.3.6	Fatty Acid Degradation	YGL205W	Pox1-p
ACOAO8p	acyl-CoA oxidase (octadecanoyl-CoA), peroxisomal	[x] : o2 + stcoa --> h2o2 + od2coa	EC-1.3.3.6	Fatty Acid Degradation	YGL205W	Pox1-p
ACOAO7p	acyl-CoA oxidase (hexadecanoyl-CoA), peroxisomal	[x] : o2 + pmtcoa --> h2o2 + hdd2coa	EC-1.3.3.6	Fatty Acid Degradation	YGL205W	Pox1-p
ACOAO6p	acyl-CpA oxidase (tetradecanoyl-CoA), peroxisomal	[x] : o2 + tdcoa --> h2o2 + td2coa	EC-1.3.3.6	Fatty Acid Degradation	YGL205W	Pox1-p
ACOAO5p	acyl-CoA oxidase (dodecanoyl-CoA), peroxisomal	[x] : ddcacoa + o2 --> dd2coa + h2o2	EC-1.3.3.6	Fatty Acid Degradation	YGL205W	Pox1-p
ACOAO4p	acyl-CoA oxidase (decanoyl-CoA), peroxisomal	[x] : dcacoa + o2 --> dc2coa + h2o2	EC-1.3.3.6	Fatty Acid Degradation	YGL205W	Pox1-p
ACACT9p	acetyl-CoA acyltransferase (tetracosanoyl-CoA), peroxisomal	[x] : 3ohxccoa + coa --> accoa + ttccoa	EC-2.3.1.16	Fatty Acid Degradation	YIL160C	Pot1-p
ACACT8p	acetyl-CoA acyltransferase (hexadecanoyl-CoA), peroxisomal	[x] : 3ohodcoa + coa --> accoa + pmtcoa	EC-2.3.1.16	Fatty Acid Degradation	YIL160C	Pot1-p
ACACT7p	acetul-CoA acyltransferase (tetradecanoyl-CoA), peroxisomal	[x] : 3ohdcoa + coa --> accoa + tdcoa	EC-2.3.1.16	Fatty Acid Degradation	YIL160C	Pot1-p
ACACT6p	acetyl-CoA C-acetyltransferase (dodecanoyl), peroxisomal	[x] : 3otdcoa + coa --> accoa + ddcacoa	EC-2.3.1.16	Fatty Acid Degradation	YIL160C	Pot1-p
ACACT5p	acetyl-CoA C-acyltransferase (decanoyl-CoA), peroxisomal	[x] : 3oddcoa + coa --> accoa + dcacoa	EC-2.3.1.16	Fatty Acid Degradation	YIL160C	Pot1-p
ACACT4p	acetyl-CoA C-acetyltransferase (octanoyl-CoA), peroxisomal	[x] : 3odcoa + coa --> accoa + occoa	EC-2.3.1.16	Fatty Acid Degradation	YIL160C	Pot1-p
THFGLUS	Tetrahydrofolate:L-glutamate gamma-ligase (ADP-forming)	[c] : atp + glu-L + thf <==> adp + h + pi + thfglu	EC-6.3.2.17	Folate Metabolism	(YKL132C or YOR241W or YMR113W)	(Rma1) or (Met7) or (Fol3)
THFATm	tetrahydrofolate aminomethyltransferase, mitochondrial	[m] : h2o + methf --> 5fthf + h	EC-2.1.2.10	Folate Metabolism	(YDR019C and YMR189W and YAL044C and (YBR221C and YER178W))	(Gcv1-m and Gcv2-m and Gcv3-m and PdE1-m)
QULNS	quinolinate synthase	[c] : dhap + iasp --> h + (2) h2o + pi + quln		Folate Metabolism		
MTHFR3	5,10-methylenetetrahydrofolatereductase (NADPH)	[c] : h + mlthf + nadph --> 5mthf + nadp	EC-1.5.1.20	Folate Metabolism	(YPL023C or YGL125W)	(Met12) or (Met13)
MTHFDm	methylenetetrahydrofolate dehydrogenase (NADP), mitochondrial	[m] : mlthf + nadp <==> h + methf + nadph	EC-1.5.1.5	Folate Metabolism	YBR084W	Mis1-m
MTHFD2	methylenetetrahydrofolate dehydrogenase (NAD)	[c] : mlthf + nad --> h + methf + nadh	EC-1.5.1.15	Folate Metabolism	YKR080W	Mtd1
MTHFD	methylenetetrahydrofolate dehydrogenase (NADP)	[c] : mlthf + nadp <==> h + methf + nadph	EC-1.5.1.5	Folate Metabolism	YGR204W	Ade3
MTHFCm	methenyltetrahydrifikate cyclohydrolase, mitochondrial	[m] : h2o + methf <==> 10fthf	EC-3.5.4.9	Folate Metabolism	YBR084W	Mis1-m
MTHFC	methenyltetrahydrofolate cyclohydrolase	[c] : h2o + methf <==> 10fthf	EC-3.5.4.9	Folate Metabolism	YGR204W	Ade3
HPPKm	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase,	[m] : 2ahhmp + atp --> 2ahhmd + amp + h	EC-2.7.6.3	Folate Metabolism	YNL256W	Fol1-m
GTPCI	GTP cyclohydrolase I	[c] : gtp + h2o --> ahdt + for	EC-3.5.4.16	Folate Metabolism	YGR267C	Fol2
FTHFLm	formate-tetrahydrofolate ligase, mitochondrial	[m] : atp + for + thf <==> 10fthf + adp + pi	EC-6.3.4.3	Folate Metabolism	YBR084W	Mis1-m
FTHFL	formate-tetrahydrofolate ligase	[c] : atp + for + thf <==> 10fthf + adp + pi	EC-6.3.4.3	Folate Metabolism	YGR204W	Ade3
FTHFI	5-Formyltetrahydrofolate:10-Formyltetrahydrofolate isomerase	[c] : 5fthf + atp + h2o --> 10fthf + adp + pi		Folate Metabolism		
FTHFCLm	5-formethyltetrahydrofolate cyclo-ligase, mitochondrial	[m] : 5fthf + atp --> adp + methf + pi	EC-6.3.3.2	Folate Metabolism		
FTHFCL	5-formethyltetrahydrofolate cyclo-ligase	[c] : 5fthf + atp --> adp + methf + pi	EC-6.3.3.2	Folate Metabolism	YER183C	Fau1
FOLDm	fold, mitochondrial	[m] : 2ahhmd + 4abz --> dhpt + ppi		Folate Metabolism	YNL256W	Fol1-m
FMETTRSm	Methionyl-tRNA formyltransferase, mitochondrial	[m] : 10fthf + mettrna --> fmettrna + h + thf	EC-2.1.2.9	Folate Metabolism	YBL013W	Fmt1-m
DNTPPA	Dihydroneopterin triphosphate pyrophosphatase	[c] : ahdt + h2o --> dhpmp + h + ppi		Folate Metabolism		
DNMPPA	Dihydroneopterin monophosphate dephosphorylase	[c] : dhpmp + h2o --> dhnpt + pi		Folate Metabolism	YDL100C	Arr4
DHPSm	dihydropteroate synthase, mitochondrial	[m] : 2ahhmp + 4abz --> dhpt + h2o	EC-2.5.1.15	Folate Metabolism	YNL256W	Fol1-m
DHNPAm	dihydroneopterin aldolase, mitochondrial	[m] : dhnpt --> 2ahhmp + gcald + h	EC-4.1.2.25	Folate Metabolism	YNL256W	Fol1-m
DHFS	dihydrofolate synthase	[c] : atp + dhpt + glu-L --> adp + dhf + pi	EC-6.3.2.12	Folate Metabolism		
DHFRim	dihydrofolate reductase, mitochondrial	[m] : dhf + h + nadph --> nadp + thf	EC-1.5.1.3	Folate Metabolism	YOR236W	Dfr1-m
DHFRi	dihydrofolate reductase (irreversible)	[c] : dhf + h + nadph --> nadp + thf	EC-1.5.1.3	Folate Metabolism	YOR236W	Dfr1
ASPOcm	aspartate oxidase	asp-L[c] + fad[m] --> fadh2[m] + iasp[c]		Folate Metabolism		
AKP1	alkaline phosphatase (Dihydroneopterin)	[c] : ahdt + (3) h2o --> dhnpt + (2) h + (3) pi	EC-3.1.3.1	Folate Metabolism	YDR481C	Pho8
ADCS	4-amino-4-deoxychorismate synthase	[c] : chor + gln-L --> 4adcho + glu-L		Folate Metabolism	YNR033W	Abz1
ADCL	4-aminobenzoate synthase	[c] : 4adcho --> 4abz + h + pyr		Folate Metabolism		
PMANM	phosphomannomutase	[c] : man1p <==> man6p	EC-5.4.2.8	Fructose and mannose metabolism	YFL045C	Sec53
PFK26	6-phosphofructo-2-kinase	[c] : atp + f6p --> adp + f26bp + h	EC-2.7.1.105	Fructose and mannose metabolism	(YIL107C or YOL136C)	(Pfk26) or (Pfk27)
MAN6PI	mannose-6-phosphate isomerase	[c] : man6p <==> f6p	EC-5.3.1.8	Fructose and mannose metabolism	YER003C	Pmi40
MAN1PT	mannose-1-phosphate guanylyltransferase	[c] : gtp + h + man1p --> gdpmann + ppi	EC-2.7.7.13	Fructose and mannose metabolism	YDL055C	Psa1
FRUK	fructose-1-phosphate kinase	[c] : atp + f1p --> adp + fdp + h	EC-2.7.1.56	Fructose and mannose metabolism		
FBP26	Fructose-2,6-bisphosphate 2-phosphatase	[c] : f26bp + h2o --> f6p + pi	EC-3.1.3.46	Fructose and mannose metabolism	YJL155C	Fbp26
UGLT	UDPglucose--hexose-1-phosphate uridylyltransferase	[c] : gal1p + udpg <==> g1p + udpgal	EC-2.7.7.12	Galactose metabolism	YBR018C	Gal7
UDPG4E	UDPglucose 4-epimerase	[c] : udpg <==> udpgal	EC-5.1.3.2	Galactose metabolism	YBR019C	Gal10
RAFGH	Raffinose galactohydrolase	[c] : h2o + raffin --> gal + sucr	EC-3.2.1.22	Galactose metabolism	YBR184W	Mel1
MELTGH	Melibiitol galactohydrolase	[c] : h2o + melt <==> gal + sbt-D	EC-3.2.1.22	Galactose metabolism	YBR184W	Mel1
MALT	alpha-glucosidase	[c] : h2o + malt --> (2) glc-D	EC-3.2.1.20	Galactose metabolism	(YBR299W or YGR292W or YJL221C or YGR287C or YIL172C or YJL216C)	(Mal32) or (Mal12) or (Fsp2) or (Mal33) or (Mal13) or (Mal14)
GGLGH	Galactosylglycerol galactohydrolase	[c] : ggl + h2o <==> gal + glyc	EC-3.2.1.22	Galactose metabolism	YBR184W	Mel1
GALU	UTP-glucose-1-phosphate uridylyltransferase	[c] : g1p + h + utp <==> ppi + udpg	EC-2.7.7.9	Galactose metabolism	(YKL035W or YHL012W)	(Ugp1) or (Ugp2)
GALT	galactose-1-phosphate uridylyltransferase	[c] : gal1p + h + utp <==> ppi + udpgal	EC-2.7.7.10	Galactose metabolism	YBR018C	Gal7
GALS3	a-galactosidase (melibiose)	[c] : h2o + melib --> gal + glc-D	EC-3.2.1.22	Galactose metabolism	YBR184W	Mel1
GALK	galactokinase	[c] : atp + gal --> adp + gal1p + h	EC-2.7.1.6	Galactose metabolism	YBR020W	Gal1
GALIGH	1-alpha-D-Galactosyl-myo-inositol galactohydrolase	[c] : 1Dgali + h2o <==> gal + inost	EC-3.2.1.22	Galactose metabolism	YBR184W	Mel1
EPMGH	Epimelibiose galactohydrolase	[c] : epm + h2o <==> gal + man		Galactose metabolism	YBR184W	Mel1
DGGH	alpha-D-glucoside glucohydrase	[c] : 6dg + h2o --> gal + glc-D		Galactose metabolism	YJL221C	Fsp2
G6PDA	glucosamine-6-phosphate deaminase	[c] : gam6p + h2o --> f6p + nh4	EC-3.5.99.6	Glucosamine Metabolism		
UDPACGLP	UDP-N-acetylglucosamine diphosphorylase	[c] : acgam1p + h + utp <==> ppi + udpacgal	EC-2.7.7.23	Glutamate metabolism	YDL103C	Qri1
SSALy	succinate-semialdehyde dehydrogenase (NADP)	[c] : h2o + nadp + sucsal --> (2) h + nadph + succ	EC-1.2.1.16	Glutamate metabolism	YBR006W	Uga2
PYR5CDm	D1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	[m] : glu5sa + h2o + nadp --> glu-L + (2) h + nadph	EC-1.5.1.12	Glutamate metabolism	YHR037W	Put2-m
PGAMT	phosphoglucosamine mutase	[c] : gam1p <==> gam6p	EC-5.4.2.10	Glutamate metabolism	YEL058W	Pcm1
P5CDm	1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	[m] : 1pyr5c + (2) h2o + nad --> glu-L + h + nadh		Glutamate metabolism		
GLUSx	glutamate synthase (NADH2)	[c] : akg + gln-L + h + nadh --> (2) glu-L + nad	EC-1.4.1.14	Glutamate metabolism	YDL171C	Glt1

GLUDy	glutamate dehydrogenase (NADP)	[c] : glu-L + h2o + nadp <==> akg + h + nadph + nh4	EC-1.4.1.4	Glutamate metabolism	(YAL062W or YOR375C)	(Gdh3) or (Gdh1)
GLUDxi	glutamate dehydrogenase (NAD)	[c] : glu-L + h2o + nad --> akg + h + nadh + nh4	EC-1.4.1.2	Glutamate metabolism	YDL215C	Gdh2
GLUDC	Glutamate Decarboxylase	[c] : glu-L + h --> 4abut + co2	EC-4.1.1.15	Glutamate metabolism	YMR250W	Gad1
CSNATirp	carnitine O-acetyltransferase, rev erse direction, peroxisomal	[x] : accoa + crn --> acrn + coa	EC-2.3.1.7	Glutamate metabolism	YML042W	Cat2-p
CHTNS	chitin synthase	[c] : udpacgal --> chitin + h + udp	EC-2.4.1.16	Glutamate metabolism	(YNL192W or YBR038W or YBR023C)	(Chs1) or (Chs2) or (Chs3)
ACGAMPM	phosphoacetylglucosamine mutase	[c] : acgam6p <==> acgam1p	EC-5.4.2.3	Glutamate metabolism	YEL058W	Pcm1
ACGAM6PS	N-acetylglucosamine-6-phosphate synthase	[c] : accoa + gam6p <==> acgam6p + coa + h	EC-2.3.1.4	Glutamate metabolism	YFL017C	Gna1
ABTA	4-aminobutyrate transaminase	[c] : 4abut + akg --> glu-L + sucsal	EC-2.6.1.19	Glutamate metabolism	YGR019W	Uga1
GLUTRSm	glutamyl-tRNA synthetase, mitochondrial	[m] : atp + glu-L + trnaglu --> amp + glutrna + ppi	EC-6.1.1.17	Glutamine Metabolism	YOL033W	Mse1-m
GLUTRS	Glutamyl-tRNA synthetase	[c] : atp + glu-L + trnaglu --> amp + glutrna + ppi	EC-6.1.1.17	Glutamine Metabolism	YGL245W	Mse2
GLUN	glutaminase	[c] : gln-L + h2o --> glu-L + nh4	EC-3.5.1.2	Glutamine Metabolism		
GLNTRS	Glutaminyl-tRNA synthetase	[c] : atp + gln-L + trnagln --> amp + glntrna + ppi	EC-6.1.1.18	Glutamine Metabolism	YOR168W	Gln4
GLNS	glutamine synthetase	[c] : atp + glu-L + nh4 --> adp + gln-L + h + pi	EC-6.3.1.2	Glutamine Metabolism	YPR035W	Gln1
GF6PTA	glutamine-fructose-6-phosphate transaminase	[c] : f6p + gln-L --> gam6p + glu-L	EC-2.6.1.16	Glutamine Metabolism	(YKL104C or YMR084W or YMR085W)	(Gfa1) or (Gfa2) or (Gfa3)
ANS	anthranilate synthase	[c] : chor + gln-L --> anth + glu-L + h + pyr	EC-4.1.3.27	Glutamine Metabolism	(YER090W or YKL211C)	(Trp2) or (Trp3)
TRIGS_SC	triglycerol synthesis	[c] : (0.01) 12dgr_SC + (0.02) dcacoa + (0.06) ddcacoa + (0.17) hdcoa + (0.09) ocdycacoa + (0.24) odecoa + (0.27) pmtcoa + (0.05) stcoa + (0.1) tdcoa --> coa + (0.01) triglyc_SC		Glycerolipid Metabolism		
GLYK	glycerol kinase	[c] : atp + glyc --> adp + glyc3p + h	EC-2.7.1.30	Glycerolipid Metabolism	YHL032C	Gut1
G3PT	glycerol-3-phosphatase	[c] : glyc3p + h2o --> glyc + pi		Glycerolipid Metabolism	(YER062C or YIL053W)	(Hor2) or (Rhr2)
G3PDm	glycerol-3-phosphate dehydrogenase (FAD), mitochondrial	[m] : fad + glyc3p --> dhap + fadh2	EC-1.1.99.5	Glycerolipid Metabolism	YIL155C	Gut2-m
G3PD1irm	glycerol-3-phosphate dehydrogenase (NAD), mitochondrial	[m] : dhap + h + nadh --> glyc3p + nad	EC-1.1.1.8	Glycerolipid Metabolism	YOL059W	Gpd2-m
G3PD1ir	glycerol-3-phosphate dehydrogenase (NAD)	[c] : dhap + h + nadh --> glyc3p + nad	EC-1.1.1.8	Glycerolipid Metabolism	YDL022W	Gpd1
DHAK	dihydroxyacetone kinase	[c] : atp + dha --> adp + dhap + h	EC-2.7.1.29	Glycerolipid Metabolism	(YML070W or YFL053W)	(Dak1) or (Dak2)
ALCD2m	alcohol dehydrogenase (ethanol), mitochondrial	[m] : etoh + nad <==> acald + h + nadh	EC-1.1.1.1	Glycerolipid Metabolism	YMR083W	Adh3-m
ALCD19y	alcohol dehydrogenase (glycerol, NADP)	[c] : glyald + h + nadph --> glyc + nadp		Glycerolipid Metabolism	YHR104W	Gre3
SERTRS	Seryl-tRNA synthetase	[c] : atp + ser-L + trnaser --> amp + ppi + sertrna	EC-6.1.1.11	Glycine and Serine Metabolism	(YDR023W or YHR011W)	(Ses1) or (Dia4)
SERD_L	L-serine deaminase	[c] : ser-L --> nh4 + pyr	EC-Undetermined	Glycine and Serine Metabolism	(YCL064C or YIL168W)	(Cha1) or (Sdl1)
PSP_L	phosphoserine phosphatase (L-serine)	[c] : h2o + pser-L --> pi + ser-L	EC-3.1.3.3	Glycine and Serine Metabolism	YGR208W	Ser2
PSERT	phosphoserine transaminase	[c] : 3php + glu-L --> akg + pser-L	EC-2.6.1.52	Glycine and Serine Metabolism	YOR184W	Ser1
PGCD	phosphoglycerate dehydrogenase	[c] : 3pg + nad --> 3php + h + nadh	EC-1.1.1.95	Glycine and Serine Metabolism	(YER081W or YIL074C)	(Ser3) or (Ser33)
HSK	homoserine kinase	[c] : atp + hom-L --> adp + h + phom	EC-2.7.1.39	Glycine and Serine Metabolism	YHR025W	Thr1
HSDyi	homoserine dehydrogenase (NADP), irreversible	[c] : aspsa + h + nadph --> hom-L + nadp	EC-1.1.1.3	Glycine and Serine Metabolism	YJR139C	Hom6
HSDxi	homoserine dehydrogenase (NADH), irreversible	[c] : aspsa + h + nadh --> hom-L + nad	EC-1.1.1.3	Glycine and Serine Metabolism	YJR139C	Hom6
GLYTRS	Glycyl-tRNA synthetase	[c] : atp + gly + trnagly --> amp + glytrna + ppi	EC-6.1.1.14	Glycine and Serine Metabolism	(YBR121C or YPR081C)	(Grs1) or (Grs2)
GLYCLm	glycine cleavage system, mitochondrial	[m] : gly + nad + thf --> co2 + mlthf + nadh + nh4	EC-2.1.2.10	Glycine and Serine Metabolism	(YDR019C and YMR189W and YAL044C and YFL018C)	(Gcv1-m and Gcv2-m and Gcv3-m and PdE3-m)
GHMT2rm	glycine hydroxymethyltransferase, reversible, mitochondrial	[m] : ser-L + thf <==> gly + h2o + mlthf	EC-2.1.2.1	Glycine and Serine Metabolism	YBR263W	Shm1-m
GHMT2r	glycine hydroxymethyltransferase, reversible	[c] : ser-L + thf <==> gly + h2o + mlthf	EC-2.1.2.1	Glycine and Serine Metabolism	YLR058C	Shm2
GCCcm	glycine-cleavage complex (lipoylprotein), mitochondrial	[m] : dhlpro + nad <==> h + lpro + nadh	EC-1.8.1.4	Glycine and Serine Metabolism	(YDR019C and YMR189W and YAL044C and YFL018C)	(Gcv1-m and Gcv2-m and Gcv3-m and PdE3-m)
GCCbim	glycine-cleavage complex (lipoylprotein) irreversible, mitochondrial	[m] : alpro + thf --> dhlpro + mlthf + nh4	EC-2.1.2.10	Glycine and Serine Metabolism	(YDR019C and YMR189W and YAL044C and YFL018C)	(Gcv1-m and Gcv2-m and Gcv3-m and PdE3-m)
GCCam	glycine-cleavage complex (lipoylprotein), mitochondrial	[m] : gly + h + lpro <==> alpro + co2	EC-1.4.4.2	Glycine and Serine Metabolism	(YDR019C and YMR189W and YAL044C and YFL018C)	(Gcv1-m and Gcv2-m and Gcv3-m and PdE3-m)
GCC2cm	glycine-cleavage complex (lipoamide), mitochondrial	[m] : dhlam + nad <==> h + lpam + nadh	EC-1.8.1.4	Glycine and Serine Metabolism	(YDR019C and YMR189W and YAL044C and YFL018C)	(Gcv1-m and Gcv2-m and Gcv3-m and PdE3-m)
GCC2bim	glycine-cleavage system (lipoamide) irreversible, mitochondrial	[m] : alpam + thf --> dhlam + mlthf + nh4	EC-2.1.2.10	Glycine and Serine Metabolism	(YDR019C and YMR189W and YAL044C and YFL018C)	(Gcv1-m and Gcv2-m and Gcv3-m and PdE3-m)
GCC2am	glycine-cleavage complex (lipoamide), mitochondrial	[m] : gly + h + lpam <==> alpam + co2	EC-1.4.4.2	Glycine and Serine Metabolism	(YDR019C and YMR189W and YAL044C and YFL018C)	(Gcv1-m and Gcv2-m and Gcv3-m and PdE3-m)
CYSTS	cystathionine beta-synthase	[c] : hcys-L + ser-L --> cyst-L + h2o	EC-4.2.1.22	Glycine and Serine Metabolism	YGR155W	Cys4
AGT	alanine-glyoxylate transaminase	[c] : ala-L + glx <==> gly + pyr	EC-2.6.1.44	Glycine and Serine Metabolism	YFL030W	Agt1
TPI	triose-phosphate isomerase	[c] : dhap <==> g3p	EC-5.3.1.1	Glycolysis/Gluconeogenesis	YDR050C	Tpi1
PYK	pyruvate kinase	[c] : adp + h + pep --> atp + pyr	EC-2.7.1.40	Glycolysis/Gluconeogenesis	(YAL038W or YOR347C)	(Cdc19) or (Pyk2)

PGM	phosphoglycerate mutase	[c] : 2pg <==> 3pg	EC-5.4.2.1	Glycolysis/Gluconeogenesis	(YKL152C or YDL021W or YOL056W)	(Gpm1) or (Gpm2) or (Gpm3)
PGK	phosphoglycerate kinase	[c] : 3pg + atp <==> 13dpg + adp	EC-2.7.2.3	Glycolysis/Gluconeogenesis	YCR012W	Pgk1
PGI	glucose-6-phosphate isomerase	[c] : g6p <==> f6p	EC-5.3.1.9	Glycolysis/Gluconeogenesis	YBR196C	Pgi1
PFK_3	phosphofructokinase, rxn3	[c] : atp + s7p --> adp + h + s17bp	EC-2.7.1.11	Glycolysis/Gluconeogenesis	(YGR240C and YMR205C)	Pfk
PFK_2	Phosphofructokinase	[c] : atp + tag6p-D --> adp + h + tagdp-D	EC-2.7.1.11	Glycolysis/Gluconeogenesis	(YGR240C and YMR205C)	Pfk
PFK	phosphofructokinase	[c] : atp + f6p --> adp + fdp + h	EC-2.7.1.11	Glycolysis/Gluconeogenesis	(YGR240C and YMR205C)	Pfk
PDHm	pyruvate dehydrogenase, mitochondrial	[m] : coa + nad + pyr --> accoa + co2 + nadh	EC-1.2.4.1	Glycolysis/Gluconeogenesis	((YBR221C and YER178W) and YNL071W and YFL018C)	(PdE1-m and PdE2-m and PdE3-m)
PDHcm	pyruvate dehydrogenase (dihydrolipoamide dehydrogenase), mitochondrial	[m] : dhlam + nad --> h + lpam + nadh	EC-1.8.1.4	Glycolysis/Gluconeogenesis	(YIL125W and YDR148C and YFL018C)	(Kgd1-m and Kgd2-m and PdE3-m)
HEX7	hexokinase (D-fructose:ATP)	[c] : atp + fru --> adp + f6p + h	EC-2.7.1.1	Glycolysis/Gluconeogenesis	(YFR053C or YGL253W)	(Hxk1) or (Hxk2)
HEX4	hexokinase (D-mannose:ATP)	[c] : atp + man --> adp + h + man6p	EC-2.7.1.1	Glycolysis/Gluconeogenesis	(YFR053C or YGL253W)	(Hxk1) or (Hxk2)
HEX1	hexokinase (D-glucose:ATP)	[c] : atp + glc-D --> adp + g6p + h	EC-2.7.1.1	Glycolysis/Gluconeogenesis	(YFR053C or YGL253W or YCL040W)	(Hxk1) or (Hxk2) or (Glk1)
GLUK	Glucokinase	[c] : atp + glc-D --> adp + g6p-B + h	EC-2.7.1.2	Glycolysis/Gluconeogenesis	YCL040W	Glk1
GAPD	glyceraldehyde-3-phosphate dehydrogenase	[c] : g3p + nad + pi <==> 13dpg + h + nadh	EC-1.2.1.12	Glycolysis/Gluconeogenesis	(YJL052W or YJR009C or YGR192C)	(Tdh1) or (Tdh2) or (Tdh3)
G6PI2	Glucose-6-phosphate isomerase	[c] : g6p-B <==> f6p-B	EC-5.3.1.9	Glycolysis/Gluconeogenesis	YBR196C	Pgi1
G6PI	Glucose-6-phosphate isomerase	[c] : g6p <==> g6p-B	EC-5.3.1.9	Glycolysis/Gluconeogenesis	YBR196C	Pgi1
FBA3	Sedoheptulose 1,7-bisphosphate D-glyceraldehyde-3-phosphate-lyase	[c] : s17bp <==> dhap + e4p	EC-4.1.2.13	Glycolysis/Gluconeogenesis	YKL060C	Fba1
FBA2	D-Fructose 1-phosphate D-glyceraldehyde-3-phosphate-lyase	[c] : f1p <==> dhap + glyald	EC-4.1.2.13	Glycolysis/Gluconeogenesis	YKL060C	Fba1
FBA	fructose-bisphosphate aldolase	[c] : fdp <==> dhap + g3p	EC-4.1.2.13	Glycolysis/Gluconeogenesis	YKL060C	Fba1
ENO	enolase	[c] : 2pg <==> h2o + pep	EC-4.2.1.11	Glycolysis/Gluconeogenesis	(YPL281C or YGR254W or YHR174W or YOR393W or YMR323W)	(Err2) or (Eno1) or (Eno2) or (Err1) or (Err3)
DPGM	Diphosphoglyceromutase	[c] : 13dpg <==> 23dpg + h		Glycolysis/Gluconeogenesis	YKL152C	Gpm1
G16MTg	Glycolipid 1,6-alpha-D-mannosyltransferase, Golgi apparatus	[g] : gdpmann + m1macchitppdol --> gdp + h + m2macchitppdol		Glycoprotein Metabolism		
G13MTg	Glycolipid 1,3-alpha-D-mannosyltransferase, Golgi apparatus	[g] : gdpmann + macchitppdol --> gdp + h + m1macchitppdol	EC-	Glycoprotein Metabolism		
G12MT2g	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus	[g] : gdpmann + m3macchitppdol --> gdp + h + m4macchitppdol	EC-2.4.1.131	Glycoprotein Metabolism	(YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C)	(Kre2-g) or (Ktr1-g) or (Ktr2-g) or (Ktr3-g) or (Ktr4-g) or (Ktr5-g) or (Ktr6-g) or (Yur1-g)
G12MT1g	Glycolipid 1,2-alpha-D-mannosyltransferase, Golgi apparatus	[g] : gdpmann + m2macchitppdol --> gdp + h + m3macchitppdol	EC-2.4.1.131	Glycoprotein Metabolism	(YDR483W or YOR099W or YKR061W or YBR205W or YBR199W or YNL029C or YPL053C or YJL139C)	(Kre2-g) or (Ktr1-g) or (Ktr2-g) or (Ktr3-g) or (Ktr4-g) or (Ktr5-g) or (Ktr6-g) or (Yur1-g)
DOLPMTcer	Dolichyl-phosphate D-mannosyltransferase	dolp[c] + gdpmann[c] --> dolmanp[r] + gdp[c]	EC-2.4.1.83	Glycoprotein Metabolism	YPR183W	Dpm1
DOLPMMer	Dolichyl-phosphate-mannose--protein mannosyltransferase, endoplasmic reticular	[r] : dolmanp --> dolp + h + mannan	EC-2.4.1.109	Glycoprotein Metabolism	((YDL095W and YAL023C) or YOR321W or YJR143C or YDL093W or YGR199W)	(Pmt1-er and Pmt2-er) or (Pmt3-er) or (Pmt4-er) or (Pmt5-er) or (Pmt6-er)
DOLK	Dolichol kinase	[c] : ctp + dolichol --> cdp + dolp + h	EC-	Glycoprotein Metabolism	YMR013C	Sec59
UGLYCHr	Ureidoglycolate hydrolase	[c] : (2) h + h2o + urdglyc <==> co2 + glx + (2) nh4	EC-3.5.3.19	Histidine Metabolism	YIR032C	Dal3
PRPPS	phosphoribosylpyrophosphate synthetase	[c] : atp + r5p <==> amp + h + prpp	EC-2.7.6.1	Histidine Metabolism	(YOL061W or YBL068W or YER099C or YHL011C or YKL181W)	(Prs5) or (Prs4) or (Prs2) or (Prs3) or (Prs1)
PRMICIi	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase (irreversible)	[c] : prfp --> prlp	EC-5.3.1.16	Histidine Metabolism	YIL020C	His6
PRATPP	phosphoribosyl-ATP pyrophosphatase	[c] : h2o + prbatp --> h + ppi + prbamp	EC-3.6.1.31	Histidine Metabolism	YCL030C	His4
PRAMPC	phosphoribosyl-AMP cyclohydrolase	[c] : h2o + prbamp --> prfp	EC-3.5.4.19	Histidine Metabolism	YCL030C	His4
IGPDH	imidazoleglycerol-phosphate dehydratase	[c] : eig3p --> h2o + imacp	EC-4.2.1.19	Histidine Metabolism	YOR202W	His3
IG3PS	Imidazole-glycerol-3-phosphate synthase	[c] : gln-L + prlp --> aicar + eig3p + glu-L + h		Histidine Metabolism	YBR248C	His7
HSTPT	histidinol-phosphate transaminase	[c] : glu-L + imacp --> akg + hisp	EC-2.6.1.9	Histidine Metabolism	YIL116W	His5
HISTRSm	histidyl-tRNA synthetase, mitochondrial	[m] : atp + his-L + trnahis --> amp + histrna + ppi	EC-6.1.1.21	Histidine Metabolism	YPR033C	Hts1-m
HISTRS	Histidyl-tRNA synthetase	[c] : atp + his-L + trnahis --> amp + histrna + ppi	EC-6.1.1.21	Histidine Metabolism	YPR033C	Hts1
HISTP	histidinol-phosphatase	[c] : h2o + hisp --> histd + pi	EC-3.1.3.15	Histidine Metabolism	YFR025C	His2

HISTD	histidinol dehydrogenase	[c] : h2o + histd + (2) nad --> (3) h + his-L + (2) nadh	EC-1.1.1.23	Histidine Metabolism	YCL030C	His4
ATPPRT	ATP phosphoribosyltransferase	[c] : atp + prpp --> ppi + prbatp	EC-2.4.2.17	Histidine Metabolism	YER055C	His1
ARMT	hnRNP arginine N-methyltransferase	[c] : amet + his-L --> NPmehis + ahcys + h		Histidine Metabolism	YBR034C	Hmt1
ALLTNr	allantoinase, reversible reaction	[c] : alltn + h2o <==> alltt + h	EC-3.5.2.5	Histidine Metabolism	YIR027C	Dal1
ALLTAHr	Allantoate aminohydrolase, reversible	[c] : alltt + h2o <==> urdglyc + urea	EC-3.5.3.4	Histidine Metabolism	YIR029W	Dal2
M1PD	mannitol-1-phosphate 5-dehydrogenase	[c] : mnl1p + nad <==> f6p + h + nadh	EC-1.1.1.17	Mannitol Metabolism		
SFGTH	S-Formylglutathione hydralase	[c] : Sfglutth + h2o <==> for + gthrd + h	EC-3.1.2.12	Methane Metabolism	YJL068C	Sfgh
FDH	formate dehydrogenase	[c] : for + nad --> co2 + nadh	EC-1.2.1.2	Methane Metabolism	(YOR388C or YPL275W or YPL276W)	(Fdh1) or (Fdh2) or (Fdh3)
SHSL4r	O-succinylhomoserine lyase (elimination), reversible	[c] : h2o + suchms <==> 2obut + h + nh4 + succ	EC-4.2.99.9	Methionine Metabolism	YML082W	Cgs1
SHSL1	O-succinylhomoserine lyase (L-cysteine)	[c] : cys-L + suchms --> cyst-L + h + succ	EC-4.2.99.9	Methionine Metabolism		
MHPGLUT	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	[c] : hcys-L + mhpglu --> hpglu + met-L	EC-2.1.1.14	Methionine Metabolism	YER091C	Met6
METTRSm	methionyl-tRNA synthetase, mitochondrial	[m] : atp + met-L + trnamet --> amp + mettrna + ppi	EC-6.1.1.10	Methionine Metabolism	YGR171C	Msm1-m
METTRS	Methionyl-tRNA synthetase	[c] : atp + met-L + trnamet --> amp + mettrna + ppi	EC-6.1.1.10	Methionine Metabolism	YGR264C	Mes1
METS	methionine synthase	[c] : 5mthf + hcys-L --> met-L + thf	EC-2.1.1.13	Methionine Metabolism	YER091C	Met6
METB1	metb1	[c] : achms + cys-L --> ac + cyst-L + h		Methionine Metabolism	YJR130C	Str2
METAT	methionine adenosyltransferase	[c] : atp + h2o + met-L --> amet + pi + ppi	EC-2.5.1.6	Methionine Metabolism	(YDR502C or YLR180W)	(Sam2) or (Sam1)
HSERTA	homoserine O-trans-acetylase	[c] : accoa + hom-L <==> achms + coa	EC-2.3.1.31	Methionine Metabolism	YNL277W	Met2
DIPS	diphthine synthase	[c] : amet + caphis --> ahcys + cmaphis + h	EC-2.1.1.98	Methionine Metabolism	YLR172C	Dph5
CYSTLp	cystathione b-lyase, peroxisomal	[x] : cyst-L + h2o --> hcys-L + nh4 + pyr	EC-4.4.1.8	Methionine Metabolism	YGL184C	Str3-p
CYSTL	cystathionine b-lyase	[c] : cyst-L + h2o --> hcys-L + nh4 + pyr	EC-4.4.1.8	Methionine Metabolism	YFR055W	Cys1
CYSTGL	cystathionine g-lyase	[c] : cyst-L + h2o --> 2obut + cys-L + nh4	EC-4.4.1.1	Methionine Metabolism	YAL012W	Cys3
AHSERL2	O-acetylhomoserine (thiol)-lyase	[c] : achms + h2s --> ac + h + hcys-L	EC-4.2.99.8	Methionine Metabolism	YLR303W	Met17
AHSERL	O-acetylhomoserine (thiol)-lyase	[c] : achms + ch4s --> ac + h + met-L	EC-4.2.99.10	Methionine Metabolism	YLR303W	Met17
AHCi	adenosylhomocysteinase	[c] : ahcys + h2o --> adn + hcys-L	EC-3.3.1.1	Methionine Metabolism	YER043C	Sah1
PUNP3m	purine-nucleoside phosphorylase (Guanosine), mitochondrial	[m] : gsn + pi <==> gua + r1p	EC-2.4.2.1	NAD Biosynthesis	YLR209C	Pnp1-m
PUNP1m	purine-nucleoside phosphorylase (Adenosine), mitochondrial	[m] : adn + pi <==> ade + r1p	EC-2.4.2.1	NAD Biosynthesis	YLR209C	Pnp1-m
NNDPRm	nicotinate-nucleotide diphosphorylase (carboxylating), mitochondrial	[m] : (2) h + prpp + quln --> co2 + nicrnt + ppi	EC-2.4.2.19	NAD Biosynthesis	YFR047C	Bna6-m
NNDPR	nicotinate-nucleotide diphosphorylase (carboxylating)	[c] : (2) h + prpp + quln --> co2 + nicrnt + ppi	EC-2.4.2.19	NAD Biosynthesis	YFR047C	Bna6
NNATm	nicotinate-nucleotide adenylyltransferase, mitochondrial	[m] : atp + h + nicrnt --> dnad + ppi	EC-2.7.7.18	NAD Biosynthesis	YLR328W	Nma1-m
NNAT	nicotinate-nucleotide adenylyltransferase	[c] : atp + h + nicrnt --> dnad + ppi	EC-2.7.7.18	NAD Biosynthesis	YLR328W	Nma1
NNAMrm	nicotinamidase, reversible, mitochondrial	[m] : h2o + ncam <==> nac + nh4	EC-3.5.1.19	NAD Biosynthesis	YGL037C	Pnc1-m
NNAMr	nicotinamidase, reversible	[c] : h2o + ncam <==> nac + nh4	EC-3.5.1.19	NAD Biosynthesis	YGL037C	Pnc1
NMNATm	nicotinamide-nucleotide adenylyltransferase, mitochondrial	[m] : atp + h + nmn --> nad + ppi	EC-2.7.7.1	NAD Biosynthesis	YLR328W	Nma1-m
NAPRTm	NAPRTase, mitochondrial	[m] : h + nac + prpp --> nicrnt + ppi	EC-2.4.2.11	NAD Biosynthesis	YOR209C	Npt1-m
NAPRT	NAPRTase	[c] : h + nac + prpp --> nicrnt + ppi	EC-2.4.2.11	NAD Biosynthesis	YOR209C	Npt1
NADS1m	NAD synthase (nh3), mitochondrial	[m] : atp + dnad + nh4 --> amp + h + nad + ppi	EC-6.3.1.5	NAD Biosynthesis	YHR074W	Qns1-m
NADS1	NAD synthase (nh3)	[c] : atp + dnad + nh4 --> amp + h + nad + ppi	EC-6.3.1.5	NAD Biosynthesis	YHR074W	Qns1
NADPPPSm	NADP phosphatase	[m] : h2o + nadp --> nad + pi		NAD Biosynthesis		
NADPPPS	NADP phosphatase	[c] : h2o + nadp --> nad + pi		NAD Biosynthesis		
NADNm	NAD nucleosidase, mitochondrial	[m] : h2o + nad --> adprib + h + ncam	EC-3.2.2.5	NAD Biosynthesis		
NADN	NAD nucleosidase	[c] : h2o + nad --> adprib + h + ncam	EC-3.2.2.5	NAD Biosynthesis		
NADKm	NAD kinase, mitochondrial	[m] : atp + nad --> adp + h + nadp	EC-2.7.1.23	NAD Biosynthesis	(YJR049C or YPL188W or YEL041W)	(Utr1-m) or (Pos5-m) or (Utr2-m)
NADK	NAD kinase	[c] : atp + nad --> adp + h + nadp	EC-2.7.1.23	NAD Biosynthesis	(YJR049C or YEL041W or YPL188W)	(Utr1) or (Utr2) or (Pos5)
UREASE	urea carboxylase	[c] : atp + hco3 + urea <==> adp + allphn + h + pi	EC-6.3.4.6	Nitrogen Metabolism	YBR208C	Dur1
NTRLASE	nitrilase	[c] : (2) h2o + ind3acnl --> ind3ac + nh4	EC-3.5.5.1	Nitrogen Metabolism	(YLR351C or YJL126W)	(Nit3) or (Nit2)
ALPHNH	allophanate hydrolase	[c] : allphn + (3) h + h2o --> (2) co2 + (2) nh4	EC-3.5.1.54	Nitrogen Metabolism	YBR208C	Dur1
XPPT	xanthine phosphoribosyltransferase	[c] : prpp + xan --> ppi + xmp	EC-2.4.2.22	Nucleotide Salvage Pathways	YJR133W	Xpt1
URIDK2rn	uridylate kinase (dUMP), nuclear	[n] : atp + dump <==> adp + dudp		Nucleotide Salvage Pathways	YKL024C	Ura6-n
URIDK2r	uridylate kinase (dUMP)	[c] : atp + dump <==> adp + dudp		Nucleotide Salvage Pathways	YKL024C	Ura6
UMPKn	UMP kinase, nuclear	[n] : atp + ump <==> adp + udp		Nucleotide Salvage Pathways	YKL024C	Ura6-n
UMPK	UMP kinase	[c] : atp + ump <==> adp + udp		Nucleotide Salvage Pathways	YKL024C	Ura6
RNTR4	ribonucleoside-triphosphate reductase (UTP)	[c] : trdrd + utp --> dutp + h2o + trdox	EC-1.17.4.2	Nucleotide Salvage Pathways		
RNTR3	ribonucleoside-triphosphate reductase (CTP)	[c] : ctp + trdrd --> dctp + h2o + trdox	EC-1.17.4.2	Nucleotide Salvage Pathways		
RNTR2	ribonucleoside-triphosphate reductase (GTP)	[c] : gtp + trdrd --> dgtp + h2o + trdox	EC-1.17.4.2	Nucleotide Salvage Pathways		
RNTR1	ribonucleoside-triphosphate reductase (ATP)	[c] : atp + trdrd --> datp + h2o + trdox	EC-1.17.4.2	Nucleotide Salvage Pathways		
RNDR4n	ribonucleoside-diphosphate reductase (UDP), nuclear	[n] : trdrd + udp --> dudp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	(YER070W and YGR180C)	Rnr14-n
RNDR4	ribonucleoside-diphosphate reductase (UDP)	[c] : trdrd + udp --> dudp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	(YER070W and YJL026W)	Rnr12
RNDR3n	ribonucleoside-diphosphate reductase (CDP), nuclear	[n] : cdp + trdrd --> dcdp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	(YER070W and YGR180C)	Rnr14-n
RNDR3	ribonucleoside-diphosphate reductase (CDP)	[c] : cdp + trdrd --> dcdp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	(YER070W and YJL026W)	Rnr12
RNDR2n	ribonucleoside-diphosphate reductase (GDP), nuclear	[n] : gdp + trdrd --> dgdp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	(YER070W and YGR180C)	Rnr14-n
RNDR2	ribonucleoside-diphosphate reductase (GDP)	[c] : gdp + trdrd --> dgdp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	(YER070W and YJL026W)	Rnr12
RNDR1n	ribonucleoside-diphosphate reductase, nuclear	[n] : adp + trdrd --> dadp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	((YER070W and YGR180C) or (YGR180C and YIL066C))	(Rnr14-n) or (Rnr34-n)

RNDR1	ribonucleoside-diphosphate reductase (ADP)	[c] : adp + trdrd --> dadp + h2o + trdox	EC-1.17.4.1	Nucleotide Salvage Pathways	((YIL066C and YJL026W) or (YER070W and YJL026W))	(Rnr32) or (Rnr12)
PYNP2r	pyrimidine-nucleoside phosphorylase (uracil)	[c] : pi + uri <==> r1p + ura	EC-2.4.2.2	Nucleotide Salvage Pathways		
PUNP7	purine-nucleoside phosphorylase (Xanthosine)	[c] : pi + xtsn <==> r1p + xan	EC-2.4.2.1	Nucleotide Salvage Pathways	YLR209C	Pnp1
PUNP6	purine-nucleoside phosphorylase (Deoxyinosine)	[c] : din + pi <==> 2dr1p + hxan	EC-2.4.2.1	Nucleotide Salvage Pathways	YLR209C	Pnp1
PUNP5	purine-nucleoside phosphorylase (Inosine)	[c] : ins + pi <==> hxan + r1p	EC-2.4.2.1	Nucleotide Salvage Pathways	YLR209C	Pnp1
PUNP4	purine-nucleoside phosphorylase (Deoxyguanosine)	[c] : dgsn + pi <==> 2dr1p + gua	EC-2.4.2.1	Nucleotide Salvage Pathways	YLR209C	Pnp1
PUNP3	purine-nucleoside phosphorylase (Guanosine)	[c] : gsn + pi <==> gua + r1p	EC-2.4.2.1	Nucleotide Salvage Pathways	YLR209C	Pnp1
PUNP2	purine-nucleoside phosphorylase (Deoxyadenosine)	[c] : dad-2 + pi <==> 2dr1p + ade	EC-2.4.2.1	Nucleotide Salvage Pathways	YLR209C	Pnp1
PUNP1	purine-nucleoside phosphorylase (Adenosine)	[c] : adn + pi <==> ade + r1p	EC-2.4.2.1	Nucleotide Salvage Pathways	YLR209C	Pnp1
NTP4	nucleoside-triphosphatase (dGTP)	[c] : dgtp + h2o --> dgdp + h + pi	EC-3.6.1.15	Nucleotide Salvage Pathways		
NTP3	nucleoside-triphosphatase (GTP)	[c] : gtp + h2o --> gdp + h + pi	EC-3.6.1.15	Nucleotide Salvage Pathways		
NTD9	5'-nucleotidase (GMP)	[c] : gmp + h2o --> gsn + pi	EC-3.1.3.5	Nucleotide Salvage Pathways		
NTD8	5'-nucleotidase (dGMP)	[c] : dgmp + h2o --> dgsn + pi	EC-3.1.3.5	Nucleotide Salvage Pathways		
NTD7	5'-nucleotidase (AMP)	[c] : amp + h2o --> adn + pi	EC-3.1.3.5	Nucleotide Salvage Pathways		
NTD6	5'-nucleotidase (dAMP)	[c] : damp + h2o --> dad-2 + pi	EC-3.1.3.5	Nucleotide Salvage Pathways		
NTD5	5'-nucleotidase (dTMP)	[c] : dtmp + h2o --> pi + thymd	EC-3.1.3.5	Nucleotide Salvage Pathways		
NTD4	5'-nucleotidase (CMP)	[c] : cmp + h2o --> cytd + pi	EC-3.1.3.5	Nucleotide Salvage Pathways		
NTD3	5'-nucleotidase (dCMP)	[c] : dcmp + h2o --> dcyt + pi	EC-3.1.3.5	Nucleotide Salvage Pathways		
NTD2	5'-nucleotidase (UMP)	[c] : h2o + ump --> pi + uri	EC-3.1.3.5	Nucleotide Salvage Pathways		
NTD11	5'-nucleotidase (IMP)	[c] : h2o + imp --> ins + pi	EC-3.1.3.5	Nucleotide Salvage Pathways		
NTD10	5'-nucleotidase (XMP)	[c] : h2o + xmp --> pi + xtsn	EC-3.1.3.5	Nucleotide Salvage Pathways		
NTD1	5'-nucleotidase (dUMP)	[c] : dump + h2o --> duri + pi	EC-3.1.3.5	Nucleotide Salvage Pathways		
NDPK9	nucleoside-diphophate kinase (ATP:IDP)	[c] : atp + idp <==> adp + itp	EC-2.7.4.6	Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK8	nucleoside-diphosphate kinase (ATP:dADP)	[c] : atp + dadp <==> adp + datp	EC-2.7.4.6	Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK7	nucleoside-diphosphate kinase (ATP:dCDP)	[c] : atp + dcdp <==> adp + dctp	EC-2.7.4.6	Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK6	nucleoside-diphosphate kinase (ATP:dUDP)	[c] : atp + dudp <==> adp + dutp	EC-2.7.4.6	Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK5	nucleoside-diphosphate kinase (ATP:dGDP)	[c] : atp + dgdp <==> adp + dgtp	EC-2.7.4.6	Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK4	nucleoside-diphosphate kinase (ATP:dTDP)	[c] : atp + dtdp <==> adp + dttp	EC-2.7.4.6	Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK3	nucleoside-diphosphate kinase (ATP:CDP)	[c] : atp + cdp <==> adp + ctp	EC-2.7.4.6	Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK2	nucleoside-diphosphate kinase (ATP:UDP)	[c] : atp + udp <==> adp + utp	EC-2.7.4.6	Nucleotide Salvage Pathways	YKL067W	Ynk1
NDPK1	nucleoside-diphosphate kinase (ATP:GDP)	[c] : atp + gdp <==> adp + gtp	EC-2.7.4.6	Nucleotide Salvage Pathways	YKL067W	Ynk1
NDP4	nucleoside-diphosphatase (dGDP)	[c] : dgdp + h2o --> dgmp + h + pi	EC-3.6.1.6	Nucleotide Salvage Pathways		
NDP3g	nucleoside-diphosphatase (GDP), Golgi apparatus	[g] : gdp + h2o --> gmp + h + pi	EC-3.6.1.6	Nucleotide Salvage Pathways	YEL042W	Gda1-g
NDP3	nucleoside-diphosphatase (GDP)	[c] : gdp + h2o --> gmp + h + pi	EC-3.6.1.6	Nucleotide Salvage Pathways		
INSK	insosine kinase	[c] : atp + ins --> adp + h + imp	EC-2.7.1.73	Nucleotide Salvage Pathways		
HXPRT	hypoxanthine phosphoribosyltransferase (Hypoxanthine)	[c] : hxan + prpp --> imp + ppi	EC-2.4.2.8	Nucleotide Salvage Pathways	YDR399W	Hpt1
GSNK	guanosine kinase	[c] : atp + gsn --> adp + gmp + h		Nucleotide Salvage Pathways		
GNNUC	gnnuc	[c] : gsn + h2o --> gua + rib-D		Nucleotide Salvage Pathways	YDR400W	Urh1
DTMPK	dTMP kinase	[c] : atp + dtmp <==> adp + dtdp	EC-2.7.4.9	Nucleotide Salvage Pathways	YJR057W	Cdc8
DCYTD	deoxycytidine deaminase	[c] : dcyt + h + h2o --> duri + nh4	EC-3.5.4.14	Nucleotide Salvage Pathways	YLR245C	Cdd1
DCTPD	dCTP deaminase	[c] : dctp + h + h2o --> dutp + nh4	EC-3.5.4.13	Nucleotide Salvage Pathways	YHR144C	Dcd1
DADK	deoxyadenylate kinase	[c] : atp + damp <==> adp + dadp	EC-2.7.4.11	Nucleotide Salvage Pathways		
DADA	Deoxyadenosine deaminase	[c] : dad-2 + h + h2o --> din + nh4		Nucleotide Salvage Pathways	YNL141W	Aah1
CYTK2	cytidylate kinase (dCMP)	[c] : atp + dcmp <==> adp + dcdp	EC-2.7.4.14	Nucleotide Salvage Pathways		
CYTK1	cytidylate kinase (CMP)	[c] : atp + cmp <==> adp + cdp	EC-2.7.4.14	Nucleotide Salvage Pathways		
CYTDK2	cytidine kinase (GTP)	[c] : cytd + gtp --> cmp + gdp + h		Nucleotide Salvage Pathways	YNR012W	Urk1
CMPN	CMP nucleosidase	[c] : cmp + h2o --> csn + r5p	EC-3.2.2.10	Nucleotide Salvage Pathways		
ATPM	ATP maintenance requirement	[c] : atp + h2o --> adp + h + pi		Nucleotide Salvage Pathways		
AMPN	AMP nucleosidase	[c] : amp + h2o --> ade + r5p	EC-3.2.2.4	Nucleotide Salvage Pathways	(YML035C or YBR284W or YJL070C)	(Amd1) or (Amd5) or (Amd3)
ADPT	adenine phosphoribosyltransferase	[c] : ade + prpp --> amp + ppi	EC-2.4.2.7	Nucleotide Salvage Pathways	(YML022W or YDR441C)	(Apt1) or (Apt2)
ADNUC	adnuc	[c] : adn + h2o --> ade + rib-D		Nucleotide Salvage Pathways	YDR400W	Urh1
ADNK1	adenosine kinase	[c] : adn + atp --> adp + amp + h	EC-2.7.1.20	Nucleotide Salvage Pathways	YJR105W	Ado1
ADK4m	adentylate kinase (ITP), mitochondrial	[m] : amp + itp <==> adp + idp	EC-2.7.4.3	Nucleotide Salvage Pathways	YER170W	Adk2-m
ADK4	adentylate kinase (ITP)	[c] : amp + itp <==> adp + idp		Nucleotide Salvage Pathways	YDR226W	Adk1
ADK3m	adentylate kinase (GTP)	[m] : amp + gtp <==> adp + gdp		Nucleotide Salvage Pathways	YER170W	Adk2-m
ADK3	adentylate kinase (GTP)	[c] : amp + gtp <==> adp + gdp		Nucleotide Salvage Pathways	YDR226W	Adk1
ADK1m	adenylate kinase, mitochondrial	[m] : amp + atp <==> (2) adp	EC-2.7.4.3	Nucleotide Salvage Pathways	YER170W	Adk2-m
ADK1	adenylate kinase	[c] : amp + atp <==> (2) adp	EC-2.7.4.3	Nucleotide Salvage Pathways	YDR226W	Adk1
ADD	adenine deaminase	[c] : ade + h + h2o --> hxan + nh4	EC-3.5.4.2	Nucleotide Salvage Pathways	YNL141W	Aah1
ADA	Adenosine deaminase	[c] : adn + h + h2o --> ins + nh4	EC-3.5.4.4	Nucleotide Salvage Pathways	YNL141W	Aah1
GUAPRT	guanine phosphoribosyltransferase	[c] : gua + prpp --> gmp + ppi		Nucleotide Savage Pathway	YDR399W	Hpt1
PEPAT	Peptide alpha-N-acetyltransferase	[c] : accoa + pepd --> apep + coa + h	EC-2.3.1.88	Other Amino Acid Metabolism	(YDL040C or YGR147C)	(Nat1) or (Nat2)
NTRLASE3	nitrilase	[c] : acybut + (2) h2o --> glu-L + nh4	EC-3.5.5.1	Other Amino Acid Metabolism	(YLR351C or YJL126W)	(Nit3) or (Nit2)
NTRLASE2	nitrilase	[c] : aprop + (2) h2o --> ala-L + nh4	EC-3.5.5.1	Other Amino Acid Metabolism	(YJL126W or YLR351C)	(Nit2) or (Nit3)
NABTNO	N4-Acetylaminobutanal:NAD+ oxidoreductase	[c] : h2o + n4abutn + nad --> 4aabutn + (2) h + nadh	EC-1.2.1.3	Other Amino Acid Metabolism		
LCADm	lactaldehyde dehydrogenase, mitochondrial	[m] : h2o + lald-L + nad <==> (2) h + lac-L + nadh	EC-1.2.1.22	Other Amino Acid Metabolism	YER073W	Ald5-m
GTMLT	g-glutamyltransferase	[c] : ala-L + gthrd --> cgly + gluala	EC-2.3.2.2	Other Amino Acid Metabolism	YLR299W	Ecm38
GTHS	glutathione synthetase	[c] : atp + glucys + gly --> adp + gthrd + h + pi	EC-6.3.2.3	Other Amino Acid Metabolism	YOL049W	Gsh2
GTHP	glutathione peridoxase	[c] : (2) gthrd + h2o2 <==> gthox + (2) h2o	EC-1.11.1.9	Other Amino Acid Metabolism	(YBR244W or YIR037W or YKL026C)	(Gpx2) or (Hyr1) or (Gpx1)
GTHO	glutathione oxidoreductase	[c] : gthox + h + nadph --> (2) gthrd + nadp	EC-1.8.1.7	Other Amino Acid Metabolism	YPL091W	Glr1
GLUCYS	gamma-glutamylcysteine synthetase	[c] : atp + cys-L + glu-L --> adp + glucys + h + pi	EC-6.3.2.2	Other Amino Acid Metabolism	YJL101C	Gsh1
GLPT	glycylpeptide N-tetradecanoyltransferase	[c] : glp + tdcoa --> coa + tglp	EC-2.3.1.97	Other Amino Acid Metabolism	YLR195C	Nmt1

APRTO2	N-acetylputrescine: oxygen oxireductase (deaminating)	[c] : aprut + h2o + o2 --> h2o2 + n4abutn + nh4	EC-1.4.3.4	Other Amino Acid Metabolism		
ABUTDm	Aminobutyraldehyde dehydrogenase, mitochondrial	[m] : 4abutn + h2o + nad --> 4abut + (2) h + nadh	EC-1.2.1.19	Other Amino Acid Metabolism	(YOR374W or YER073W)	(Ald4-m) or (Ald5-m)
AABTN	4-acetamidobutyrate deacetylase	[c] : 4aabutn + h2o --> 4abut + ac	EC-3.5.1.63	Other Amino Acid Metabolism		
SUCD3-u6m	succinate dehydrogenase (ubiquinone-6), mitochondrial	[m] : fadh2 + q6 <==> fad + q6h2	EC-1.3.5.1	Oxidative phosphorylation	((YDR178W and YKL141W and YKL148C and YLL041C) or (YKL141W and YKL148C and YLL041C and YLR164W) or (YDR178W and YKL148C and YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C))	(Sdh-m) or (Sdh2-m) or (Sdh3-m) or (Sdh4-m)
SUCD1m	succinate dehydrogenase, mitochondrial	[m] : fad + succ <==> fadh2 + fum	EC-1.3.99.1	Oxidative phosphorylation	((YDR178W and YKL141W and YKL148C and YLL041C) or (YKL141W and YKL148C and YLL041C and YLR164W) or (YDR178W and YKL148C and YLL041C and YMR118C) or (YDR178W and YJL045W and YKL141W and YLL041C))	(Sdh-m) or (Sdh2-m) or (Sdh3-m) or (Sdh4-m)
PPAm	inorganic diphosphatase, mitochondrial	[m] : h2o + ppi --> h + (2) pi	EC-3.6.1.1	Oxidative phosphorylation	YMR267W	Ppa2-m
PPA	inorganic diphosphatase	[c] : h2o + ppi --> h + (2) pi	EC-3.6.1.1	Oxidative phosphorylation	YBR011C	Ipp1
NADH2-u6m	NADH dehydrogenase, mitochondrial	[m] : h + nadh + q6 --> nad + q6h2	EC-1.6.99.3	Oxidative phosphorylation	(YML120C or YKL192C)	(Ndi1-m) or (Acp1-m)
NADH2-u6cm	NADH dehydrogenase, cytosolic/mitochondrial	h[c] + nadh[c] + q6[m] --> nad[c] + q6h2[m]	EC-1.6.99.3	Oxidative phosphorylation	(YMR145C or YDL085W)	(Nde1-m) or (Nde2-m)
MDHp	malate dehydrogenase, peroxisomal	[x] : mal-L + nad <==> h + nadh + oaa	EC-1.1.1.37	Oxidative phosphorylation	YDL078C	Mdh3-p
MDHm	malate dehydrogenase, mitochondrial	[m] : mal-L + nad <==> h + nadh + oaa	EC-1.1.1.37	Oxidative phosphorylation	YKL085W	Mdh1-m
MDH	malate dehydrogenase	[c] : mal-L + nad <==> h + nadh + oaa	EC-1.1.1.37	Oxidative phosphorylation	YOL126C	Mdh2
FUMm	fumarase, mitochondrial	[m] : fum + h2o <==> mal-L	EC-4.2.1.2	Oxidative phosphorylation	YPL262W	Fum1-m
FUM	fumarase	[c] : fum + h2o <==> mal-L	EC-4.2.1.2	Oxidative phosphorylation	YPL262W	Fum1
FRDm	fumarate reductase, mitochondrial	[m] : fadh2 + fum --> fad + succ	EC-1.3.99.1	Oxidative phosphorylation	YJR051W	Osm1-m
FDNG	formate dehydrogenase, cytosolic/mitochondrial	for[c] + h[c] + q6[m] --> co2[c] + q6h2[m]	EC-1.2.2.1	Oxidative phosphorylation		
CYOR_u6m	ubiquinol-6 cytochrome c reductase	(2) ficytc[m] + (1.5) h[m] + q6h2[m] --> (2) focytc[m] + (1.5) h[c] + q6[m]	EC-1.10.2.2	Oxidative phosphorylation	(Q0105 and YBL045C and YDR529C and YEL024W and YFR033C and YGR183C and YHR001W-A and YJL166W and YOR065W and YPR191W)	Cbc1-m
CYOOm	cytochrome c oxidase, mitochondrial	(4) focytc[m] + (6) h[m] + o2[m] --> (4) ficytc[m] + (6) h[c] + (2) h2o[m]	EC-1.9.3.1	Oxidative phosphorylation	((Q0045 and Q0250 and Q0275 and YDL067C and YGL187C and YGL191W and YHR051W and YLR038C and YLR395C and YMR256C and YNL052W) or (Q0045 and Q0250 and Q0275 and YDL067C and YGL187C and YGL191W and YHR051W and YIL111W and YLR038C and YLR395C and YMR256C))	(Cco1-m) or (Cco2-m)
ATPS3v	ATP synthase, vacuole	adp[v] + (3) h[c] + pi[v] --> atp[v] + (2) h[v] + h2o[v]	EC-3.6.3.14	Oxidative phosphorylation	(YBR127C and YDL185W and YEL027W and YEL051W and YGR020C and YHR026W and YHR039C-A and YKL080W and YLR447C and YOR270C and YOR332W and YPL234C and YPR036W)	Hatp-v

ATPS3m	ATP synthase, mitochondrial	adp[m] + (3) h[c] + pi[m] --> atp[m] + (2) h[m] + h2o[m]	EC-3.6.3.14	Oxidative phosphorylation	((Q0080 and Q0085 and Q0130 and YBL099W and YBR039W and YDL004W and YDL181W and YDR298C and YDR322C-A and YDR377W and YJR121W and YKL016C and YLR295C and YML081C-A and YOL077W-A and YPL078C and YPL271W and YPR020W) or (Q0080 and Q0085 and Q0130 and YBL099W and YBR039W and YDL004W and YDL181W and YDR298C and YDR377W and YJR121W and YKL016C and YLR295C and YML081C-A and YPL078C and YPL271W))	(Atps2-m) or (Atps1-m)
ATPS3g	ATP synthase, Golgi Apparatus	adp[g] + (3) h[c] + pi[g] --> atp[g] + (2) h[g] + h2o[g]		Oxidative phosphorylation	(YBR127C and YDL185W and YEL027W and YEL051W and YGR020C and YHR026W and YHR039C-A and YKL080W and YLR447C and YMR054W and YOR332W and YPL234C and YPR036W)	Hatp-g
PTPATim	pantetheine-phosphate adenylyltransferase	[m] : atp + h + pan4p --> dpcoa + ppi	EC-2.7.7.3	Pantothenate and CoA Biosynthesis		
PTPATi	pantetheine-phosphate adenylyltransferase	[c] : atp + h + pan4p --> dpcoa + ppi	EC-2.7.7.3	Pantothenate and CoA Biosynthesis		
PPNCL2	phosphopantothenate-cysteine ligase	[c] : 4ppan + ctp + cys-L --> 4ppcys + cmp + h + ppi	EC-6.3.2.5	Pantothenate and CoA Biosynthesis		
PPCDC	phosphopantothenoylcysteine decarboxylase	[c] : 4ppcys + h --> co2 + pan4p	EC-4.1.1.36	Pantothenate and CoA Biosynthesis		
PNTK	pantothenate kinase	[c] : atp + pnto-R --> 4ppan + adp + h	EC-2.7.1.33	Pantothenate and CoA Biosynthesis	YDR531W	Pnk1
PANTS	pantothenate synthase	[c] : ala-B + atp + pant-R --> amp + h + pnto-R + ppi	EC-6.3.2.1	Pantothenate and CoA Biosynthesis	YIL145C	Pan6
MOHMT	3-methyl-2-oxobutanoate hydroxymethyltransferase	[c] : 3mob + h2o + mlthf --> 2dhp + thf	EC-2.1.2.11	Pantothenate and CoA Biosynthesis	YBR176W	Ecm31
DPRm	2-dehydropantoate 2-reductase, mitochondrial	[m] : 2dhp + h + nadph --> nadp + pant-R	EC-	Pantothenate and CoA Biosynthesis	YLR355C	Ilv5-m
DPR	2-dehydropantoate 2-reductase	[c] : 2dhp + h + nadph --> nadp + pant-R	EC-	Pantothenate and CoA Biosynthesis	YHR063C	Pan5
DPCOAKm	dephospho-CoA kinase, mitochondrial	[m] : atp + dpcoa --> adp + coa + h	EC-2.7.1.24	Pantothenate and CoA Biosynthesis		
DPCOAK	dephospho-CoA kinase	[c] : atp + dpcoa --> adp + coa + h	EC-2.7.1.24	Pantothenate and CoA Biosynthesis		
DBTSr	dethiobiotin synthase	[c] : atp + co2 + dann <==> adp + dtbt + (3) h + pi	EC-6.3.3.3	Pantothenate and CoA Biosynthesis	YNR057C	Bio4
BTSr	biotin synthase	[c] : dtbt + s <==> btn + (2) h	EC-2.8.1.6	Pantothenate and CoA Biosynthesis	YGR286C	Bio2
ASP1DC	aspartate 1-decarboxylase	[c] : asp-L + h --> ala-B + co2	EC-4.1.1.11	Pantothenate and CoA Biosynthesis		
AMAOTr	adenosylmethionine-8-amino-7-oxononanoate transaminase	[c] : 8aonn + amet <==> amob + dann	EC-2.6.1.62	Pantothenate and CoA Biosynthesis	YNR058W	Bio3
ACPSm	acyl carrier protein synthase, mitochondrial	[m] : coa + h2o --> (2) h + pan4p + pap		Pantothenate and CoA Biosynthesis	YPL148C	Ppt2-m
TKT2	transketolase	[c] : e4p + xu5p-D <==> f6p + g3p	EC-2.2.1.1	Pentose Phosphate Cycle	(YPR074C or YBR117C)	(Tkl1) or (Tkl2)
TKT1	transketolase	[c] : r5p + xu5p-D <==> g3p + s7p	EC-2.2.1.1	Pentose Phosphate Cycle	(YBR117C or YPR074C)	(Tkl2) or (Tkl1)
TALA	transaldolase	[c] : g3p + s7p <==> e4p + f6p	EC-2.2.1.2	Pentose Phosphate Cycle	(YLR354C or YGR043C)	(Tal1) or (Tal2)
RPI	ribose-5-phosphate isomerase	[c] : r5p <==> ru5p-D	EC-5.3.1.6	Pentose Phosphate Cycle	YOR095C	Rki1
RPE	ribulose 5-phosphate 3-epimerase	[c] : ru5p-D <==> xu5p-D	EC-5.1.3.1	Pentose Phosphate Cycle	YJL121C	Rpe1
RBK	ribokinase	[c] : atp + rib-D --> adp + h + r5p	EC-2.7.1.15	Pentose Phosphate Cycle	YCR036W	Rbk1
PPM	phosphopentomutase	[c] : r1p <==> r5p	EC-5.4.2.7	Pentose Phosphate Cycle	(YKL127W or YMR105C)	(Pgm1) or (Pgm2)
PGMT	phosphoglucomutase	[c] : g1p <==> g6p	EC-5.4.2.2	Pentose Phosphate Cycle	(YKL127W or YMR105C)	(Pgm1) or (Pgm2)
PGL	6-phosphogluconolactonase	[c] : 6pgl + h2o --> 6pgc + h	EC-3.1.1.31	Pentose Phosphate Cycle	(YNR034W or YHR163W or YGR248W or YCR073W-A)	(Sol1) or (Sol3) or (Sol4) or (Sol2)
GND	phosphogluconate dehydrogenase	[c] : 6pgc + nadp --> co2 + nadph + ru5p-D	EC-1.1.1.44	Pentose Phosphate Cycle	(YGR256W or YHR183W)	(Gnd2) or (Gnd1)
G6PDH2er	glucose 6-phosphate dehydrogenase, endoplasmic reticular	[r] : g6p + nadp --> 6pgl + h + nadph		Pentose Phosphate Cycle		
G6PDH2	glucose 6-phosphate dehydrogenase	[c] : g6p + nadp --> 6pgl + h + nadph	EC-1.1.1.49	Pentose Phosphate Cycle	YNL241C	Zwf1
DRBK	Deoxyribokinase	[c] : atp + drib --> 2dr5p + adp + h	EC-2.7.1.15	Pentose Phosphate Cycle	YCR036W	Rbk1
PSERSm_SC	phosphatidylserine synthase, yeast-specific, mitochondrial	[m] : (0.01) cdpdag_SC + ser-L <==> cmp + h + (0.01) ps_SC	EC-2.7.8.8	Phospholipid Biosynthesis	YER026C	Cho1-m
PSERS_SC	phosphatidylserine synthase, yeast-specific	[c] : (0.01) cdpdag_SC + ser-L <==> cmp + h + (0.01) ps_SC	EC-2.7.8.8	Phospholipid Biosynthesis	YER026C	Cho1
PSERDv_SC	phosphatidylserine decarboxylase, yeast-specific, vacuolar	[v] : h + (0.01) ps_SC --> co2 + (0.01) pe_SC	EC-4.1.1.65	Phospholipid Biosynthesis	YGR170W	Psd2-v
PSERDm_SC	phosphatidylserine decarboxylase, yeast-specific, mitochondrial	[m] : h + (0.01) ps_SC --> co2 + (0.01) pe_SC	EC-4.1.1.65	Phospholipid Biosynthesis	YNL169C	Psd1-m
PSERDg_SC	phosphatidylserine decarboxylase, yeast-specific, Golgi apparatus	[g] : h + (0.01) ps_SC --> co2 + (0.01) pe_SC	EC-4.1.1.65	Phospholipid Biosynthesis	YGR170W	Psd2-g
PMETM_SC	Phosphatidyl-N-methylethanolamine N-methyltransferase, yeast-specific	[c] : amet + (0.01) ptd2meeta_SC --> ahcys + h + (0.01) pc_SC	EC-2.1.1.16	Phospholipid Biosynthesis	YJR073C	Opi3
PINOS_SC	phosphatidylinositol synthase, yeast-specific	[c] : (0.01) cdpdag_SC + inost --> cmp + h + (0.01) ptd1ino_SC	EC-2.7.8.11	Phospholipid Biosynthesis	YPR113W	Pis1
PIN4Kn_SC	phosphatidylinositol 4-kinase, nuclear, yeast-specifc	[n] : atp + (0.01) ptd1ino_SC --> adp + h + (0.01) ptd4ino_SC	EC-2.7.1.67	Phospholipid Biosynthesis	YNL267W	Pik1-n
PIN4K_SC	phosphatidylinositol 4-kinase, yeast-specific	[c] : atp + (0.01) ptd1ino_SC --> adp + h + (0.01) ptd4ino_SC	EC-2.7.1.67	Phospholipid Biosynthesis	(YNL267W or YLR305C)	(Pik1) or (Stt4)

PIN3K_SC	1-phosphatidylinositol 3-kinase, yeast-specific	[c] : atp + (0.01) ptd1ino_SC --> adp + h + (0.01) ptd3ino_SC	EC-2.7.1.137	Phospholipid Biosynthesis	(YKL203C or YLR240W or YJR066W)	(Tor2) or (Vps34) or (Tor1)
PI4P5K_SC	phosphatidylinositol-4-phosphate 5-kinase, yeast-specfic	[c] : atp + (0.01) ptd4ino_SC --> adp + h + (0.01) ptd145bp_SC	EC-2.7.1.68	Phospholipid Biosynthesis	(YDR208W or YFR019W)	(Mss4) or (Fab1)
PI45BPP_SC	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase, yeast-specific	[c] : h2o + (0.01) ptd145bp_SC --> (0.01) 12dgr_SC + h + mi145tp-D	EC-3.1.4.11	Phospholipid Biosynthesis	YPL268W	Plc1
PI3P4K_SC	phosphatidylinositol-3-phosphate 4-kinase, yeast-specific	[c] : atp + (0.01) ptd3ino_SC --> adp + h + (0.01) ptd134bp_SC		Phospholipid Biosynthesis		
PGPPAm_SC	phosphatidylglycerol phosphate phosphatase A, yeast-specific, mitochondrial	[m] : h2o + (0.01) pgp_SC --> (0.01) pg_SC + pi	EC-3.1.3.27	Phospholipid Biosynthesis		
PETOHM_SC	phosphatidylethanolamine N-methyltransferase, yeast-specific	[c] : amet + (0.01) pe_SC --> ahcys + h + (0.01) ptdmeeta_SC	EC-2.1.1.17	Phospholipid Biosynthesis	YGR157W	Cho2
PETHCT	phosphoethanolamine cytidyltransferase	[c] : ctp + ethamp + h --> cdpea + ppi	EC-2.7.7.14	Phospholipid Biosynthesis	YGR007W	Muq1
PAK_SC	phosphatidate kinase, yeast-specific	[c] : atp + (0.01) pa_SC --> adp + (0.01) dagpy_SC		Phospholipid Biosynthesis		
MI1PS	myo-Inositol-1-phosphate synthase	[c] : g6p --> mi1p-D	EC-5.5.1.4	Phospholipid Biosynthesis	YJL153C	Ino1
MI1PP	myo-inositol 1-phosphatase	[c] : h2o + mi1p-D --> inost + pi	EC-3.1.3.25	Phospholipid Biosynthesis	YHR046C	Inm1
MFAPS_SC	methylene-fatty-acyl-phospholipid synthase, yeast-specific	[c] : amet + (0.01) ptdmeeta_SC --> ahcys + h + (0.01) ptd2meeta_SC	EC-2.1.1.16	Phospholipid Biosynthesis	YJR073C	Opi3
LPP_SC	lipid phosphate phosphatase, yeast-specific	[c] : (0.01) dagpy_SC + h2o --> h + (0.01) pa_SC + pi		Phospholipid Biosynthesis	(YDR284C or YDR503C)	(Dpp1) or (Lpp1)
GAT2_SC	glycerol 3-phosphate acyltransferase (glycerone phosphate), yeast-specific	[c] : (0.02) dcacoa + (0.06) ddcacoa + dhap + (0.17) hdcoa + (0.09) ocdycacoa + (0.24) odecoa + (0.27) pmtcoa + (0.05) stcoa + (0.1) tdcoa --> (0.01) 1agly3p_SC + coa		Phospholipid Biosynthesis		
GAT1_SC	glycerol 3-phosphate acyltransferase (glycerol 3-phosphate), yeast-specific	[c] : (0.02) dcacoa + (0.06) ddcacoa + glyc3p + (0.17) hdcoa + (0.09) ocdycacoa + (0.24) odecoa + (0.27) pmtcoa + (0.05) stcoa + (0.1) tdcoa --> (0.01) 1ag3p_SC + coa		Phospholipid Biosynthesis		
ETHAPT_SC	Ethanolaminephosphotransferase, yeast-specific	[c] : (0.01) 12dgr_SC + cdpea <==> cmp + h + (0.01) pe_SC	EC-2.7.8.1	Phospholipid Biosynthesis	YHR123W	Ept1
ETHAK	Ethanolamine kinase	[c] : atp + etha --> adp + ethamp + h	EC-2.7.1.82	Phospholipid Biosynthesis	YDR147W	Eki1
DASYNm_SC	CDP-Diacylglycerol synthetase, yeast-specific, mitochondrial	[m] : ctp + h + (0.01) pa_SC <==> (0.01) cdpdag_SC + ppi	EC-2.7.7.41	Phospholipid Biosynthesis	YBR029C	Cds1-m
DASYN_SC	CDP-Diacylglycerol synthetase, yeast-specific	[c] : ctp + h + (0.01) pa_SC <==> (0.01) cdpdag_SC + ppi	EC-2.7.7.41	Phospholipid Biosynthesis	YBR029C	Cds1
DAGPYP_SC	diacylglycerol pyrophosphate phosphatase, yeast-specific	[c] : h2o + (0.01) pa_SC --> (0.01) 12dgr_SC + pi	EC-3.1.3.4	Phospholipid Biosynthesis	(YDR284C or YDR503C)	(Dpp1) or (Lpp1)
DAGCPT_SC	diacylglycerol cholinephosphotransferase, yeast-specific	[c] : (0.01) 12dgr_SC + cdpchol --> cmp + h + (0.01) pc_SC	EC-2.7.8.2	Phospholipid Biosynthesis	(YNL130C or YHR123W)	(Cpt1) or (Ept1)
CLPNSm_SC	cardiolipin synthase, yeast-specific, mitochondrial	[m] : (0.01) cdpdag_SC + (0.01) pg_SC --> (0.01) clpn_SC + cmp + h	EC-2.7.8.5	Phospholipid Biosynthesis	YDL142C	Crd1-m
CHOLK	Choline kinase	[c] : atp + chol --> adp + cholp + h	EC-2.7.1.32	Phospholipid Biosynthesis	YLR133W	Cki1
CHLPCTD	choline phosphate cytididyltransferase	[c] : cholp + ctp + h --> cdpchol + ppi	EC-2.7.7.15	Phospholipid Biosynthesis	YGR202C	Pct1
CDPDGPm_SC	CDP-diacylglycerol--serine O-phosphatidyltransferae, yeast-specific, mitochondrial	[m] : (0.01) cdpdag_SC + glyc3p <==> cmp + h + (0.01) pgp_SC	EC-2.7.8.8	Phospholipid Biosynthesis	YCL004W	Pgs1-m
AGAT_SC	1-Acyl-glycerol-3-phosphate acyltransferase, yeast-specific	[c] : (0.01) 1ag3p_SC + (0.02) dcacoa + (0.06) ddcacoa + (0.17) hdcoa + (0.09) ocdycacoa + (0.24) odecoa + (0.27) pmtcoa + (0.05) stcoa + (0.1) tdcoa --> coa + (0.01) pa_SC	EC-2.3.1.51	Phospholipid Biosynthesis	YDL052C	Slc1
ADHAPR_SC	acyldihydroxyacetonephosphate reductase, yeast-specific	[c] : (0.01) 1agly3p_SC + h + nadph --> (0.01) 1ag3p_SC + nadp		Phospholipid Biosynthesis		
UPPDC1	uroporphyrinogen decarboxylase (uroporphyrinogen III)	[c] : (4) h + uppg3 --> (4) co2 + cpppg3	EC-4.1.1.37	Porphyrin and Chlorophyll Metabolism	YDR047W	Hem12
UPP3S	uroporphyrinogen-III synthase	[c] : hmbil --> h2o + uppg3	EC-4.2.1.75	Porphyrin and Chlorophyll Metabolism	YOR278W	Hem4
UPP3MT	uroporphyrinogen methyltransferase	[c] : (2) amet + uppg3 --> (2) ahcys + h + shcl	EC-2.1.1.107	Porphyrin and Chlorophyll Metabolism	YKR069W	Met1
PPPGOm	protoporphyrinogen oxidase, mitochondrial	[m] : (3) o2 + (2) pppg9 --> (6) h2o + (2) ppp9	EC-1.3.3.4	Porphyrin and Chlorophyll Metabolism	YER014W	Hem14-m
PPBNGS	porphobilinogen synthase	[c] : (2) 5aop --> h + (2) h2o + ppbng	EC-4.2.1.24	Porphyrin and Chlorophyll Metabolism	YGL040C	Hem2
HMBS	hydroxymethylbilane synthase	[c] : h2o + (4) ppbng --> hmbil + (4) nh4	EC-4.3.1.8	Porphyrin and Chlorophyll Metabolism	YDL205C	Hem3
FCLTm	Ferrochelatase, mitochondrial	[m] : fe2 + ppp9 --> (2) h + pheme	EC-4.99.1.1	Porphyrin and Chlorophyll Metabolism	YOR176W	Hem15-m
CPPPGO	coproporphyrinogen oxidase (O2 required)	[c] : cpppg3 + (2) h + o2 --> (2) co2 + (2) h2o + pppg9	EC-1.3.3.3	Porphyrin and Chlorophyll Metabolism	YDR044W	Hem13
ALASm	5-aminolevulinate synthase, mitochondrial	[m] : gly + h + succoa --> 5aop + co2 + coa	EC-2.3.1.37	Porphyrin and Chlorophyll Metabolism	YDR232W	Hem1-m
YUMPS	yUMP synthetase	[c] : r5p + ura <==> h2o + psd5p	EC-4.2.1.70	Purine and Pyrimidine Biosynthesis	(YFL001W or YPL212C or YGL063W or YNL292W)	(Deg1) or (Pus1) or (Pus2) or (Pus4)
URIK2	uridine kinase (GTP:Uridine)	[c] : gtp + uri --> gdp + h + ump	EC-2.7.1.48	Purine and Pyrimidine Biosynthesis	YNR012W	Urk1
URIK1	uridine kinase (ATP:Uridine)	[c] : atp + uri --> adp + h + ump	EC-2.7.1.48	Purine and Pyrimidine Biosynthesis	YNR012W	Urk1
UPPRT	uracil phosphoribosyltransferase	[c] : prpp + ura --> ppi + ump	EC-2.4.2.9	Purine and Pyrimidine Biosynthesis	YHR128W	Fur1
TRDRm	thioredoxin reductase (NADPH), mitochondrial	[m] : h + nadph + trdox --> nadp + trdrd	EC-1.8.1.9	Purine and Pyrimidine Biosynthesis	YHR106W	Trr2-m
TRDR	thioredoxin reductase (NADPH)	[c] : h + nadph + trdox --> nadp + trdrd	EC-1.8.1.9	Purine and Pyrimidine Biosynthesis	YDR353W	Trr1
TMDS	thymidylate synthase	[c] : dump + mlthf --> dhf + dtmp	EC-2.1.1.45	Purine and Pyrimidine Biosynthesis	YOR074C	Cdc21
TMDPP	thymidine phosphorylase	[c] : pi + thymd <==> 2dr1p + thym	EC-2.4.2.4	Purine and Pyrimidine Biosynthesis	YLR209C	Pnp1
TMDK1	thymidine kinase (ATP:thymidine)	[c] : atp + thymd --> adp + dtmp + h	EC-2.7.1.21	Purine and Pyrimidine Biosynthesis		
PRFGS	phosphoribosylformylglycinamidine synthase	[c] : atp + fgam + gln-L + h2o --> adp + fpram + glu-L + h + pi	EC-6.3.5.3	Purine and Pyrimidine Biosynthesis	YGR061C	Ade6
PRASCS	phosphoribosylaminoimidazolesuccinocarboxamide synthase	[c] : 5aizc + asp-L + atp <==> 25aics + adp + h + pi	EC-6.3.2.6	Purine and Pyrimidine Biosynthesis	YAR015W	Ade1
PRAIS	phosphoribosylaminoimidazole synthase	[c] : atp + fpram --> adp + air + (2) h + pi	EC-6.3.3.1	Purine and Pyrimidine Biosynthesis	YGL234W	Ade5,7
PRAGSr	phosphoribosylglycinamide synthase	[c] : atp + gly + pram <==> adp + gar + h + pi	EC-6.3.4.13	Purine and Pyrimidine Biosynthesis	YGL234W	Ade5,7
PDE5	3',5'-cyclic-nucleotide phosphodiesterase	[c] : 35ccmp + h2o --> cmp + h	EC-3.1.4.17	Purine and Pyrimidine Biosynthesis	YOR360C	Pde2
PDE4	3',5'-cyclic-nucleotide phosphodiesterase	[c] : 35cgmp + h2o --> gmp + h	EC-3.1.4.17	Purine and Pyrimidine Biosynthesis	YOR360C	Pde2
PDE3	3',5'-cyclic-nucleotide phosphodiesterase	[c] : 35cimp + h2o --> h + imp	EC-3.1.4.17	Purine and Pyrimidine Biosynthesis	YOR360C	Pde2
PDE2	3',5'-cyclic-nucleotide phosphodiesterase	[c] : 35cdamp + h2o --> damp + h	EC-3.1.4.17	Purine and Pyrimidine Biosynthesis	YOR360C	Pde2
PDE1	3',5'-cyclic-nucleotide phosphodiesterase	[c] : camp + h2o --> amp + h	EC-3.1.4.17	Purine and Pyrimidine Biosynthesis	(YOR360C or YGL248W)	(Pde2) or (Pde1)
ORPT	orotate phosphoribosyltransferase	[c] : orot5p + ppi <==> orot + prpp	EC-2.4.2.10	Purine and Pyrimidine Biosynthesis	(YML106W or YMR271C)	(Ura5) or (Ura10)
OMPDC	orotidine-5'-phosphate decarboxylase	[c] : h + orot5p --> co2 + ump	EC-4.1.1.23	Purine and Pyrimidine Biosynthesis	YEL021W	Ura3

IMPD	IMP dehydrogenase	[c] : h2o + imp + nad --> h + nadh + xmp	EC-1.1.1.205	Purine and Pyrimidine Biosynthesis	(YAR073W or YHR216W or YML056C or YLR432W or YAR075W)	(Imd1) or (Imd2) or (Imd4) or (Imd3) or (Imd5)
IMPC	IMP cyclohydrolase	[c] : h2o + imp <==> fprica	EC-3.5.4.10	Purine and Pyrimidine Biosynthesis	(YLR028C or YMR120C)	(Ade16) or (Ade17)
GMPS2	GMP synthase	[c] : atp + gln-L + h2o + xmp --> amp + glu-L + gmp + (2) h + ppi	EC-6.3.5.2	Purine and Pyrimidine Biosynthesis	YMR217W	Gua1
GLUPRT	glutamine phosphoribosyldiphosphate amidotransferase	[c] : gln-L + h2o + prpp --> glu-L + ppi + pram	EC-2.4.2.14	Purine and Pyrimidine Biosynthesis	YMR300C	Ade4
GK2	guanylate kinase (GMP:dATP)	[c] : datp + gmp <==> dadp + gdp	EC-2.7.4.8	Purine and Pyrimidine Biosynthesis	YDR454C	Guk1
GK1	guanylate kinase (GMP:ATP)	[c] : atp + gmp <==> adp + gdp	EC-2.7.4.8	Purine and Pyrimidine Biosynthesis	YDR454C	Guk1
GARFTi	phosphoribosylglycinamide formyltransferase, irreversible	[c] : 10fthf + gar --> fgam + h + thf	EC-2.1.2.2	Purine and Pyrimidine Biosynthesis	YDR408C	Ade8
DUTPDP	dUTP diphosphatase	[c] : dutp + h2o --> dump + h + ppi	EC-3.6.1.23	Purine and Pyrimidine Biosynthesis	YBR252W	Dut1
DURIPP	deoxyuridine phosphorylase	[c] : duri + pi <==> 2dr1p + ura		Purine and Pyrimidine Biosynthesis	YLR209C	Pnp1
DURIK1	deoxyuridine kinase (ATP:Deoxyuridine)	[c] : atp + duri --> adp + dump + h		Purine and Pyrimidine Biosynthesis		
DHORTSn	dihydroorotase, nuclear	[n] : dhor-S + h2o <==> cbasp + h	EC-3.5.2.3	Purine and Pyrimidine Biosynthesis	YJL130C	Ura2-n
DHORTS	dihydroorotase	[c] : dhor-S + h2o <==> cbasp + h	EC-3.5.2.3	Purine and Pyrimidine Biosynthesis	YLR420W	Ura4
DHORD4	dihydoorotic acid (ubiquinone-6)	dhor-S[c] + q6[m] <==> orot[c] + q6h2[m]	EC-1.3.3.1	Purine and Pyrimidine Biosynthesis	YKL216W	Ura1
DHORD	dihydoorotic acid dehydrogenase	[c] : dhor-S + o2 <==> h2o2 + orot	EC-1.3.3.1	Purine and Pyrimidine Biosynthesis	YKL216W	Ura1
DGK1	deoxyguanylate kinase (dGMP:ATP)	[c] : atp + dgmp <==> adp + dgdp	EC-2.7.4.8	Purine and Pyrimidine Biosynthesis	YDR454C	Guk1
DCMPDA	dCMP deaminase	[c] : dcmp + h + h2o <==> dump + nh4	EC-3.5.4.12	Purine and Pyrimidine Biosynthesis	YHR144C	Dcd1
CYTD	cytidine deaminase	[c] : cytd + h + h2o --> nh4 + uri	EC-3.5.4.5	Purine and Pyrimidine Biosynthesis	YLR245C	Cdd1
CTPS2	CTP synthase (glutamine)	[c] : atp + gln-L + h2o + utp --> adp + ctp + glu-L + (2) h + pi	EC-6.3.4.2	Purine and Pyrimidine Biosynthesis	(YBL039C or YJR103W)	(Ura7) or (Ura8)
CTPS1	CTP synthase (NH3)	[c] : atp + nh4 + utp --> adp + ctp + (2) h + pi	EC-6.3.4.2	Purine and Pyrimidine Biosynthesis	(YBL039C or YJR103W)	(Ura7) or (Ura8)
CSND	Cytosine deaminase	[c] : csn + h + h2o --> nh4 + ura	EC-3.5.4.1	Purine and Pyrimidine Biosynthesis	YPR062W	Fcy1
ATPATF3	ATP adenylyltransferase	[c] : gdp + gtp + h --> gp4g + pi	EC-2.7.7.53	Purine and Pyrimidine Biosynthesis	YCL050C	Apa1
ATPATF2	ATP adenylyltransferase	[c] : adp + gtp + h --> ap4g + pi	EC-2.7.7.53	Purine and Pyrimidine Biosynthesis	YCL050C	Apa1
ATPATF1	ATP adenylyltransferase	[c] : adp + atp + h --> ap4a + pi	EC-2.7.7.53	Purine and Pyrimidine Biosynthesis	YDR530C	Apa2
ASPCTn	aspartate carbamoyltransferase, nuclear	[n] : asp-L + cbp --> cbasp + h + pi	EC-2.1.3.2	Purine and Pyrimidine Biosynthesis	YJL130C	Ura2-n
AP4AHr	Ap4A hydrolase, reversible	[c] : ap4a + h2o <==> (2) adp + (2) h	EC-3.6.1.41	Purine and Pyrimidine Biosynthesis	YDR305C	Hnt2
AMPDA	Adenosine monophosphate deaminase	[c] : amp + h + h2o --> imp + nh4		Purine and Pyrimidine Biosynthesis	YML035C	Amd1
AIRCr	phosphoribosylaminoimidazole carboxylase	[c] : air + co2 <==> 5aizc + h	EC-4.1.1.21	Purine and Pyrimidine Biosynthesis	YOR128C	Ade2
AICART	phosphoribosylaminoimidazolecarboxamide formyltransferase	[c] : 10fthf + aicar <==> fprica + thf	EC-2.1.2.3	Purine and Pyrimidine Biosynthesis	(YLR028C or YMR120C)	(Ade16) or (Ade17)
ADSS	adenylosuccinate synthase	[c] : asp-L + gtp + imp --> dcamp + gdp + (2) h + pi	EC-6.3.4.4	Purine and Pyrimidine Biosynthesis	YNL220W	Ade12
ADSL2r	adenylosuccinate lyase	[c] : 25aics <==> aicar + fum	EC-4.3.2.2	Purine and Pyrimidine Biosynthesis	YLR359W	Ade13
ADSL1r	adenylsuccinate lyase	[c] : dcamp <==> amp + fum	EC-4.3.2.2	Purine and Pyrimidine Biosynthesis	YLR359W	Ade13
ADNCYC	adenylate cyclase	[c] : atp --> camp + ppi	EC-4.6.1.1	Purine and Pyrimidine Biosynthesis	YJL005W	Cyr1
PYDXO	pyridoxal oxidase	[c] : (2) h2o + nh4 + (0.5) o2 + pydx <==> (2) h2o2 + pydam	EC-1.4.3.5	Pyridoxine Metabolism	YBR035C	Pdx3
PYDXNO	pyridoxine oxidase	[c] : o2 + pydxn <==> h2o2 + pydx	EC-1.4.3.5	Pyridoxine Metabolism	YBR035C	Pdx3
PYDXNK	pyridoxine kinase	[c] : atp + pydxn --> adp + h + pdx5p	EC-2.7.1.35	Pyridoxine Metabolism		
PYDXK	pyridoxal kinase	[c] : atp + pydx --> adp + h + pydx5p	EC-2.7.1.35	Pyridoxine Metabolism		
PYDAMK	pyridoxamine kinase	[c] : atp + pydam --> adp + h + pyam5p	EC-2.7.1.35	Pyridoxine Metabolism		
PYAM5PO	pyridoxamine 5'-phosphate oxidase	[c] : h2o + o2 + pyam5p --> h2o2 + nh4 + pydx5p	EC-1.4.3.5	Pyridoxine Metabolism	YBR035C	Pdx3
PDX5PO	pyridoxine 5'-phosphate oxidase	[c] : o2 + pdx5p <==> h2o2 + pydx5p	EC-1.4.3.5	Pyridoxine Metabolism	YBR035C	Pdx3
OHPBAT	O-Phospho-4-hydroxy-L-threonine:2-oxoglutarate aminotransferase	[c] : glu-L + ohpb <==> akg + phthr	EC-2.6.1.52	Pyridoxine Metabolism	YOR184W	Ser1
HYPOE	hypothetical enyme	[c] : h2o + pyam5p --> pi + pydam		Pyridoxine Metabolism		
PYRDC	pyruvate decarboxylase	[c] : h + pyr --> acald + co2	EC-4.1.1.1	Pyruvate metabolism	(YGR087C or YLR134W or YLR044C)	(Pdc6) or (Pdc5) or (Pdc1)
HCITSn	homocitrate synthase, nuclear	[n] : accoa + akg + h2o --> coa + h + hcit	EC-4.1.3.21	Pyruvate metabolism	(YDL131W or YDL182W)	(Lys21-n) or (Lys20-n)
HCITSm	homocitrate synthase, mitochondrial	[m] : accoa + akg + h2o --> coa + h + hcit	EC-4.1.3.21	Pyruvate metabolism		
FALDH	formaldehyde dehydrogenase	[c] : fald + gthrd + nad <==> Sfglutth + h + nadh	EC-1.2.1.1	Pyruvate metabolism	YDL168W	Sfa1
ALCD2x	alcohol dehydrogenase (ethanol)	[c] : etoh + nad <==> acald + h + nadh	EC-1.1.1.1	Pyruvate metabolism	(YGL256W or YBR145W or YDL168W or YOL086C or YMR303C)	(Adh4) or (Adh5) or (Sfa1) or (Adh1) or (Adh2)
ACSp	acetyl-CoA synthetase	[x] : ac + atp + coa --> accoa + amp + ppi	EC-6.2.1.1	Pyruvate metabolism	YAL054C	Acs1-p
ACSm	acetyl-CoA synthetase, mitochondrial	[m] : ac + atp + coa --> accoa + amp + ppi	EC-6.2.1.1	Pyruvate metabolism	YAL054C	Acs1-m
ACS	acetyl-CoA synthetase	[c] : ac + atp + coa --> accoa + amp + ppi	EC-6.2.1.1	Pyruvate metabolism	YLR153C	Acs2
ACOAH	acetyl-CoA hydrolase	[c] : ac + coa + h --> accoa + h2o	EC-3.1.2.1	Pyruvate metabolism	YBL015W	Ach1
OPHHX6	2-Octaprenylphenol hydroxylase	[c] : 2oph_5 + (0.5) o2 --> 2ohph_5		Quinone Biosynthesis		
OPHBDC6	Octaprenyl-hydroxybenzoate decarboxylase	[c] : 3ophb_5 + h --> 2oph_5 + co2		Quinone Biosynthesis	YDR538W	Pad1
OMPHHX6m	2-octaprenyl-6-methoxyphenol hydroxylase, mitochondrial	[m] : 2omph_5 + (0.5) o2 --> 2ombzl_5		Quinone Biosynthesis		
OMMBLHX6m	2-Octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase, mitochodnrial	[m] : 2ommbl_5 + (0.5) o2 --> 2omhmbl_5		Quinone Biosynthesis	YGR255C	Coq6-m
OMBZLM6m	2-Octaprenyl-6-methoxy-benzoquinol methylase, mitochodnrial	[m] : 2ombzl_5 + amet --> 2ommbl_5 + ahcys + h		Quinone Biosynthesis	YML110C	Coq5-m
OHPHM6n	2-octaprenyl-6-hydroxyphenol methylase, nuclear	[n] : 2ohph_5 + amet --> 2omph_5 + ahcys + h		Quinone Biosynthesis	YPL266W	Dim1-n
HBZOPT6m	Hydroxybenzoate octaprenyltransferase, mitochondrial	[m] : 4hbz + octdp_5 --> 3ophb_5 + ppi		Quinone Biosynthesis	(YPL172C or YNR041C or YBR003W)	(Cox10-m) or (Coq2-m) or (Coq1-m)
HBZOPT6	Hydroxybenzoate octaprenyltransferase	[c] : 4hbz + octdp_5 --> 3ophb_5 + ppi		Quinone Biosynthesis	((YGL155W and YKL019W) or (YJL031C and YPR176C) or YMR101C or (YDL090C and YKL019W) or YBR002C)	(Ggt1) or (Bet24) or (Srt1) or (Ram12) or (Rer2)
DMQMT6m	3-Dimethylubiquinonol 3-methyltransferase, mitochondrial	[m] : 2omhmbl_5 + amet --> ahcys + h + q6h2		Quinone Biosynthesis	YOL096C	Coq3-m
CHRPL	Chorismate pyruvate lyase	[c] : chor --> 4hbz + pyr		Quinone Biosynthesis	(YKL211C or YER090W)	(Trp3) or (Trp2)

RBFSb	riboflavin synthase	[c] : (2) dmlz --> 4r5au + ribflv	EC-2.5.1.9	Riboflavin Metabolism	YBR256C	Rib5
RBFSa	riboflavin synthase	[c] : 4r5au + db4p --> dmlz + (2) h2o + pi	EC-2.5.1.9	Riboflavin Metabolism	YOL143C	Rib4
RBFKm	riboflavin kinase, mitochondrial	[m] : atp + ribflv --> adp + fmn + h	EC-2.7.1.26	Riboflavin Metabolism	YDR236C	Fmn1-m
RBFK	riboflavin kinase	[c] : atp + ribflv --> adp + fmn + h	EC-2.7.1.26	Riboflavin Metabolism	YDR236C	Fmn1
PMDPHT	pyrimidine phosphatase	[c] : 5aprbu + h2o --> 4r5au + pi		Riboflavin Metabolism		
GTPCII	GTP cyclohydrolase II	[c] : gtp + (3) h2o --> 25dhpp + for + (2) h + ppi	EC-3.5.4.25	Riboflavin Metabolism	YBL033C	Rib1
FMNATm	FMN adenylyltransferase, mitochondrial	[m] : atp + fmn + h --> fad + ppi	EC-2.7.7.2	Riboflavin Metabolism		
FMNAT	FMN adenylyltransferase	[c] : atp + fmn + h --> fad + ppi	EC-2.7.7.2	Riboflavin Metabolism	YDL045C	Fad1
DHPPDA	diaminohydroxyphosphoribosylaminopyrimidine deaminase	[c] : 25dhpp + h + h2o --> 5apru + nh4	EC-3.5.4.26	Riboflavin Metabolism	YBR153W	Rib7
DB4PS	3,4-Dihydroxy-2-butanone-4-phosphate	[c] : ru5p-D --> db4p + for + h		Riboflavin Metabolism		
APRAUR	5-amino-6-(5-phosphoribosylamino)uracil reductase	[c] : 5apru + h + nadph --> 5aprbu + nadp	EC-	Riboflavin Metabolism	YBR153W	Rib7
ACP1e	acid phosphatase, extracellular (secreted)	[e] : fmn + h2o --> pi + ribflv	EC-3.1.3.2	Riboflavin Metabolism	YAR071W	Pho11-e
SPHPL	sphinganine phosphate lyase	[c] : sph1p --> ethamp + hxdcal		Sphingolipid Metabolism	YDR294C	Dpl1
SLCBK2	sphingolipid long chain base kinase (phytosphingosine)	[c] : atp + psphings --> adp + h + psph1p		Sphingolipid Metabolism	(YOR171C or YLR260W)	(Lcb4) or (Lcb5)
SLCBK1	sphingolipid long chain base kinase (sphinganine)	[c] : atp + sphgn --> adp + h + sph1p		Sphingolipid Metabolism	(YLR260W or YOR171C)	(Lcb5) or (Lcb4)
SERPT	serine C-palmitoyltransferase	[c] : h + pmtcoa + ser-L --> 3dsphgn + co2 + coa	EC-2.3.1.50	Sphingolipid Metabolism	(YDR062W and YMR296C)	Lcb
SBPP2	sphingoid base-phosphate phosphatase (phytosphingosine 1-phosphate)	[c] : h2o + psph1p --> pi + psphings		Sphingolipid Metabolism	(YJL134W or YKR053C)	(Lcb3) or (Ysr3)
SBPP1	sphingoid base-phosphate phosphatase (sphinganine 1-phosphatase)	[c] : h2o + sph1p --> pi + sphgn		Sphingolipid Metabolism	(YJL134W or YKR053C)	(Lcb3) or (Ysr3)
PSPHS	Phytosphingosine synthesis	[c] : h + nadph + o2 + sphgn --> h2o + nadp + psphings		Sphingolipid Metabolism	YDR297W	Sur2
PSPHPL	phytosphingosine phosphate lyase	[c] : psph1p --> 2hhxdal + ethamp		Sphingolipid Metabolism	YDR294C	Dpl1
MIPCS326_SC	mannose-inositol phosphorylceramide synthase (ceramide-3, 26C), yeast-specific	[c] : gdpmann + (0.01) ipc326_SC --> gdp + h + (0.01) mipc326_SC		Sphingolipid Metabolism	(YBR036C or YPL057C)	(Csg2) or (Sur1)
MIPCS324_SC	mannose-inositol phosphorylceramide synthase (ceramide-3, 24C), yeast-specific	[c] : gdpmann + (0.01) ipc324_SC --> gdp + h + (0.01) mipc324_SC		Sphingolipid Metabolism	(YBR036C or YPL057C)	(Csg2) or (Sur1)
MIPCS226_SC	mannose-inositol phosphorylceramide synthase (ceramide-2, 26C), yeast-specific	[c] : gdpmann + (0.01) ipc226_SC --> gdp + h + (0.01) mipc226_SC		Sphingolipid Metabolism	(YBR036C or YPL057C)	(Csg2) or (Sur1)
MIPCS224_SC	mannose-inositol phosphorylceramide synthase (ceramide-2, 24C), yeast-specific	[c] : gdpmann + (0.01) ipc224_SC --> gdp + h + (0.01) mipc224_SC		Sphingolipid Metabolism	(YBR036C or YPL057C)	(Csg2) or (Sur1)
MIPCS126_SC	mannose-inositol phosphorylceramide synthase (ceramide-1, 26C), yeast-specific	[c] : gdpmann + (0.01) ipc126_SC --> gdp + h + (0.01) mipc126_SC		Sphingolipid Metabolism	(YBR036C or YPL057C)	(Csg2) or (Sur1)
MIPCS124_SC	mannose-inositiol phophorylceramide synthase (ceramide-1, 24C), yeast-specific	[c] : gdpmann + (0.01) ipc124_SC --> gdp + h + (0.01) mipc124_SC		Sphingolipid Metabolism	(YBR036C or YPL057C)	(Csg2) or (Sur1)
MIP2CS326_SC	mannose-(inositol-P)2-ceramide synthase (ceramide-3, 26C), yeast-specific	[c] : (0.01) mipc326_SC + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) mip2c326_SC		Sphingolipid Metabolism	YDR072C	Ipt1
MIP2CS324_SC	mannose-(inositol-P)2-ceramide synthase (ceramide-3, 24C), yeast specific	[c] : (0.01) mipc324_SC + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) mip2c324_SC		Sphingolipid Metabolism	YDR072C	Ipt1
MIP2CS226_SC	mannose-(inositol-P)2-ceramide synthase (ceramide-2, 24C), yeast-specific	[c] : (0.01) mipc226_SC + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) mip2c226_SC		Sphingolipid Metabolism	YDR072C	Ipt1
MIP2CS224_SC	mannose-(inositol-P)2-ceramide synthase (ceramide-2, 26C), yeast specific	[c] : (0.01) mipc224_SC + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) mip2c224_SC		Sphingolipid Metabolism	YDR072C	Ipt1
MIP2CS126_SC	mannose-(inositol-P)2-ceramide synthase (ceramide-1, 26C), yeast-specific	[c] : (0.01) mipc126_SC + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) mip2c126_SC		Sphingolipid Metabolism	YDR072C	Ipt1
MIP2CS124_SC	mannose-(inositol-P)2-ceramide synthase (ceramide-1, 24C), yeast-specific	[c] : (0.01) mipc124_SC + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) mip2c124_SC		Sphingolipid Metabolism	YDR072C	Ipt1
IPCS326_SC	Inositol phosphorylceramide synthase (ceramide-3, 26C), yeast-specific	[c] : cer3_26 + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) ipc326_SC		Sphingolipid Metabolism	YKL004W	Aur1
IPCS324_SC	Inositol phosphorylceramide synthase (ceramide-3, 24C), yeast-specific	[c] : cer3_24 + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) ipc324_SC		Sphingolipid Metabolism	YKL004W	Aur1
IPCS226_SC	Inositol phosphoryceramide synthase (ceramide-2, 26C), yeast-specific	[c] : cer2_26 + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) ipc226_SC		Sphingolipid Metabolism	YKL004W	Aur1
IPCS224_SC	Inositol phosphorylceramide synthase (ceramide-2, 24C), yeast-specific	[c] : cer2_24 + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) ipc224_SC		Sphingolipid Metabolism	YKL004W	Aur1
IPCS126_SC	Inositol phosphorylceramide synthase (ceramide-1, 26C), yeast-specific	[c] : cer1_26 + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) ipc126_SC		Sphingolipid Metabolism	YKL004W	Aur1
IPCS124_SC	Inositol phosphorylceramide synthase (ceramide-1, 24C), yeast-specific	[c] : cer1_24 + (0.01) ptd1ino_SC --> (0.01) 12dgr_SC + (0.01) ipc124_SC		Sphingolipid Metabolism	YKL004W	Aur1
CERS326	Ceramide-3 synthase (26C)	[c] : cer2_26 + h + nadph + o2 --> cer3_26 + h2o + nadp		Sphingolipid Metabolism	YMR272C	Scs7
CERS324	Ceramide-3 synthase (24C)	[c] : cer2_24 + h + nadph + o2 --> cer3_24 + h2o + nadp		Sphingolipid Metabolism	YMR272C	Scs7
CERS226	Ceramide-2 synthase (26C)	[c] : hexccoa + psphings --> cer2_26 + coa + h		Sphingolipid Metabolism		
CERS224	Ceramide-2 synthase (24C)	[c] : psphings + ttccoa --> cer2_24 + coa + h		Sphingolipid Metabolism		
CERS2'26	Ceramide-2' synthase (26C)	[c] : cer1_26 + h + nadph + o2 --> cer2'_26 + h2o + nadp		Sphingolipid Metabolism	YMR272C	Scs7
CERS2'24	Ceramide-2' synthase (24C)	[c] : cer1_24 + h + nadph + o2 --> cer2'_24 + h2o + nadp		Sphingolipid Metabolism	YMR272C	Scs7
CERS126	Ceramide-1 synthase (26C)	[c] : hexccoa + sphgn --> cer1_26 + coa + h		Sphingolipid Metabolism		
CERS124	Ceramide-1 synthase (24C)	[c] : sphgn + ttccoa --> cer1_24 + coa + h		Sphingolipid Metabolism		
CERH126	Ceramide-1 hydroxylase (26C)	[c] : cer1_26 + h + nadph + o2 --> cer2_26 + h2o + nadp		Sphingolipid Metabolism	YDR297W	Sur2
CERH124	Ceramide-1 hydroxylase (24C)	[c] : cer1_24 + h + nadph + o2 --> cer2_24 + h2o + nadp		Sphingolipid Metabolism	YDR297W	Sur2
3DSPHR	3-Dehydrosphinganine reductase	[c] : 3dsphgn + h + nadph --> nadp + sphgn	EC-	Sphingolipid Metabolism	YBR265W	Tsc10
13BGHe	Exo-1,3-beta-glucan glucohydrase, extracellular	[e] : 13BDglcn + h2o --> glc-D	EC-3.2.1.58	Starch and sucrose metabolism	(YOR190W or YDR261C or YLR300W)	(Spr1-e) or (Exg2-e) or (Exg1-e)
13BGH	Endo-1,3-beta-glucan glucohydrase	[c] : 13BDglcn + h2o --> glc-D	EC-3.2.1.58	Starch and sucrose metabolism	YGR282C	Bgl2
SQLS	Squalene synthase	[c] : (2) frdp + h + nadph --> nadp + (2) ppi + sql	EC-2.5.1.21	Sterol Biosynthesis	YHR190W	Erg9
SQLEer	Squalene epoxidase, endoplasmic reticular	[r] : h + nadph + o2 + sql --> Ssq23epx + h2o + nadp	EC-	Sterol Biosynthesis	YGR175C	Erg1-er
SAM24MT	S-adenosyl-methionine delta-24-sterol-c-methyltransferase	[c] : amet + zymst --> ahcys + fecost + h	EC-2.1.1.41	Sterol Biosynthesis	YML008C	Erg6
PMEVK	phosphomevalonate kinase	[c] : 5pmev + atp --> 5dpmev + adp	EC-2.7.4.2	Sterol Biosynthesis	YMR220W	Erg8
MEVK4	mevalonate kinase (utp)	[c] : mev-R + utp --> 5pmev + h + udp	EC-2.7.1.36	Sterol Biosynthesis	YMR208W	Erg12
MEVK3	mevalonate kinase (gtp)	[c] : gtp + mev-R --> 5pmev + gdp + h	EC-2.7.1.36	Sterol Biosynthesis	YMR208W	Erg12
MEVK2	mevalonate kinase (ctp)	[c] : ctp + mev-R --> 5pmev + cdp + h	EC-2.7.1.36	Sterol Biosynthesis	YMR208W	Erg12
MEVK1	mevalonate kinase (atp)	[c] : atp + mev-R --> 5pmev + adp + h	EC-2.7.1.36	Sterol Biosynthesis	YMR208W	Erg12
LNSTLS	lanosterol synthase	[c] : Ssq23epx --> lanost	EC-5.4.99.7	Sterol Biosynthesis	YHR072W	Erg7
LNS14DM	cytochrome P450 lanosterol 14-alpha-demethylase	[c] : (2) h + lanost + (3) nadph + (3) o2 --> 44mctr + for + (4) h2o + (3) nadp	EC-	Sterol Biosynthesis	YHR007C	Erg11
IPDDI	isopentenyl-diphosphate D-isomerase	[c] : ipdp <==> dmpp	EC-5.3.3.2	Sterol Biosynthesis	YPL117C	Idi1
HMGCOASm	Hydroxymethylglutaryl CoA synthase, mitochondrial	[m] : coa + h + hmgcoa <==> aacoa + accoa + h2o	EC-4.1.3.5	Sterol Biosynthesis	YML126C	Erg13-m
HMGCOAS	Hydroxymethylglutaryl CoA synthase	[c] : coa + h + hmgcoa <==> aacoa + accoa + h2o	EC-4.1.3.5	Sterol Biosynthesis	YML126C	Erg13
HMGCOAR	Hydroxymethylglutaryl CoA reductase	[c] : coa + mev-R + (2) nadp <==> (2) h + hmgcoa + (2) nadph	EC-1.1.1.34	Sterol Biosynthesis	(YLR450W or YML075C)	(Hmg2) or (Hmg1)
GRTT	geranyltranstransferase	[c] : grdp + ipdp --> frdp + ppi	EC-2.5.1.10	Sterol Biosynthesis	YJL167W	Erg20
DPMVD	diphosphomevalonate decarboxylase	[c] : 5dpmev + atp --> adp + co2 + ipdp + pi	EC-4.1.1.33	Sterol Biosynthesis	YNR043W	Mvd1
DMATT	dimethylallyltranstransferase	[c] : dmpp + ipdp --> grdp + ppi	EC-2.5.1.1	Sterol Biosynthesis	YJL167W	Erg20
CHLSTI	cholestenol delta-isomerase, lumped reaction	[c] : amet + o2 + zymst --> ahcys + ergtetrol + h + (2) h2o	EC-5.3.3.5	Sterol Biosynthesis		

C8STI	C-8 sterol isomerase	[c] : fecost --> epist		Sterol Biosynthesis	YMR202W	Erg2
C5STDS	C-5 sterol desaturase	[c] : epist + h + nadph + o2 --> ergtrol + (2) h2o + nadp		Sterol Biosynthesis	YLR056W	Erg3
C4STMO2	C-4 sterol methyl oxidase (4-methylzymosterol)	[c] : 4mzym + (3) h + (3) nadph + (3) o2 --> (4) h2o + (3) nadp + zym_int1		Sterol Biosynthesis	YGR060W	Erg25
C4STMO1	C-4 sterol methyl oxidase (4,4-dimethylzymosterol)	[c] : 44mzym + (3) h + (3) nadph + (3) o2 --> 4mzym_int1 + (4) h2o + (3) nadp		Sterol Biosynthesis	YGR060W	Erg25
C3STKR2	C-3 sterol keto reductase (zymosterol)	[c] : h + nadph + zym_int2 --> nadp + zymst		Sterol Biosynthesis	YLR100W	Erg27
C3STKR1	C-3 sterol keto reductase (4-methylzymosterol)	[c] : 4mzym_int2 + h + nadph --> 4mzym + nadp		Sterol Biosynthesis	YLR100W	Erg27
C3STDH2	C-3 sterol dehydrogenase (zymosterol)	[c] : nad + zym_int1 --> co2 + h + nadh + zym_int2	EC-5.3.3.1	Sterol Biosynthesis	YGL001C	Erg26
C3STDH1	C-3 sterol dehydrogenase (4-methylzymosterol)	[c] : 4mzym_int1 + nad --> 4mzym_int2 + co2 + h + nadh	EC-5.3.3.1	Sterol Biosynthesis	YGL001C	Erg26
C24STRer	C-s24 sterol reductase, endoplamic reticular	[r] : ergtetrol + h + nadph --> ergst + nadp		Sterol Biosynthesis	YGL012W	Erg4-er
C22STDS	C-22 sterol desaturase	[c] : ergtrol + h + nadph + o2 --> ergtetrol + (2) h2o + nadp		Sterol Biosynthesis	YMR015C	Erg5
C14STR	C-14 sterol reductase	[c] : 44mctr + h + nadph --> 44mzym + nadp		Sterol Biosynthesis	YNL280C	Erg24
TMPPP	thiamine-phosphate diphosphorylase	[c] : 2mahmp + 4mpetz + h --> ppi + thmmp	EC-2.5.1.3	Thiamine Metabolism	YPL214C	Thi6
TMPKr	thiamine-phosphate kinase	[c] : atp + thmmp <==> adp + thmpp	EC-2.7.4.16	Thiamine Metabolism		
TMN	thiaminase	[c] : h2o + thm --> 4ahmmp + 4mhetz + h	EC-3.5.99.2	Thiamine Metabolism		
TMDPPK	thiamine-diphosphate kinase	[c] : atp + thmpp --> adp + thmtp	EC-2.7.4.15	Thiamine Metabolism	YOR143C	Thi80
TMDPK	thiamine diphosphokinase	[c] : atp + thm --> amp + h + thmpp	EC-2.7.6.2	Thiamine Metabolism	YOR143C	Thi80
THZPSN2_SC	thiazole phosphate synthesis (ribose 5-phosphate), yeast-specifc	[c] : achms + cys-L + gly + h + r5p --> 4abut + 4mpetz + ac + co2 + (3) h2o + nh4 + pyr		Thiamine Metabolism		
THZPSN1_SC	thiazole phosphate synthesis (xylulose 5-phosphate), yeast-specific	[c] : achms + cys-L + gly + h + xu5p-D --> 4abut + 4mpetz + ac + co2 + (3) h2o + nh4 + pyr		Thiamine Metabolism		
THMPe	thiamin phosphatase, extracellular	[e] : h2o + thmmp --> pi + thm	EC-3.1.3.2	Thiamine Metabolism	YBR092C	Pho3-e
THMP	thiamin phosphatase	[c] : h2o + thmmp --> pi + thm		Thiamine Metabolism		
THMDPe	thiamin diphosphatase, extracellular	[e] : (2) h2o + thmpp --> h + (2) pi + thm	EC-3.1.3.2	Thiamine Metabolism	YBR092C	Pho3-e
PMPK	phosphomethylpyrimidine kinase	[c] : 4ampm + atp --> 2mahmp + adp	EC-2.7.4.7	Thiamine Metabolism	(YOL055C or YPL258C)	(Thi20) or (Thi21)
HMPK1	hydroxymethylpyrimidine kinase (ATP)	[c] : 4ahmmp + atp --> 4ampm + adp + h	EC-2.7.1.49	Thiamine Metabolism	(YOL055C or YPL258C or YPR121W)	(Thi20) or (Thi21) or (Thi22)
HETZK	hydroxyethylthiazole kinase	[c] : 4mhetz + atp --> 4mpetz + adp + h	EC-2.7.1.50	Thiamine Metabolism	YPL214C	Thi6
AHMMPS	4-amino-5-hydroxymethyl-2-methylpyrimidine synthetase	[c] : air + (2) h --> 4ahmmp + gcald + pi		Thiamine Metabolism		
THRTRSm	threonyl-tRNA synthetase, mitochondrial	[m] : atp + thr-L + trnathr --> amp + ppi + thrtrna	EC-6.1.1.3	Threonine and Lysine Metabolism	YKL194C	Mst1-m
THRTRS	Threonyl-tRNA synthetase	[c] : atp + thr-L + trnathr --> amp + ppi + thrtrna	EC-6.1.1.3	Threonine and Lysine Metabolism	YIL078W	Ths1
THRS	threonine synthase	[c] : h2o + phom --> pi + thr-L	EC-4.2.3.1	Threonine and Lysine Metabolism	YCR053W	Thr4
THRD_Lm	L-threonine deaminase, mitochondrial	[m] : thr-L --> 2obut + nh4	EC-4.3.1.19	Threonine and Lysine Metabolism	YER086W	Ilv1-m
THRD_L	L-threonine deaminase	[c] : thr-L --> 2obut + nh4		Threonine and Lysine Metabolism	(YCL064C or YKL218C)	(Cha1) or (Sry1)
THRA	Threonine aldolase	[c] : acald + gly --> thr-L	EC-4.1.2.5	Threonine and Lysine Metabolism	YEL046C	Gly1
SACCD2	saccharopine dehydrogenase (NAD, L-lysine forming)	[c] : h2o + nad + saccrp-L <==> akg + h + lys-L + nadh	EC-1.5.1.7	Threonine and Lysine Metabolism	YIR034C	Lys1
SACCD1	saccharopine dehydrogenase (NADP, L-glutamate forming)	[c] : L2aadp6sa + glu-L + h + nadph <==> h2o + nadp + saccrp-L	EC-1.5.1.10	Threonine and Lysine Metabolism	YNR050C	Lys9
OXAGm	non-enzymatic reaction, mitochondrial	[m] : h + oxag <==> 2oxoadp + co2		Threonine and Lysine Metabolism		
MCITDm	2-methylcitrate dehydratase, mitochondrial	[m] : hcit <==> b124tc + h2o	EC-4.2.1.79	Threonine and Lysine Metabolism		
LYSTRSm	Lysyl-tRNA synthetase, mitochondrial	[m] : atp + lys-L + trnalys --> amp + lystrna + ppi	EC-6.1.1.6	Threonine and Lysine Metabolism	YNL073W	Msk1-m
LYSTRS	Lysyl-tRNA synthetase	[c] : atp + lys-L + trnalys --> amp + lystrna + ppi	EC-6.1.1.6	Threonine and Lysine Metabolism	YDR037W	Krs1
HICITDm	homoisocitrate dehydrogenase, mitochondrial	[m] : hicit + nad <==> h + nadh + oxag	EC-	Threonine and Lysine Metabolism	YIL094C	Lys12-m
HACNHm	homoacontinate hydratase, mitochondrial	[m] : b124tc + h2o <==> hicit	EC-4.2.1.36	Threonine and Lysine Metabolism	YDR234W	Lys4-m
AATA	2-aminoadipate transaminase	[c] : 2oxoadp + glu-L <==> L2aadp + akg	EC-2.6.1.39	Threonine and Lysine Metabolism		
AASAD2	L-aminoadipate-semialdehyde dehydrogenase (NADH)	[c] : L2aadp + atp + h + nadh --> L2aadp6sa + amp + nad + ppi	EC-1.2.1.31	Threonine and Lysine Metabolism	(YBR115C and YGL154C)	Lys25
AASAD1	L-aminoadipate-semialdehyde dehydrogenase (NADPH)	[c] : L2aadp + atp + h + nadph --> L2aadp6sa + amp + nadp + ppi	EC-1.2.1.31	Threonine and Lysine Metabolism	(YBR115C and YGL154C)	Lys25
4HTHRS	4-Hydroxy-L-threonine synthase	[c] : h2o + phthr --> 4hthr + pi		Threonine and Lysine Metabolism	YCR053W	Thr4
SQLter	squalene endoplamic reticular transport	sql[c] <==> sql[r]		Transport, Endoplasmic Reticular		
SQ23EPXter	Squalene-2,3-epoxide endoplamic reticular transport	Ssq23epx[r] <==> Ssq23epx[c]		Transport, Endoplasmic Reticular		
O2ter	O2 endoplamic reticulum transport	o2[c] <==> o2[r]		Transport, Endoplasmic Reticular		
MANNANter	mannan endoplasmic reticulum transport via diffusion	mannan[c] <==> mannan[r]		Transport, Endoplasmic Reticular		
H2Oter	H2O endoplasmic reticulum transport	h2o[c] <==> h2o[r]		Transport, Endoplasmic Reticular		
G6Pter	glucose 6-phosphate endoplasmic reticular transport via diffusion	g6p[c] <==> g6p[r]		Transport, Endoplasmic Reticular		
ERGTETROLter	Ergosta-5,6,22,24,(28)-tetraen-3beta-ol endoplamic reticular transport	ergtetrol[c] <==> ergtetrol[r]		Transport, Endoplasmic Reticular		
ERGSTter	ergosterol endoplasmic reticular transport	ergst[r] <==> ergst[c]		Transport, Endoplasmic Reticular		
DOLPt2er	dolichol phosphate endoplasmic reticular transport via proton symport	dolp[c] + h[c] <==> dolp[r] + h[r]		Transport, Endoplasmic Reticular		
6PGLter	6-phospho-D-glucono-1,5-lactone endoplasmic reticular transport via diffusion	6pgl[c] <==> 6pgl[r]		Transport, Endoplasmic Reticular		
ZYMSTt	zymosterol reversible transport	zymst[e] <==> zymst[c]		Transport, Extracellular	YOR011W	Aus1
XYLt	D-xylose reversible transport	xyl-D[e] <==> xyl-D[c]		Transport, Extracellular		
XYLTt	Xylitol transport via passive diffusion	xylt[e] <==> xylt[c]		Transport, Extracellular		
XTSNt2	xanthosine transport in via proton symport	h[e] + xtsn[e] --> h[c] + xtsn[c]		Transport, Extracellular		
XANt	xanthine reversible transport	xan[e] <==> xan[c]		Transport, Extracellular		
VALt2r	L-valine reversible transport via proton symport	h[e] + val-L[e] <==> h[c] + val-L[c]		Transport, Extracellular	(YKR039W or YCL025C or YDR046C or YBR069C or YBR068C)	(Gap1) or (Agp1) or (Bap3) or (Tat1) or (Bap2)
URIt2	uridine transport in via proton symport	h[e] + uri[e] --> h[c] + uri[c]		Transport, Extracellular	YBL042C	Fui1
UREA2t2	urea reversible transport via proton symport (2 H+)	(2) h[e] + urea[e] <==> (2) h[c] + urea[c]		Transport, Extracellular	YHL016C	Dur3
URAt2	uracil transport in via proton symport	h[e] + ura[e] --> h[c] + ura[c]		Transport, Extracellular	YBR021W	Fur4
TYRt2r	L-tyrosine reversible transport via proton symport	h[e] + tyr-L[e] <==> h[c] + tyr-L[c]		Transport, Extracellular	(YBR069C or YKR039W or YCL025C or YBR068C or YOL020W or YDR046C)	(Tat1) or (Gap1) or (Agp1) or (Bap2) or (Tat2) or (Bap3)
TTDCAt	Tetradecanoate (n-C14:0) transport in via uniport	ttdca[e] --> ttdca[c]		Transport, Extracellular		
TRPt2r	L-tryptophan reversible transport via proton symport	h[e] + trp-L[e] <==> h[c] + trp-L[c]		Transport, Extracellular	(YBR069C or YKR039W or YOL020W or YBR068C or YDR046C)	(Tat1) or (Gap1) or (Tat2) or (Bap2) or (Bap3)

TREt2	trehalose transport in via proton symporter	h[e] + tre[e] --> h[c] + tre[c]		Transport, Extracellular		
THYMt3r	thymine reversible transport via proton antiport	h[e] + thym[c] <==> h[c] + thym[e]		Transport, Extracellular		
THRt2r	L-threonine reversible transport via proton symport	h[e] + thr-L[e] <==> h[c] + thr-L[c]		Transport, Extracellular	(YBR069C or YCL025C or YKR039W or YDR508C)	(Tat1) or (Agp1) or (Gap1) or (Gnp1)
THMt2	Thiamine transport in via proton symport	h[e] + thm[e] --> h[c] + thm[c]		Transport, Extracellular	(YLR237W or YOR071C or YOR192C)	(Thi7) or (Thm1) or (Thm2)
THMDt2	thymidine transport in via proton symport	h[e] + thymd[e] --> h[c] + thymd[c]		Transport, Extracellular		
SUCRt2	sucrose transport in via proton symport	h[e] + sucr[e] --> h[c] + sucr[c]		Transport, Extracellular		
SUCCt2r	succinate transport via proton symport	h[e] + succ[e] <==> h[c] + succ[c]		Transport, Extracellular		
SRB_Lt	L-sorbose reversible transport	srb-L[e] <==> srb-L[c]		Transport, Extracellular		
SPRMti	spermine irreversible uniport	sprm[e] --> sprm[c]		Transport, Extracellular		
SPMDt2	spermidine transport in via proton symport	h[e] + spmd[e] --> h[c] + spmd[c]		Transport, Extracellular		
SO4ti	sulfate irreversible uniport	so4[e] --> so4[c]		Transport, Extracellular	(YBR294W or YLR092W or YGR125W)	(Sul1) or (Sul2) or (Sul3)
SERt2r	L-serine reversible transport via proton symport	h[e] + ser-L[e] <==> h[c] + ser-L[c]		Transport, Extracellular	(YFL055W or YCL025C or YDR508C or YKR039W or YPL265W)	(Agp3) or (Agp1) or (Gnp1) or (Gap1) or (Dip5)
SBT_Lt	L-sorbitol transport via passive diffusion	sbt-L[e] <==> sbt-L[c]		Transport, Extracellular		
SBT_Dt	D-sorbitol transport via passive diffusion	sbt-D[e] <==> sbt-D[c]		Transport, Extracellular		
RIBt2	ribose transport in via proton symporter	h[e] + rib-D[e] --> h[c] + rib-D[c]		Transport, Extracellular		
RIBFLVt2	riboflavin transport in via proton symport	h[e] + ribflv[e] --> h[c] + ribflv[c]		Transport, Extracellular		
PYRt2	pyruvate transport in via proton symport	h[e] + pyr[e] --> h[c] + pyr[c]		Transport, Extracellular	YKL217W	Jen1
PTRCt2	putrescine transport in via proton symport	h[e] + ptrc[e] --> h[c] + ptrc[c]		Transport, Extracellular		
PROt2r	L-proline reversible transport via proton symport	h[e] + pro-L[e] <==> h[c] + pro-L[c]		Transport, Extracellular	(YKR039W or YOR348C)	(Gap1) or (Put4)
PNTOt2	Pantothenate reversible transport via proton symport	h[e] + pnto-R[e] <==> h[c] + pnto-R[c]		Transport, Extracellular	YCR028C	Fen2
PIt2r	phosphate reversible transport via symport	h[e] + pi[e] <==> h[c] + pi[c]		Transport, Extracellular	(YML123C or YCR037C or YBR296C or YJL198W or YNR013C or YCR098C)	(Pho84) or (Pho87) or (Pho89) or (Pho90) or (Pho91) or (Git1)
PHEt2r	L-phenylalanine reversible transport via proton symport	h[e] + phe-L[e] <==> h[c] + phe-L[c]		Transport, Extracellular	(YKR039W or YCL025C or YOL020W or YBR068C or YDR046C)	(Gap1) or (Agp1) or (Tat2) or (Bap2) or (Bap3)
PEPDt3	peptide transport in via proton symport	h[e] + pepd[e] --> h[c] + pepd[c]		Transport, Extracellular	YKR093W	Ptr2
PAPt	PAP reversible uniport	pap[e] <==> pap[c]		Transport, Extracellular		
ORNt2r	orntithine reversible transport in via proton symport	h[e] + orn[e] <==> h[c] + orn[c]		Transport, Extracellular	(YKR039W or YEL063C)	(Gap1) or (Can1)
OCDCYAt	Octadecynoate (n-C18:2) transport in via uniport	ocdcya[e] --> ocdcya[c]		Transport, Extracellular		
OCDCEAt	Octadecenoate (n-C18:1) transport in via uniport	ocdcea[e] --> ocdcea[c]		Transport, Extracellular		
OCDCAt	Octadecanoate (n-C18:0) transport in via uniport	ocdca[e] --> ocdca[c]		Transport, Extracellular		
O2t	o2 transport (diffusion)	o2[e] <==> o2[c]		Transport, Extracellular		
NMNTP	nmntp	h[e] + nmn[e] --> h[c] + nmn[c]		Transport, Extracellular		
NH4t	ammonia reversible transport	nh4[e] <==> nh4[c]		Transport, Extracellular	(YGR121C or YNL142W or YPR138C)	(Mep1) or (Mep2) or (Mep3)
NAt3_1	sodium proton antiporter (H:NA is 1:1)	h[e] + na1[c] <==> h[c] + na1[e]		Transport, Extracellular	YLR138W	Nha1
MMETt2	S-methylmethionine permease	h[e] + mmet[e] --> h[c] + mmet[c]		Transport, Extracellular	YLL061W	Mmp1
METt2r	L-methionine reversible transport via proton symport	h[e] + met-L[e] <==> h[c] + met-L[c]		Transport, Extracellular	(YKR039W or YCL025C or YDR508C or YBR068C or YDR046C or YGR055W or YHL036W)	(Gap1) or (Agp1) or (Gnp1) or (Bap2) or (Bap3) or (Mup1) or (Mup3)
MELIBt2	melibiose transport in via symport	h[e] + melib[e] --> h[c] + melib[c]		Transport, Extracellular		
MANt2	D-mannose transport in via proton symport	h[e] + man[e] --> h[c] + man[c]		Transport, Extracellular	(YHR094C or YFL011W or YOL156W or YEL069C or YDL245C or YJR158W or YNR072W or YMR011W or YDR345C or YHR092C or YHR096C or YDR343C or YDR342C or YJL214W or YJL219W)	(Hxt1) or (Hxt10) or (Hxt11) or (Hxt13) or (Hxt15) or (Hxt16) or (Hxt17) or (Hxt2) or (Hxt3) or (Hxt4) or (Hxt5) or (Hxt6) or (Hxt7) or (Hxt8) or (Hxt9)
MALt2r	L-malate reversible transport via proton symport	h[e] + mal-L[e] <==> h[c] + mal-L[c]		Transport, Extracellular		

MALTt2	maltose transport in via proton symport	h[e] + malt[e] --> h[c] + malt[c]		Transport, Extracellular	(YGR289C or YBR298C or YDL247W or YJR160C)	(Mal11) or (Mal31) or (Mph2) or (Mph3)
LYSt2r	L-lysine reversible transport via proton symport	h[e] + lys-L[e] <==> h[c] + lys-L[c]		Transport, Extracellular	(YNL268W or YKR039W)	(Lyp1) or (Gap1)
LEUt2r	L-leucine reversible transport via proton symport	h[e] + leu-L[e] <==> h[c] + leu-L[c]		Transport, Extracellular	(YBR069C or YKR039W or YCL025C or YBR068C or YDR046C or YDR508C)	(Tat1) or (Gap1) or (Agp1) or (Bap2) or (Bap3) or (Gnp1)
L-LACt2r	L-lactate reversible transport via proton symport	h[e] + lac-L[e] <==> h[c] + lac-L[c]		Transport, Extracellular	YKL217W	Jen1
Kt2r	potassium reversible transport via proton symport	h[e] + k[e] <==> h[c] + k[c]		Transport, Extracellular		
INSt2	inosine transport in via proton symport	h[e] + ins[e] --> h[c] + ins[c]		Transport, Extracellular		
INSTt2	inositol transport in via proton symport	h[e] + inost[e] --> h[c] + inost[c]		Transport, Extracellular	(YDR497C or YOL103W)	(Itr1) or (Itr2)
ILEt2r	L-isoleucine reversible transport via proton symport	h[e] + ile-L[e] <==> h[c] + ile-L[c]		Transport, Extracellular	(YBR069C or YKR039W or YCL025C or YBR068C or YDR046C)	(Tat1) or (Gap1) or (Agp1) or (Bap2) or (Bap3)
HXANt2r	hypoxanthine reversible transport via proton symport	h[e] + hxan[e] <==> h[c] + hxan[c]		Transport, Extracellular		
HISt2r	L-histidine reversible transport via proton symport	h[e] + his-L[e] <==> h[c] + his-L[c]		Transport, Extracellular	(YGR191W or YKR039W or YCL025C or YBR069C)	(Hip1) or (Gap1) or (Agp1) or (Tat1)
HDCEAt	hexadecenoate (n-C16:1) transport in via uniport	hdcea[e] --> hdcea[c]		Transport, Extracellular		
HDCAt	Hexadecanoate (n-C16:0) transport in via uniport	hdca[e] --> hdca[c]		Transport, Extracellular		
H2Ot	H2O transport via diffusion	h2o[e] <==> h2o[c]		Transport, Extracellular		
GUAt2r	guanine reversible transport via proton symport	gua[e] + h[e] <==> gua[c] + h[c]		Transport, Extracellular	(YER056C or YER060W or YER060W-A or YGL186C)	(Fcy2) or (Fcy21) or (Fcy22) or (Fcy23)
GTHOXti	oxidized glutathione irreversible uniport	gthox[e] --> gthox[c]		Transport, Extracellular		
GSNt2	guanosine transport in via proton symport	gsn[e] + h[e] --> gsn[c] + h[c]		Transport, Extracellular		
GLYt2r	glycine reversible transport via proton symport	gly[e] + h[e] <==> gly[c] + h[c]		Transport, Extracellular	(YKR039W or YOL020W or YPL265W or YOR348C)	(Gap1) or (Tat2) or (Dip5) or (Put4)
GLYCt	glycerol transport via channel	glyc[c] <==> glyc[e]		Transport, Extracellular	YLL043W	Fps1
GLUt2r	L-glutamate transport via proton symport, reversible	glu-L[e] + h[e] <==> glu-L[c] + h[c]		Transport, Extracellular	(YFL055W or YDR536W or YKR039W or YCL025C or YPL265W)	(Agp3) or (Stl1) or (Gap1) or (Agp1) or (Dip5)
GLNt2r	L-glutamine reversible transport via proton symport	gln-L[e] + h[e] <==> gln-L[c] + h[c]		Transport, Extracellular	(YKR039W or YCL025C or YDR508C or YPL265W)	(Gap1) or (Agp1) or (Gnp1) or (Dip5)
GLCt1	glucose transport (uniport)	glc-D[e] --> glc-D[c]		Transport, Extracellular	(YHR092C or YLR081W or YOL156W or YDR536W or YHR094C or YEL069C or YDL245C or YJR158W or YFL011W or YNR072W or YMR011W or YDR345C or YHR096C or YDR343C or YDR342C or YJL214W or YJL219W)	(Hxt4) or (Gal2) or (Hxt11) or (Stl1) or (Hxt1) or (Hxt13) or (Hxt15) or (Hxt16) or (Hxt10) or (Hxt17) or (Hxt2) or (Hxt3) or (Hxt5) or (Hxt6) or (Hxt7) or (Hxt8) or (Hxt9)
GCALDt	Glycoaldehydye reversible transport	gcald[e] <==> gcald[c]		Transport, Extracellular		
GAM6Pt	D-glucosamine 6-phosphate reversible uniport	gam6p[e] <==> gam6p[c]		Transport, Extracellular		
GALt2	D-galactose transport in via proton symport	gal[e] + h[e] --> gal[c] + h[c]		Transport, Extracellular	(YLR081W or YFL011W or YOL156W or YNL318C or YJL219W or YDR536W)	(Gal2) or (Hxt10) or (Hxt11) or (Hxt14) or (Hxt9) or (Stl1)
FUMt2r	fumarate reversible transport via symport	fum[e] + h[e] <==> fum[c] + h[c]		Transport, Extracellular		

FRUt2	D-fructose transport in via proton symport	fru[e] + h[e] --> fru[c] + h[c]		Transport, Extracellular	(YHR094C or YFL011W or YOL156W or YEL069C or YDL245C or YJR158W or YNR072W or YMR011W or YDR345C or YHR092C or YHR096C or YDR343C or YDR342C or YJL214W or YJL219W)	(Hxt1) or (Hxt10) or (Hxt11) or (Hxt13) or (Hxt15) or (Hxt16) or (Hxt17) or (Hxt2) or (Hxt3) or (Hxt4) or (Hxt5) or (Hxt6) or (Hxt7) or (Hxt8) or (Hxt9)
FORt	formate transport via diffusion	for[e] <==> for[c]		Transport, Extracellular		
ETOHt	ethanol reversible transport	etoh[e] <==> etoh[c]		Transport, Extracellular		
ERGSTt	ergosterol reversible transport	ergst[e] <==> ergst[c]		Transport, Extracellular	YOR011W	Aus1
DURIt2	deoxyuridine transport in via proton symport	duri[e] + h[e] --> duri[c] + h[c]		Transport, Extracellular		
DTTPt	dTTP reversible uniport	dttp[e] <==> dttp[c]		Transport, Extracellular		
DINSt2	deoxyinosine transport in via proton symport	din[e] + h[e] --> din[c] + h[c]		Transport, Extracellular		
DGSNt2	deoxyguanosine transport in via proton symport	dgsn[e] + h[e] --> dgsn[c] + h[c]		Transport, Extracellular		
DCYTt2	deoxycytidine transport in via proton symport	dcyt[e] + h[e] --> dcyt[c] + h[c]		Transport, Extracellular		
DANNt2	7,8-Diaminononanoate reversible transport via proton symport	dann[e] + h[e] <==> dann[c] + h[c]		Transport, Extracellular		
DADNt2	deoxyadenosine transport in via proton symport	dad-2[e] + h[e] --> dad-2[c] + h[c]		Transport, Extracellular		
CYTDt2	cytidine transport in via proton symport	cytd[e] + h[e] --> cytd[c] + h[c]		Transport, Extracellular		
CYSt2r	L-cysteine reversible transport via proton symport	cys-L[e] + h[e] <==> cys-L[c] + h[c]		Transport, Extracellular	(YKR039W or YDR508C or YBR068C or YDR046C or YBR069C or YOL020W)	(Gap1) or (Gnp1) or (Bap2) or (Bap3) or (Tat1) or (Tat2)
CSNt2	cytosine transport in via proton symport	csn[e] + h[e] --> csn[c] + h[c]		Transport, Extracellular	(YER056C or YER060W or YER060W-A or YGL186C)	(Fcy2) or (Fcy21) or (Fcy22) or (Fcy23)
CRNt	L-carnitine reversible transport	crn[e] <==> crn[c]		Transport, Extracellular	YBR132C	Agp2
CO2t	CO2 transporter via diffusion	co2[e] <==> co2[c]		Transport, Extracellular		
CITt2r	citrate reversible transport via symport	cit[e] + h[e] <==> cit[c] + h[c]		Transport, Extracellular		
CHLt2	choline transport via proton symport	chol[e] + h[e] --> chol[c] + h[c]		Transport, Extracellular	YGL077C	Hnm1
BTNt2i	Biotin uptake	btn[e] + h[e] --> btn[c] + h[c]		Transport, Extracellular	(YGR065C or YNR056C)	(Vht1) or (Bio5)
ATPS	ATPase, cytosolic	atp[c] + h2o[c] --> adp[c] + h[e] + pi[c]	EC-3.6.3.6	Transport, Extracellular	((YCR024C-A and YEL017C-A and YGL008C) or (YCR024C-A and YEL017C-A and YPL036W))	(Pma1) or (Pma2)
ASPt2r	L-aspartate reversible transport via proton symport	asp-L[e] + h[e] <==> asp-L[c] + h[c]		Transport, Extracellular	(YFL055W or YKR039W or YPL265W)	(Agp3) or (Gap1) or (Dip5)
ASNt2r	L-asparagine reversible transport via proton symport	asn-L[e] + h[e] <==> asn-L[c] + h[c]		Transport, Extracellular	(YKR039W or YCL025C or YDR508C or YPL265W)	(Gap1) or (Agp1) or (Gnp1) or (Dip5)
ARGt2r	L-arganine reversible transport via proton symport	arg-L[e] + h[e] <==> arg-L[c] + h[c]		Transport, Extracellular	(YKR039W or YEL063C or YNL270C)	(Gap1) or (Can1) or (Alp1)
ARAB-Lt	L-arabinoase extracellular transport	arab-L[e] <==> arab-L[c]		Transport, Extracellular		
ARAB-Dt	D-arabinose reversible transport	arab-D[e] <==> arab-D[c]		Transport, Extracellular		
AMETt2	S-adenosyl-L-methionine transport in via proton symport	amet[e] + h[e] --> amet[c] + h[c]		Transport, Extracellular	YPL274W	Sam3
ALLTTti	allantoate irreversible uniport	alltt[e] --> alltt[c]		Transport, Extracellular	YJR152W	Dal5
ALLTNti	allantoin irreversible uniport	alltn[e] --> alltn[c]		Transport, Extracellular	YIR028W	Dal4
ALAt2r	L-alanine reversible transport via proton symport	ala-L[e] + h[e] <==> ala-L[c] + h[c]		Transport, Extracellular	(YKR039W or YPL265W or YCL025C or YOL020W or YOR348C)	(Gap1) or (Dip5) or (Agp1) or (Tat2) or (Put4)
AKGt2r	2-oxoglutarate reversible transport via symport	akg[e] + h[e] <==> akg[c] + h[c]		Transport, Extracellular		
AKGMAL	alpha-ketoglutarate/malate transporter	akg[c] + mal-L[e] <==> akg[e] + mal-L[c]		Transport, Extracellular		
ADNt2	adenosine transport in via proton symport	adn[e] + h[e] --> adn[c] + h[c]		Transport, Extracellular		
ADEt2	adenine transport in via proton symport	ade[e] + h[e] --> ade[c] + h[c]		Transport, Extracellular	(YER056C or YER060W or YER060W-A or YGL186C)	(Fcy2) or (Fcy21) or (Fcy22) or (Fcy23)
ACt2r	acetate reversible transport via proton symport	ac[e] + h[e] <==> ac[c] + h[c]		Transport, Extracellular	YCR032W	Bph1
ACALDt	acetaldehyde reversible transport	acald[e] <==> acald[c]		Transport, Extracellular		
ABUTt2	4-aminobutyrate transport in via proton symport	4abut[e] + h[e] --> 4abut[c] + h[c]		Transport, Extracellular	(YOR348C or YDL210W)	(Put4) or (Uga4)
ABTt	L-arabinitol transport via passive diffusion	abt[e] <==> abt[c]		Transport, Extracellular		
8AONNt2	8-Amino-7-oxononanoate reversible transport via proton symport	8aonn[e] + h[e] <==> 8aonn[c] + h[c]		Transport, Extracellular		
5AOPt2	5-Amino-4-oxopentanoate transport in via proton symport	5aop[e] + h[e] --> 5aop[c] + h[c]		Transport, Extracellular	YDL210W	Uga4
PStg_SC	phosphatidylserine Golgi transport, yeast-specific	ps_SC[c] <==> ps_SC[g]		Transport, Golgi Apparatus		

PEtg_SC	phosphatidylethanolamine Golgi transport, yeast-specific	pe_SC[c] <==> pe_SC[g]		Transport, Golgi Apparatus		
GDPt3g	GDP Golgi transport via proton anitport	gdp[g] + h[c] <==> gdp[c] + h[g]		Transport, Golgi Apparatus		
CO2tg	CO2 Golgi transport	co2[c] <==> co2[g]		Transport, Golgi Apparatus		
VALt2m	Valine reversible mitochondrial transport via proton symport	h[c] + val-L[c] <==> h[m] + val-L[m]		Transport, Mitochondrial		
TYRt2m	tyrosine mitochondrial transport via proton symport	h[c] + tyr-L[c] <==> h[m] + tyr-L[m]		Transport, Mitochondrial		
TRPt2m	tryptophan mitochondrial transport via proton symport	h[c] + trp-L[c] <==> h[m] + trp-L[m]		Transport, Mitochondrial		
THRt2m	threonine mitochondrial transport via proton symport	h[c] + thr-L[c] <==> h[m] + thr-L[m]		Transport, Mitochondrial		
THFtm	5,6,7,8-Tetrahydrofolate transport, diffusion, mitochondrial	thf[c] <==> thf[m]		Transport, Mitochondrial		
SUCFUMtm	succinate-fumarate transport, mitochondrial	fum[m] + succ[c] --> fum[c] + succ[m]		Transport, Mitochondrial	YJR095W	Sfc1-m
SUCCtm	succinate transport, mitochondrial	pi[m] + succ[c] --> pi[c] + succ[m]		Transport, Mitochondrial	YLR348C	Dic1-m
SERt2m	serine mitochondrial transport via proton symport	h[c] + ser-L[c] <==> h[m] + ser-L[m]		Transport, Mitochondrial		
RIBFLVtm	Riboflavin reversible mitochondrial transport	ribflv[c] <==> ribflv[m]		Transport, Mitochondrial		
QULNtm	Quinolinate reversible mitochondrial transport	quln[c] <==> quln[m]		Transport, Mitochondrial		
PYRt2m	pyruvate mitochondrial transport via proton symport	h[c] + pyr[c] <==> h[m] + pyr[m]		Transport, Mitochondrial		
PStm_SC	phosphatidylserine mitochondrial transport, yeast-specific	ps_SC[c] <==> ps_SC[m]		Transport, Mitochondrial		
PRPPtm	PRPP reversible transport, mitochondrial	prpp[c] <==> prpp[m]		Transport, Mitochondrial		
PROtm	L-proline transport, diffusion, mitochondrial	pro-L[c] <==> pro-L[m]		Transport, Mitochondrial		
PPPG9tm	protoporphyrinogen IX mitochondrial transport	pppg9[c] <==> pppg9[m]		Transport, Mitochondrial		
PIt5m	phosphate transport via hydroxide ion symport, mitochondrial	oh1[m] + pi[c] <==> oh1[c] + pi[m]		Transport, Mitochondrial	YER053C	Phc1-m
PIt2m	phosphate transporter, mitochondrial	h[c] + pi[c] <==> h[m] + pi[m]		Transport, Mitochondrial	YJR077C	Mir1-m
PHEt2m	Phenylalanine mitochondrial transport via proton symport	h[m] + phe-L[m] <==> h[c] + phe-L[c]		Transport, Mitochondrial		
PEtm_SC	phosphatidylethanolamine mitochondrial transport, yeast-specific	pe_SC[c] <==> pe_SC[m]		Transport, Mitochondrial		
PAtm_SC	phosphatidate reversible transport, mitochondrial, yeast-specific	pa_SC[c] <==> pa_SC[m]		Transport, Mitochondrial		
PAPtm	Adenosine 3',5'-bisphosphate mitochondrial transport	pap[c] <==> pap[m]		Transport, Mitochondrial		
PANTtm	pantothenate mitochondrial transport	pant-R[c] <==> pant-R[m]		Transport, Mitochondrial		
PAN4Ptm	panthetheine 4'-phosphate reversible mitochondrial transport	pan4p[c] <==> pan4p[m]		Transport, Mitochondrial		
OXO2Ctm	2-oxodicarboylate transporter, mitochondrial	akg[m] + oxag[c] <==> akg[c] + oxag[m]		Transport, Mitochondrial	(YPL134C or YOR222W)	(Odc1-m) or (Odc2-m)
ORNt3m	ornithine mitochondrial transport via proton antiport	h[c] + orn[m] <==> h[m] + orn[c]		Transport, Mitochondrial	YOR130C	Ort1-m
OCTDP_5tm	all-trans-Octaprenyl diphosphate	octdp_5[c] <==> octdp_5[m]		Transport, Mitochondrial		
OAAt2m	oxaloacetate transport, mitochondrial	h[c] + oaa[c] <==> h[m] + oaa[m]		Transport, Mitochondrial	YKL120W	Oac1-m
O2tm	O2 transport (diffusion)	o2[c] <==> o2[m]		Transport, Mitochondrial		
NMNt2m	NMN mitochondrial transport via proton symport	h[c] + nmn[c] <==> h[m] + nmn[m]		Transport, Mitochondrial		
NH4tm	NH3 mitochondrial transport	nh4[c] <==> nh4[m]		Transport, Mitochondrial		
MLTHFtm	5,10-Methylenetetrahydrofolate transport, diffusion, mitochondrial	mlthf[c] <==> mlthf[m]		Transport, Mitochondrial		
METt2m	methionine mitochondrial transport via proton symport	h[m] + met-L[m] <==> h[c] + met-L[c]		Transport, Mitochondrial		
MALtm	malate transport, mitochondrial	mal-L[c] + pi[m] <==> mal-L[m] + pi[c]		Transport, Mitochondrial	YLR348C	Dic1-m
LYSt2m	Lysine mitochondrial transport via proton symport	h[c] + lys-L[c] <==> h[m] + lys-L[m]		Transport, Mitochondrial		
IND3ACtm	indole-3-acetate mitochondrial transport via diffusion	ind3ac[c] <==> ind3ac[m]		Transport, Mitochondrial		
ID3ACALDtm	indole-3-acetaldehyde mitochondrial transport via diffusion	id3acald[c] <==> id3acald[m]		Transport, Mitochondrial		
HMGCOAtm	Hydroxymethylglutaryl-CoA reversible mitochondrial transport	hmgcoa[c] <==> hmgcoa[m]		Transport, Mitochondrial		
HISt2m	histidine mitochondrial transport via proton symport	h[m] + his-L[m] <==> h[c] + his-L[c]		Transport, Mitochondrial		
H2Otm	H2O transport, mitochondrial	h2o[c] <==> h2o[m]		Transport, Mitochondrial		
GUAtm	guanine mitochondrial transport via diffusion	gua[c] <==> gua[m]		Transport, Mitochondrial		
GSNt2m	guanosine mitochondrial transport via proton symport	gsn[c] + h[c] <==> gsn[m] + h[m]		Transport, Mitochondrial		
GLYt2m	glycine mitochondrial transport via proton symport	gly[c] + h[c] <==> gly[m] + h[m]		Transport, Mitochondrial		
GLYC3Ptm	glycerol-3-phosphate shuttle	glyc3p[c] --> glyc3p[m]		Transport, Mitochondrial		
GLUt5m	L-glutamate transport into mitochondria via hydroxide ion antiport	glu-L[c] + oh1[m] --> glu-L[m] + oh1[c]		Transport, Mitochondrial		
GLUt2m	L-glutamate reversible transport via proton symport, mitochondrial	glu-L[c] + h[c] <==> glu-L[m] + h[m]		Transport, Mitochondrial		
GCALDtm	glycoaldehyde mitochondrial transport	gcald[c] <==> gcald[m]		Transport, Mitochondrial		
FRDcm	fumarate reductase, cytosolic/mitochondrial	fadh2[m] + fum[c] --> fad[m] + succ[c]	EC-1.3.99.1	Transport, Mitochondrial	YEL047C	Frds1
FORtm	formate mitochondrial transport	for[m] --> for[c]		Transport, Mitochondrial		
FADFMNtm	FAD/FMN antiport	fad[c] + fmn[m] --> fad[m] + fmn[c]		Transport, Mitochondrial	YIL134W	Flx1-m
FA182ACPtm	fatty-acyl-ACP mitochondrial transport	ocdcyaACP[m] --> ocdcyaACP[c]		Transport, Mitochondrial		
FA181ACPtm	fatty-acyl-ACP mitochondrial transport	octeACP[m] --> octeACP[c]		Transport, Mitochondrial		
FA180ACPtm	fatty-acyl-ACP mitochondrial transport	ocdcaACP[m] --> ocdcaACP[c]		Transport, Mitochondrial		
FA161ACPtm	fatty-acyl-ACP mitochondrial transport	hdeACP[m] --> hdeACP[c]		Transport, Mitochondrial		
FA160ACPtm	fatty-acyl-ACP mitochondrial transport	palmACP[m] --> palmACP[c]		Transport, Mitochondrial		
FA141ACPtm	fatty-acyl-ACP mitochondrial transport	tdeACP[m] --> tdeACP[c]		Transport, Mitochondrial		
FA140ACPtm	fatty-acyl-ACP mitochondrial transport	myrsACP[m] --> myrsACP[c]		Transport, Mitochondrial		
FA120ACPtm	fatty-acyl-ACP mitochondrial transport	ddcaACP[m] --> ddcaACP[c]		Transport, Mitochondrial		
ETOHtm	ethanol transport to mitochondria (diffusion)	etoh[c] <==> etoh[m]		Transport, Mitochondrial		
E4Ptm	D-erythrose 4-phosphate mtiochondrial transport via diffusion	e4p[c] <==> e4p[m]		Transport, Mitochondrial		
E4HGLUtm	L-erythro-4-hydroxyglutamate mitochondrial transport via diffusion	e4hglu[c] <==> e4hglu[m]		Transport, Mitochondrial		
DICtm	dicarboxylate transport, mitochondrial	mal-L[c] + succ[m] <==> mal-L[m] + succ[c]		Transport, Mitochondrial	YLR348C	Dic1-m
DHPTtm	Dihydropteroate mitochondrial transport via diffusion	dhpt[c] <==> dhpt[m]		Transport, Mitochondrial		
DHNPTtm	dhnpt mitochondrial transport	dhnpt[c] <==> dhnpt[m]		Transport, Mitochondrial		
DHFtm	dihydrofolate reversible mitochondrial transport	dhf[c] <==> dhf[m]		Transport, Mitochondrial		
DHAPtm	dihydroxyacetone phosphate transport, mitochondrial	dhap[m] --> dhap[c]		Transport, Mitochondrial		
D-LACtm	D-lactate transport, mitochondrial	h[c] + lac-D[c] <==> h[m] + lac-D[m]		Transport, Mitochondrial		
CRNtim	L-carnitine transport out of mitochondria via diffusion	crn[m] --> crn[c]		Transport, Mitochondrial		
CRNCARtm	carnithine-acetylcarnithine carrier, mitochondrial	acrn[c] + crn[m] --> acrn[m] + crn[c]		Transport, Mitochondrial	YOR100C	Crc1-m
CO2tm	CO2 transport (diffusion), mitochondrial	co2[c] <==> co2[m]		Transport, Mitochondrial		
CMPtm	CMP transport, diffusion, mitochondrial	cmp[c] <==> cmp[m]		Transport, Mitochondrial		
CITtcm	citrate transport, mitochondrial	cit[c] + icit[m] <==> cit[m] + icit[c]		Transport, Mitochondrial	YBR291C	Ctp1-m
CITtbm	citrate transport, mitochondrial	cit[c] + pep[m] <==> cit[m] + pep[c]		Transport, Mitochondrial	YBR291C	Ctp1-m
CITtam	citrate transport, mitochondrial	cit[c] + mal-L[m] <==> cit[m] + mal-L[c]		Transport, Mitochondrial	YBR291C	Ctp1-m
ATPtm-H	ADP/ATP transporter, mitochondrial	adp[c] + atp[m] + h[c] --> adp[m] + atp[c] + h[m]		Transport, Mitochondrial	(YBR085W or YBL030C or YMR056C)	(Aac3-m) or (Pet9-m) or (Aac1-m)
ASPt2m	aspartate mitochondrial transport via proton symport	asp-L[c] + h[c] <==> asp-L[m] + h[m]		Transport, Mitochondrial		
ASNt2m	asparagine mitochondrial transport via proton transport	asn-L[c] + h[c] <==> asn-L[m] + h[m]		Transport, Mitochondrial		
ARGt2m	arginine mitochondrial transport via proton symport	arg-L[c] + h[c] <==> arg-L[m] + h[m]		Transport, Mitochondrial		

AMETtm	S-Adenosyl-L-methionine reversible transport, mitochondrial	amet[c] <==> amet[m]		Transport, Mitochondrial		
AHCYStm	S-adenosyl-L-homocysteine reversible transport, mitochondrial	ahcys[c] <==> ahcys[m]		Transport, Mitochondrial		
ADEtm	adenine reversible transport, mitochondria	ade[c] <==> ade[m]		Transport, Mitochondrial		
ACtm	acetate transport, mitochondrial	ac[c] <==> ac[m]		Transport, Mitochondrial		
ACRNtim	O-acetylcarnintine transport into mitochondria via diffusion	acrn[c] --> acrn[m]		Transport, Mitochondrial		
5MTHFtm	5-Methyltetrahydrofolate mitochondrial transport via diffusion	5mthf[c] <==> 5mthf[m]		Transport, Mitochondrial		
5AOPtm	5-Amino-4-oxopentanoate mitochondrial transport	5aop[c] <==> 5aop[m]		Transport, Mitochondrial		
4HPRO-LTtm	trans-4-hydroxy-L-proline mitochondrial transport via diffusion	4hpro-LT[c] <==> 4hpro-LT[m]		Transport, Mitochondrial		
4HBZtm	4-Hydroxybenzoate mitochondrial transport	4hbz[c] <==> 4hbz[m]		Transport, Mitochondrial		
4H2OGLTtm	4-hydroxy-2-oxoglutarate mitochondrial transport via diffusion	4h2oglt[c] <==> 4h2oglt[m]		Transport, Mitochondrial		
4ABZtm	4-Aminobenzoate mitochondrial transport via diffusion	4abz[c] <==> 4abz[m]		Transport, Mitochondrial		
4ABUTtm	4-aminobutanoate mitochondrial transport via diffusion	4abut[c] <==> 4abut[m]		Transport, Mitochondrial		
4ABUTNtm	4-aminobutanal mitochondrial transport via diffusion	4abutn[c] <==> 4abutn[m]		Transport, Mitochondrial		
3OPHB_5tm	3-Octaprenyl-4-hydroxybenzoate mitochondrial transport	3ophb_5[c] <==> 3ophb_5[m]		Transport, Mitochondrial		
3MOPtm	3-Methyl-2-oxopentanoate transport, diffusion, mitochondrial	3mop[c] <==> 3mop[m]		Transport, Mitochondrial		
3MOBtm	3-methyl-2-oxobutanoate transport, diffusion, mitochondrial	3mob[c] <==> 3mob[m]		Transport, Mitochondrial		
3C4MOPtm	3-Carboxy-4-methyl-2-oxopentanoate transport, diffusion, mitochondrial	3c4mop[c] <==> 3c4mop[m]		Transport, Mitochondrial		
3C3HMPtm	2-Isopropylmalate transport, diffusion, mitochondrial	3c3hmp[c] <==> 3c3hmp[m]		Transport, Mitochondrial		
34HPPt2m	3-(4-hydroxyphenyl)pyruvate mitochondrial transport via proton symport	34hpp[c] + h[c] <==> 34hpp[m] + h[m]		Transport, Mitochondrial		
2OXOADPtim	2-oxoadipate transport out of mitochondria via diffusion	2oxoadp[m] --> 2oxoadp[c]		Transport, Mitochondrial		
2OMPH_5tm	2-Octaprenyl-6-methoxyprenol mitochondrial transport	2omph_5[c] <==> 2omph_5[m]		Transport, Mitochondrial		
2MCITtm	2-methylcitrate mitochondrial transport via diffusion	2mcit[c] <==> 2mcit[m]		Transport, Mitochondrial		
2DHPtm	2-Dehydropantoate mitochondrial transport	2dhp[c] <==> 2dhp[m]		Transport, Mitochondrial		
2DDA7Ptm	2-Dehydro-3-deoxy-D-arabino-heptonate7-phohsphate mitochondrial transport via diffusion	2dda7p[c] <==> 2dda7p[m]		Transport, Mitochondrial		
UMPtn	UMP nuclear transport	ump[c] <==> ump[n]		Transport, Nuclear		
PTD4INOtn_SC	phosphatidyl-1D-myo-4-inositol nuclear transport, yeast-specific	ptd4ino_SC[c] <==> ptd4ino_SC[n]		Transport, Nuclear		
PTD1INOtn_SC	phosphatidyl-1D-myo-insoitol nuclear transport, yeast-specific	ptd1ino_SC[c] <==> ptd1ino_SC[n]		Transport, Nuclear		
PIt2n	phosphate nuclear transport via proton symport	h[c] + pi[c] <==> h[n] + pi[n]		Transport, Nuclear		
H2Otn	H2O transport, nuclear	h2o[n] <==> h2o[c]		Transport, Nuclear		
GLUt2n	glutamate nuclear transport via proton symport	glu-L[c] + h[c] <==> glu-L[n] + h[n]		Transport, Nuclear		
GLNt2n	glutamine nuclear transport via proton symport	gln-L[c] + h[c] <==> gln-L[n] + h[n]		Transport, Nuclear		
GDPtn	GDP nuclear transport	gdp[c] <==> gdp[n]		Transport, Nuclear		
DUMPtn	dUMP nuclear transport	dump[c] <==> dump[n]		Transport, Nuclear		
DHORtn	(S)-Dihydrooroate nuclear transport	dhor-S[c] <==> dhor-S[n]		Transport, Nuclear		
DGDPtn	dGDP nuclear transport	dgdp[c] <==> dgdp[n]		Transport, Nuclear		
DCDPtn	dCDP nuclear transport	dcdp[c] <==> dcdp[n]		Transport, Nuclear		
DADPtn	DADP nuclear transport	dadp[c] <==> dadp[n]		Transport, Nuclear		
CO2tn	CO2 nuclear transport via diffusion	co2[n] <==> co2[c]		Transport, Nuclear		
CDPtn	CDP nuclear transport	cdp[c] <==> cdp[n]		Transport, Nuclear		
CBPtn	carbamoyl phosphate nuclear transport via diffusion	cbp[c] <==> cbp[n]		Transport, Nuclear		
CBASPtn	N-carbomoyl-L-aspartate transport, diffusion	cbasp[n] <==> cbasp[c]		Transport, Nuclear		
ASPt2n	aspartate nuclear transport via proton symport	asp-L[c] + h[c] <==> asp-L[n] + h[n]		Transport, Nuclear		
AMETtn	S-adenosyl-L-methionine nuclear transport	amet[c] <==> amet[n]		Transport, Nuclear		
AKGt2n	2-oxoglutarate nuclear transport via proton symport	akg[c] + h[c] <==> akg[n] + h[n]		Transport, Nuclear		
AHCYStn	S-adenosyl-L-homocysteine nuclear transport	ahcys[c] <==> ahcys[n]		Transport, Nuclear		
2OMPH_5tn	2-Octaprenyl-6-methoxyprenol nuclear transport	2omph_5[c] <==> 2omph_5[n]		Transport, Nuclear		
2OHPH_5tn	2-Octaprenyl-6-hydroxyphenol nuclear transport	2ohph_5[c] <==> 2ohph_5[n]		Transport, Nuclear		
TYRt2p	tyrosine peroxisomal transport via proton symport	h[c] + tyr-L[c] <==> h[x] + tyr-L[x]		Transport, Peroxisomal		
PYRt2p	pyruvate peroxisomal transport via proton symport	h[c] + pyr[c] <==> h[x] + pyr[x]		Transport, Peroxisomal		
PIt2p	phosphate peroxisomal transport via proton symport	h[c] + pi[c] <==> h[x] + pi[x]		Transport, Peroxisomal		
NMNt2p	NMN peroxisomal transport via proton symport	h[c] + nmn[c] <==> h[x] + nmn[x]		Transport, Peroxisomal		
NH4tp	ammonia peroxisomal transport	nh4[c] <==> nh4[x]		Transport, Peroxisomal		
MALOAAtp	malate/oxaloacetate shuttle	mal-L[x] + oaa[c] <==> mal-L[c] + oaa[x]		Transport, Peroxisomal		
HCYSt2p	Homocysteine peroxisomal transport via proton symport	h[c] + hcys-L[c] <==> h[x] + hcys-L[x]		Transport, Peroxisomal		
H2Otp	water transport by diffusion, peroxisomal	h2o[c] <==> h2o[x]		Transport, Peroxisomal		
GLXtp	glyoxylate transport, peroxisomal	glx[c] <==> glx[x]		Transport, Peroxisomal		
FA80tp	fatty acid peroxisomal transport	octa[c] --> octa[x]		Transport, Peroxisomal		
FA260tp	fatty acid peroxisomal transport	hexc[c] --> hexc[x]		Transport, Peroxisomal	YBR041W	Fat1-p
FA240tp	fatty acid peroxisomal transport	ttc[c] --> ttc[x]		Transport, Peroxisomal	YBR041W	Fat1-p
FA182COAabcp	fatty acyl-CoA peroxisomal transport via ABC system	atp[x] + h2o[x] + ocdycacoa[c] --> adp[x] + h[x] + ocdycacoa[x] + pi[x]		Transport, Peroxisomal	(YPL147W and YKL188C)	(Pxa1-p and Pxa2-p)
FA181COAabcp	fatty acyl-CoA peroxisomal transport via ABC system	atp[x] + h2o[x] + odecoa[c] --> adp[x] + h[x] + odecoa[x] + pi[x]		Transport, Peroxisomal	(YPL147W and YKL188C)	(Pxa1-p and Pxa2-p)
FA180COAabcp	fatty acyl-CoA transport via ABC system	atp[x] + h2o[x] + stcoa[c] --> adp[x] + h[x] + pi[x] + stcoa[x]		Transport, Peroxisomal	(YPL147W and YKL188C)	(Pxa1-p and Pxa2-p)
FA161tp	fatty acid peroxisomal transport	hdcea[c] --> hdcea[x]		Transport, Peroxisomal		
FA161COAabcp	fatty acyl-CoA peroxisomal transport via ABC system	atp[x] + h2o[x] + hdcoa[c] --> adp[x] + h[x] + hdcoa[x] + pi[x]		Transport, Peroxisomal	(YPL147W and YKL188C)	(Pxa1-p and Pxa2-p)
FA160tp	fatty acid peroxisomal transport	hdca[c] --> hdca[x]		Transport, Peroxisomal		
FA160COAabcp	fatty acyl-CoA peroxisomal transport via ABC system	atp[x] + h2o[x] + pmtcoa[c] --> adp[x] + h[x] + pi[x] + pmtcoa[x]		Transport, Peroxisomal	(YPL147W and YKL188C)	(Pxa1-p and Pxa2-p)
FA141tp	fatty acid peroxisomal transport	ttdcea[c] --> ttdcea[x]		Transport, Peroxisomal		
FA141COAabcp	fatty acid peroxisomal transport via ABC system	atp[x] + h2o[x] + tdecoa[c] --> adp[x] + h[x] + pi[x] + tdecoa[x]		Transport, Peroxisomal	(YPL147W and YKL188C)	(Pxa1-p and Pxa2-p)
FA140tp	fatty acid peroxisomal transport	ttdca[c] --> ttdca[x]		Transport, Peroxisomal		
FA140COAabcp	fatty acid peroxisomal transport via ABC system	atp[x] + h2o[x] + tdcoa[c] --> adp[x] + h[x] + pi[x] + tdcoa[x]		Transport, Peroxisomal	(YPL147W and YKL188C)	(Pxa1-p and Pxa2-p)
FA120tp	fatty acid peroxisomal transport	ddca[c] --> ddca[x]		Transport, Peroxisomal		
FA100tp	fatty acid peroxisomal transport	dca[c] --> dca[x]		Transport, Peroxisomal		
E4HGLUtp	L-erythro-4-hydroxyglutamate peroxisomal transport via diffusion	e4hglu[c] <==> e4hglu[x]		Transport, Peroxisomal		
CYSTtp	cystathione peroxisomal transport	cyst-L[c] <==> cyst-L[x]		Transport, Peroxisomal		
CRNtp	carnitine transport into peroxsiome	crn[c] --> crn[x]		Transport, Peroxisomal		

CRNCARtp	carnitine-acetylcarnitine carrier, peroxisomal	acrn[x] + crn[c] --> acrn[c] + crn[x]		Transport, Peroxisomal		
CO2tp	CO2 peroxisomal transport	co2[c] <==> co2[x]		Transport, Peroxisomal		
CITtcp	citrate/isocitrate antiport into peroxisome	cit[c] + icit[x] <==> cit[x] + icit[c]		Transport, Peroxisomal		
CITtap	citrate/malate antiport into peroxisome	cit[x] + mal-L[c] <==> cit[c] + mal-L[x]		Transport, Peroxisomal		
ATPtp-H	ADP/ATP transporter, peroxisomal	adp[x] + atp[c] + h[x] --> adp[c] + atp[x] + h[c]		Transport, Peroxisomal	YPR128C	Ant1-p
ATP2tp_H	AMP/ATP transporter, peroxisomal	amp[x] + atp[c] + h[x] --> amp[c] + atp[x] + h[c]		Transport, Peroxisomal	YPR128C	Ant1-p
ASPGLUtp	aspartate-glutamate peroxisomal shuttle	asp-L[c] + glu-L[x] <==> asp-L[x] + glu-L[c]		Transport, Peroxisomal		
ACtp	acetate transport, peroxisomal	ac[c] <==> ac[x]		Transport, Peroxisomal		
ACRNtp	acetylcarnitine transport out of peroxisome	acrn[x] --> acrn[c]		Transport, Peroxisomal		
4H2OGLTtp	4-hydroxy-2-oxoglutarate peroxisomal transport via diffusion	4h2oglt[c] <==> 4h2oglt[x]		Transport, Peroxisomal		
34HPPt2p	3-(4-hydroxyphenyl)pyruvate peroxisomal transport via proton symport	34hpp[c] + h[c] <==> 34hpp[x] + h[x]		Transport, Peroxisomal		
TREt2v	trehalose vacuolar transport via proton symport	h[c] + tre[c] <==> h[v] + tre[v]		Transport, Vacuolar		
PStv_SC	phosphatidylserine vacuolar transport, yeast-specific	ps_SC[c] <==> ps_SC[v]		Transport, Vacuolar		
PIt2v	phosphate vacuolar transport via proton symport	h[c] + pi[c] <==> h[v] + pi[v]		Transport, Vacuolar		
PEtv_SC	phosphatidylethanolamine vacuolar transport, yeast-specific	pe_SC[c] <==> pe_SC[v]		Transport, Vacuolar		
H2Otv	H2O transport, vacuolar	h2o[c] <==> h2o[v]		Transport, Vacuolar		
GLCtv	glucose transport, vacuolar	glc-D[c] <==> glc-D[v]		Transport, Vacuolar		
CO2tv	CO2 vacuolar transport	co2[c] <==> co2[v]		Transport, Vacuolar		
TYRTRSm	tyrosyl-tRNA synthetase, mitochondrial	[m] : atp + trnatyr + tyr-L --> amp + ppi + tyrtrna	EC-6.1.1.1	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YPL097W	Msy1-m
TYRTRS	tyrosyl-tRNA synthetase	[c] : atp + trnatyr + tyr-L --> amp + ppi + tyrtrna	EC-6.1.1.1	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YGR185C	Tys1
TYRTAp	tyrosine transaminase, peroxisomal	[x] : akg + tyr-L <==> 34hpp + glu-L	EC-2.6.1.5	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YLR027C	Aat2-p
TYRTAm	tyrosine transaminase, mitochondrial	[m] : akg + tyr-L <==> 34hpp + glu-L	EC-2.6.1.5	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YKL106W	Aat1-m
TYRTAi	tyrosine transaminase, irreversible	[c] : 34hpp + glu-L --> akg + tyr-L	EC-2.6.1.5	Tyrosine, Tryptophan, and Phenylalanine Metabolism	(YGL202W or YHR137W)	(Aro8) or (Aro9)
TYRTA	tyrosine transaminase	[c] : akg + tyr-L <==> 34hpp + glu-L	EC-2.6.1.5	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YLR027C	Aat2
TRPTRSm	Tryptophanyl-tRNA synthetase, mitochondrial	[m] : atp + trnatrp + trp-L --> amp + ppi + trptrna	EC-6.1.1.2	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR268W	Msw1-m
TRPTRS	Tryptophanyl-tRNA synthetase	[c] : atp + trnatrp + trp-L --> amp + ppi + trptrna	EC-6.1.1.2	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YOL097C	Wrs1
TRPS1	tryptophan synthase (indoleglycerol phosphate)	[c] : 3ig3p + ser-L --> g3p + h2o + trp-L	EC-4.2.1.20	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YGL026C	Trp5
TRPO2	L-Tryptophan:oxygen 2,3-oxidoreductase (decyclizing)	[c] : o2 + trp-L --> Lfmkynr	EC-1.13.11.11	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YJR078W	Bna2
SPMDAT1	Spermidine acetyltransferase	[c] : accoa + spmd --> N1aspmd + coa + h	EC-2.3.1.57	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
SHKK	shikimate kinase	[c] : atp + skm --> adp + h + skm5p	EC-2.7.1.71	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR127W	Aro1
SHK3D	shikimate dehydrogenase	[c] : 3dhsk + h + nadph --> nadp + skm	EC-1.1.1.25	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR127W	Aro1
PSCVTi	3-phosphoshikimate 1-carboxyvinyltransferase, irreversible	[c] : pep + skm5p --> 3psme + pi	EC-2.5.1.19	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR127W	Aro1
PRAIi	phosphoribosylanthranilate isomerase (irreversible)	[c] : pran --> 2cpr5p	EC-5.3.1.24	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR007W	Trp1
PPNDH	prephenate dehydratase	[c] : h + pphn --> co2 + h2o + phpyr	EC-4.2.1.51	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YNL316C	Pha2
PPND2	prephenate dehydrogenase (NADP)	[c] : nadp + pphn --> 34hpp + co2 + nadph	EC-1.3.1.13	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YBR166C	Tyr1
PPND	prephenate dehydrogenase	[c] : nad + pphn --> 34hpp + co2 + nadh	EC-1.3.1.12	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
POLYAO2	poylamine oxidase	[c] : N1sprm + h2o + o2 --> N1aspmd + aproa + h2o2	EC-1.5.3.11	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
POLYAO	polyamine oxidase	[c] : N1aspmd + h2o + o2 --> aproa + aprut + h2o2	EC-1.5.3.11	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
PHETRSm	phenylalanyl-tRNA synthetase, mitochondrial	[m] : atp + phe-L + trnaphe --> amp + phetrna + ppi	EC-6.1.1.20	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YPR047W	Msf1-m
PHETRS	Phenylalanyl-tRNA synthetase	[c] : atp + phe-L + trnaphe --> amp + phetrna + ppi	EC-6.1.1.20	Tyrosine, Tryptophan, and Phenylalanine Metabolism	(YFL022C and YLR060W)	Frs
PHETA1	phenylalanine transaminase	[c] : akg + phe-L <==> glu-L + phpyr	EC-2.6.1.58	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YHR137W	Aro9
PCLAD	picolinic acid decarboxylase	[c] : cmusa + h --> am6sa + co2	EC-4.1.1.45	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
MACACI	maleylacetoacetate isomerase	[c] : 4mlacac --> 4fumacac	EC-5.2.1.2	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
KYN3OX	kynurenine 3-monooxygenase	[c] : Lkynr + h + nadph + o2 --> h2o + hLkynr + nadp	EC-1.14.13.9	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YBL098W	Bna4
KYN	kynureninase	[c] : Lkynr + h2o --> ala-L + anth + h	EC-3.7.1.3	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YLR231C	Bna5
INDPYRD	Indole-3-pyruvate carboxylase	[c] : h + indpyr <==> co2 + id3acald	EC-4.1.1.74	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR380W	Aro10
IGPS	indole-3-glycerol-phosphate synthase	[c] : 2cpr5p + h --> 3ig3p + co2 + h2o	EC-4.1.1.48	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YKL211C	Trp3
HKYNH	3-Hydroxy-L-kynurenine hydrolase	[c] : h2o + hLkynr --> 3hanthrn + ala-L	EC-3.7.1.3	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YLR231C	Bna5
HGNTOR	Homogentisate:oxygen 1,2-oxidoreductase (decyclizing)	[c] : hgentis + o2 --> 4mlacac + h	EC-1.13.11.5	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
FUMAC	fumarylacetoacetase	[c] : 4fumacac + h2o --> acac + fum + h	EC-3.7.1.2	Tyrosine, Tryptophan, and Phenylalanine Metabolism		

FKYNH	N-Formyl-L-kynurenine amidohydrolase	[c] : Lfmkynr + h2o --> Lkynr + for + h	EC-3.5.1.9	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
DIAT	diamine transaminase	[c] : accoa + sprm --> N1sprm + coa + h	EC-2.6.1.29	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
DHQTi	3-dehydroquinate dehydratase, irreversible	[c] : 3dhq --> 3dhsk + h2o	EC-4.2.1.10	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR127W	Aro1
DHQS	3-dehydroquinate synthase	[c] : 2dda7p --> 3dhq + pi		Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR127W	Aro1
DDPAm	2-deoxy-D-arabino-heptulosonate 7-phosphate synthetase, mitochondrial	[m] : e4p + h2o + pep --> 2dda7p + pi	EC-4.1.2.15	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR035W	Aro3-m
DDPA	3-deoxy-D-arabino-heptulosonate 7-phosphate synthetase	[c] : e4p + h2o + pep --> 2dda7p + pi	EC-4.1.2.15	Tyrosine, Tryptophan, and Phenylalanine Metabolism	(YBR249C or YDR035W)	(Aro4) or (Aro3)
CHORS	chorismate synthase	[c] : 3psme --> chor + pi	EC-4.2.3.5	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YGL148W	Aro2
CHORM	chorismate mutase	[c] : chor --> pphn	EC-5.4.99.5	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YPR060C	Aro7
CATp	catalase A, peroxisomal	[x] : (2) h2o2 --> (2) h2o + o2	EC-1.11.1.6	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR256C	Cta1-p
CAT	catalase	[c] : (2) h2o2 --> (2) h2o + o2	EC-1.11.1.6	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YGR088W	Ctt1
ANPRT	anthranilate phosphoribosyltransferase	[c] : anth + prpp --> ppi + pran	EC-2.4.2.18	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR354W	Trp4
AMID3	amidase	[c] : h2o + iad --> ind3ac + nh4	EC-3.5.1.4	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR242W	Amd2
AMID2	amidase	[c] : h2o + pad --> nh4 + pac	EC-3.5.1.4	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YDR242W	Amd2
AM6SAD	aminomuconate-semialdehyde dehydrogenase	[c] : am6sa + h2o + nad --> amuco + (2) h + nadh	EC-1.2.1.32	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
ALDD2ym	aldehyde dehydrogenase (acetylaldehyde, NADP), mitochondrial	[m] : acald + h2o + nadp --> ac + (2) h + nadph	EC-1.2.1.4	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YOR374W	Ald4-m
ALDD2y	aldehyde dehydrogenase (acetaldehyde, NADP)	[c] : acald + h2o + nadp --> ac + (2) h + nadph	EC-1.2.1.4	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YPL061W	Ald6
ALDD2xm	aldehyde dehydrogenase (acetylaldehyde, NAD), mitochondrial	[m] : acald + h2o + nad --> ac + (2) h + nadh	EC-1.2.1.3	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YOR374W	Ald4-m
ALDD20ym	aldehyde dehydrogenase (indole-3-acetaldehyde, NADP), mitochondrial	[m] : h2o + id3acald + nadp --> (2) h + ind3ac + nadph		Tyrosine, Tryptophan, and Phenylalanine Metabolism	(YOR374W or YER073W)	(Ald4-m) or (Ald5-m)
ALDD20y	aldehyde dehydrogenase (indole-3-acetaldehyde, NADP)	[c] : h2o + id3acald + nadp --> (2) h + ind3ac + nadph		Tyrosine, Tryptophan, and Phenylalanine Metabolism	YPL061W	Ald6
ALDD20xm	aldehyde dehydrogenase (indole-3-acetaldehyde, NAD), mitochondrial	[m] : h2o + id3acald + nad --> (2) h + ind3ac + nadh		Tyrosine, Tryptophan, and Phenylalanine Metabolism	YOR374W	Ald4-m
ALDD19x	aldehyde dehydrogenase (phenylacetaldehyde, NAD)	[c] : h2o + nad + pacald --> (2) h + nadh + pac	EC-1.2.1.39	Tyrosine, Tryptophan, and Phenylalanine Metabolism	(YMR170C or YMR169C)	(Ald2) or (Ald3)
3HAO	3-hydroxyanthranilate 3,4-dioxygenase	[c] : 3hanthrn + o2 --> cmusa + h	EC-1.13.11.6	Tyrosine, Tryptophan, and Phenylalanine Metabolism	YJR025C	Bna1
34HPPOR	4-Hydroxyphenylpyruvate:oxygen oxidoreductase	[c] : 34hpp + o2 --> co2 + hgentis	EC-1.13.11.27	Tyrosine, Tryptophan, and Phenylalanine Metabolism		
VALTRSm	valyl-tRNA synthetase, mitochondrial	[m] : atp + trnaval + val-L --> amp + ppi + valtrna	EC-6.1.1.9	Valine, leucine, and isoleucine metabolism	YGR094W	Vas1-m
VALTRS	Valyl-tRNA synthetase	[c] : atp + trnaval + val-L --> amp + ppi + valtrna	EC-6.1.1.9	Valine, leucine, and isoleucine metabolism	YGR094W	Vas1
VALTA	valine transaminase	[c] : akg + val-L <==> 3mob + glu-L	EC-2.6.1.42	Valine, leucine, and isoleucine metabolism	YJR148W	Bat2
OMCDCm	2-oxo-4-methyl-3-carboxypentanoate decarboxylation, mitochondrial	[m] : 3c4mop + h --> 4mop + co2		Valine, leucine, and isoleucine metabolism	YHR208W	Bat1-m
OMCDC	2-Oxo-4-methyl-3-carboxypentanoate decarboxylation	[c] : 3c4mop + h --> 4mop + co2		Valine, leucine, and isoleucine metabolism	YJR148W	Bat2
LEUTRSm	leucyl-tRNA synthetase, mitochondrial	[m] : atp + leu-L + trnaleu --> amp + leutrna + ppi	EC-6.1.1.4	Valine, leucine, and isoleucine metabolism	YLR382C	Nam2-m
LEUTRS	Leucyl-tRNA synthetase	[c] : atp + leu-L + trnaleu --> amp + leutrna + ppi	EC-6.1.1.4	Valine, leucine, and isoleucine metabolism	YPL160W	Cdc60
LEUTAm	leucine transaminase, mitochondrial	[m] : akg + leu-L <==> 4mop + glu-L	EC-2.6.1.6	Valine, leucine, and isoleucine metabolism	YHR208W	Bat1-m
LEUTA	leucine transaminase	[c] : akg + leu-L <==> 4mop + glu-L	EC-2.6.1.6	Valine, leucine, and isoleucine metabolism	YJR148W	Bat2
KARA2im	ketol-acid reductoisomerase (2-Aceto-2-hydroxybutanoate), mitochondrial	[m] : 2ahbut + h + nadph --> 23dhmp + nadp	EC-1.1.1.86	Valine, leucine, and isoleucine metabolism	YLR355C	Ilv5-m
KARA1im	acetohydroxy acid isomeroreductase, mitochondrial	[m] : alac-S + h + nadph --> 23dhmb + nadp	EC-1.1.1.86	Valine, leucine, and isoleucine metabolism	YLR355C	Ilv5-m
IPPSm	2-isopropylmalate synthase, mitochondrial	[m] : 3mob + accoa + h2o --> 3c3hmp + coa + h	EC-4.1.3.12	Valine, leucine, and isoleucine metabolism	YNL104C	Leu4-m
IPPS	2-isopropylmalate synthase	[c] : 3mob + accoa + h2o --> 3c3hmp + coa + h	EC-4.1.3.12	Valine, leucine, and isoleucine metabolism	(YNL104C or YOR108W)	(Leu4) or (Leu5)
IPPMIb	2-isopropylmalate hydratase	[c] : 2ippm + h2o <==> 3c3hmp	EC-4.2.1.33	Valine, leucine, and isoleucine metabolism	YGL009C	Leu1
IPPMIa	3-isopropylmalate dehydratase	[c] : 3c2hmp <==> 2ippm + h2o	EC-4.2.1.33	Valine, leucine, and isoleucine metabolism	YGL009C	Leu1
IPMD	3-isopropylmalate dehydrogenase	[c] : 3c2hmp + nad --> 3c4mop + h + nadh	EC-1.1.1.85	Valine, leucine, and isoleucine metabolism	YCL018W	Leu2
ILETRSm	isoleucyl-tRNA synthetase, mitochondrial	[m] : atp + ile-L + trnaile --> amp + iletrna + ppi	EC-6.1.1.5	Valine, leucine, and isoleucine metabolism	YPL040C	Ism1-m
ILETRS	Isoleucyl-tRNA synthetase	[c] : atp + ile-L + trnaile --> amp + iletrna + ppi	EC-6.1.1.5	Valine, leucine, and isoleucine metabolism	YBL076C	Ils1

ILETAm	isoleucine transaminase, mitochondrial	[m] : akg + ile-L <==> 3mop + glu-L	EC-2.6.1.42	Valine, leucine, and isoleucine metabolism	YHR208W	Bat1-m
ILETA	isoleucine transaminase	[c] : akg + ile-L <==> 3mop + glu-L	EC-2.6.1.42	Valine, leucine, and isoleucine metabolism	YJR148W	Bat2
DHAD2m	dihydroxy-acid dehydratase (2,3-dihydroxy-3-methylpentanoate), mitochondrial	[m] : 23dhmp --> 3mop + h2o		Valine, leucine, and isoleucine metabolism	YJR016C	Ilv3-m
DHAD1m	dihydroxy-acid dehydratase (2,3-dihydroxy-3-methylbutanoate), mitochondrial	[m] : 23dhmb --> 3mob + h2o	EC-4.2.1.9	Valine, leucine, and isoleucine metabolism	YJR016C	Ilv3-m
ACLSm	acetolactate synthase, mitochondrial	[m] : h + (2) pyr --> alac-S + co2	EC-4.1.3.18	Valine, leucine, and isoleucine metabolism	(YCL009C and YMR108W)	Ilv26-m
ACHBSm	2-aceto-2-hydroxybutanoate synthase, mitochondrial	[m] : 2obut + h + pyr --> 2ahbut + co2	EC-4.1.3.18	Valine, leucine, and isoleucine metabolism	(YCL009C and YMR108W)	Ilv26-m
XYLTD_D	xylitol dehydrogenase (D-xyulose-forming)	[c] : nad + xylt --> h + nadh + xylu-D	EC-1.1.1.9	Xylose Metabolism	YLR070C	Xyl2
XYLR	xylose reductase	[c] : h + nadph + xyl-D --> nadp + xylt	EC-1.1.1.21	Xylose Metabolism	YHR104W	Gre3
XYLK	xylulokinase	[c] : atp + xylu-D --> adp + h + xu5p-D	EC-2.7.1.17	Xylose Metabolism	YGR194C	Xks1

BIOMASS REACTION
(1.1348) 13BDglcn + (0.4588) ala-L + (0.046) amp + (0.1607) arg-L + (0.1017) asn-L + (0.2975) asp-L + (59.276) atp + (0.0447) cmp + (0.0066) cys-L + (0.0036) damp + (0.0024) dcmp + (0.0024) dgmp + (0.0036) dtmp + (0.0007) ergst + (0.1054) gln-L + (0.3018) glu-L + (0.2904) gly + (0.5185) glycogen + (0.046) gmp + (59.276) h2o + (0.0663) his-L + (0.1927) ile-L + (0.2964) leu-L + (0.2862) lys-L + (0.8079) mannan + (0.0507) met-L + (0.000006) pa_SC + (0.00006) pc_SC + (0.000045) pe_SC + (0.1339) phe-L + (0.1647) pro-L + (0.000017) ps_SC + (0.000053) ptd1ino_SC + (0.1854) ser-L + (0.02) so4 + (0.1914) thr-L + (0.0234) tre + (0.000066) triglyc_SC + (0.0284) trp-L + (0.102) tyr-L + (0.0599) ump + (0.2646) val-L + (0.0015) zymst --> (59.276) adp + (58.7162) h + (59.305) pi

ABBREVIATION	METABOLITE NAME	COMPARTMENT	FORMULA	CHARGE
10fthf	10-Formyltetrahydrofolate	cytosol	C20H22N7O7	-1
10fthf	10-Formyltetrahydrofolate	mitochondrion	C20H22N7O7	-1
* 12dgr_SC	1,2-Diacylglycerol, yeast-specific	cytosol	C3540H6644O500	0
13BDglcn	1,3-beta-D-Glucan	cytosol	C6H10O5	0
13BDglcn	1,3-beta-D-Glucan	extracellular	C6H10O5	0
13dampp	1,3-Diaminopropane	cytosol	C3H12N2	2
13dpg	3-Phospho-D-glyceroyl phosphate	cytosol	C3H4O10P2	-4
14glun	(1,4-alpha-D-Glucosyl)n	cytosol	C6H12O6	0
1Dgali	1-alpha-D-Galactosyl-myo-inositol	cytosol	C12H22O11	0
* 1ag3p_SC	1-Acyl-sn-glycerol 3-phosphate	cytosol	C1920H3622O700P100	-200
* 1agly3p_SC	1-Acyl-glycerone 3-phosphate, yeast-specific	cytosol	C1920H3422O700P100	-200
1p3h5c	L-1-Pyrroline-3-hydroxy-5-carboxylate	cytosol	C5H6NO3	-1
1p3h5c	L-1-Pyrroline-3-hydroxy-5-carboxylate	mitochondrion	C5H6NO3	-1
1pyr5c	1-Pyrroline-5-carboxylate	cytosol	C5H6NO2	-1
1pyr5c	1-Pyrroline-5-carboxylate	mitochondrion	C5H6NO2	-1
23dhmb	(R)-2,3-Dihydroxy-3-methylbutanoate	mitochondrion	C5H9O4	-1
23dhmp	(R)-2,3-Dihydroxy-3-methylpentanoate	mitochondrion	C6H11O4	-1
23dpg	3-Phospho-D-glycerol phosphate	cytosol	C3H3O10P2	-5
25aics	(S)-2-[5-Amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido]succinate	cytosol	C13H15N4O12P	-4
25dhpp	2,5-Diamino-6-hydroxy-4-(5'-phosphoribosylamino)-pyrimidine	cytosol	C9H14N5O8P	-2
2ahbut	(S)-2-Aceto-2-hydroxybutanoate	mitochondrion	C6H9O4	-1
2ahhmd	2-Amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine diphosphate	mitochondrion	C7H8N5O8P2	-3
2ahhmp	2-Amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine	mitochondrion	C7H9N5O2	0
2cpr5p	1-(2-Carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate	cytosol	C12H13NO9P	-3
2dda7p	2-Dehydro-3-deoxy-D-arabino-heptonate 7-phosphate	cytosol	C7H10O10P	-3
2dda7p	2-Dehydro-3-deoxy-D-arabino-heptonate 7-phosphate	mitochondrion	C7H10O10P	-3
2dhp	2-Dehydropantoate	cytosol	C6H9O4	-1
2dhp	2-Dehydropantoate	mitochondrion	C6H9O4	-1
2dr1p	2-Deoxy-D-ribose 1-phosphate	cytosol	C5H9O7P	-2
2dr5p	2-Deoxy-D-ribose 5-phosphate	cytosol	C5H9O7P	-2
2hhxdal	2-Hydroxy-hexadecanal	cytosol	C16H32O2	0
2ippm	2-Isopropylmaleate	cytosol	C7H8O4	-2
2mahmp	2-Methyl-4-amino-5-hydroxymethylpyrimidine diphosphate	cytosol	C6H8N3O7P2	-3
2mcit	2-Methylcitrate	cytosol	C7H7O7	-3
2mcit	2-Methylcitrate	mitochondrion	C7H7O7	-3
2obut	2-Oxobutanoate	cytosol	C4H5O3	-1
2obut	2-Oxobutanoate	mitochondrion	C4H5O3	-1
2ohph_5	2-Octaprenyl-6-hydroxyphenol (5 repeating units)	cytosol	C36H54O2	0
2ohph_5	2-Octaprenyl-6-hydroxyphenol (5 repeating units)	nucleus	C36H54O2	0
2ombzl_5	2-Octaprenyl-6-methoxy-1,4-benzoquinol (5 repeating units)	mitochondrion	C37H56O3	0
2omhmbl_5	2-Octaprenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinol (5 repeating units)	mitochondrion	C38H58O4	0
2ommbl_5	2-Octaprenyl3-methyl-6-methoxy-1,4-benzoquinol (5 repeating units)	mitochondrion	C38H58O3	0
2omph_5	2-Octaprenyl-6-methoxyphenol (5 repeating units)	cytosol	C37H56O2	0
2omph_5	2-Octaprenyl-6-methoxyphenol (5 repeating units)	mitochondrion	C37H56O2	0
2omph_5	2-Octaprenyl-6-methoxyphenol (5 repeating units)	nucleus	C37H56O2	0
2oph_5	2-Octaprenylphenol (5 repeating units)	cytosol	C36H54O	0
2oxoadp	2-Oxoadipate	cytosol	C6H6O5	-2
2oxoadp	2-Oxoadipate	mitochondrion	C6H6O5	-2
2pg	D-Glycerate 2-phosphate	cytosol	C3H4O7P	-3
34hpp	3-(4-Hydroxyphenyl)pyruvate	cytosol	C9H7O4	-1
34hpp	3-(4-Hydroxyphenyl)pyruvate	mitochondrion	C9H7O4	-1
34hpp	3-(4-Hydroxyphenyl)pyruvate	peroxisome	C9H7O4	-1
35ccmp	3',5'-Cyclic CMP	cytosol	C9H11N3O7P	-1

35cdamp	3',5'-Cyclic dAMP	cytosol	C10H11N5O5P	-1
35cgmp	3',5'-Cyclic GMP	cytosol	C10H11N5O7P	-1
35cimp	3',5'-Cyclic IMP	cytosol	C10H10N4O7P	-1
3c2hmp	3-Carboxy-2-hydroxy-4-methylpentanoate	cytosol	C7H10O5	-2
3c3hmp	3-Carboxy-3-hydroxy-4-methylpentanoate	cytosol	C7H10O5	-2
3c3hmp	3-Carboxy-3-hydroxy-4-methylpentanoate	mitochondrion	C7H10O5	-2
3c4mop	3-Carboxy-4-methyl-2-oxopentanoate	cytosol	C7H8O5	-2
3c4mop	3-Carboxy-4-methyl-2-oxopentanoate	mitochondrion	C7H8O5	-2
3dhq	3-Dehydroquinate	cytosol	C7H9O6	-1
3dhsk	3-Dehydroshikimate	cytosol	C7H7O5	-1
3dsphgn	3-Dehydrosphinganine	cytosol	C18H38NO2	1
3hacoa	(S)-3-Hydroxyacyl-CoA	peroxisome	C24H35N7O18P3RS	-4
3hanthrn	3-Hydroxyanthranilate	cytosol	C7H7NO3	0
3hdcoa	(S)-3-Hydroxydecanoyl-CoA	peroxisome	C31H50N7O18P3S	-4
3hddcoa	(S)-3-Hydroxydodecanoyl-CoA	peroxisome	C33H54N7O18P3S	-4
3hhdcoa	(S)-3-Hydroxyhexadecanoyl-CoA	peroxisome	C37H62N7O18P3S	-4
3hodcoa	(S)-3-Hydroxyoctadecanoyl-CoA	peroxisome	C39H66N7O18P3S	-4
3htdcoa	(S)-3-Hydroxytetradecanoyl-CoA	peroxisome	C35H58N7O18P3S	-4
3hxccoa	(S)-3-Hydroxyhexacosyl-CoA	peroxisome	C47H82N7O18P3S	-4
3ig3p	C'-(3-Indolyl)-glycerol 3-phosphate	cytosol	C11H12NO6P	-2
3mob	3-Methyl-2-oxobutanoate	cytosol	C5H7O3	-1
3mob	3-Methyl-2-oxobutanoate	mitochondrion	C5H7O3	-1
3mop	(S)-3-Methyl-2-oxopentanoate	cytosol	C6H9O3	-1
3mop	(S)-3-Methyl-2-oxopentanoate	mitochondrion	C6H9O3	-1
3oacoa	3-Oxoacyl-CoA	peroxisome	C24H33N7O18P3RS	-4
3odcoa	3-Oxodecanoyl-CoA	peroxisome	C31H48N7O18P3S	-4
3oddcoa	3-Oxododecanoyl-CoA	peroxisome	C33H52N7O18P3S	-4
3ohdcoa	3-Oxohexadecanoyl-CoA	peroxisome	C37H60N7O18P3S	-4
3ohodcoa	3-Oxooctadecanoyl-CoA	peroxisome	C39H64N7O18P3S	-4
3ohxccoa	3-Oxohexacosyl-CoA	peroxisome	C47H80N7O18P3S	-4
3ophb_5	3-Octaprenyl-4-hydroxybenzoate (5 repeating units)	cytosol	C37H53O3	-1
3ophb_5	3-Octaprenyl-4-hydroxybenzoate (5 repeating units)	mitochondrion	C37H53O3	-1
3otdcoa	3-Oxotetradecanoyl-CoA	peroxisome	C35H56N7O18P3S	-4
3pg	3-Phospho-D-glycerate	cytosol	C3H4O7P	-3
3php	3-Phosphohydroxypyruvate	cytosol	C3H2O7P	-3
3psme	5-O-(1-Carboxyvinyl)-3-phosphoshikimate	cytosol	C10H9O10P	-4
44mctr	4,4-dimethylcholesta-8,14,24-trienol	cytosol	C29H46O	0
44mzym	4,4-dimethylzymosterol	cytosol	C29H48O	0
4aabutn	4-Acetamidobutanoate	cytosol	C6H10NO3	-1
4abut	4-Aminobutanoate	cytosol	C4H9NO2	0
4abut	4-Aminobutanoate	extracellular	C4H9NO2	0
4abut	4-Aminobutanoate	mitochondrion	C4H9NO2	0
4abutn	4-Aminobutanal	cytosol	C4H10NO	1
4abutn	4-Aminobutanal	mitochondrion	C4H10NO	1
4abz	4-Aminobenzoate	cytosol	C7H6NO2	-1
4abz	4-Aminobenzoate	mitochondrion	C7H6NO2	-1
4adcho	4-amino-4-deoxychorismate	cytosol	C10H10NO5	-1
4ahmmp	4-Amino-5-hydroxymethyl-2-methylpyrimidine	cytosol	C6H9N3O	0
4ampm	4-Amino-2-methyl-5-phosphomethylpyrimidine	cytosol	C6H8N3O4P	-2
4fumacac	4-Fumarylacetoacetate	cytosol	C8H6O6	-2
4gudbd	4-Guanidinobutanamide	cytosol	C5H13N4O	1
4gudbutn	4-Guanidinobutanoate	cytosol	C5H11N3O2	0
4h2oglt	4-Hydroxy-2-oxoglutarate	cytosol	C5H4O6	-2
4h2oglt	4-Hydroxy-2-oxoglutarate	mitochondrion	C5H4O6	-2
4h2oglt	4-Hydroxy-2-oxoglutarate	peroxisome	C5H4O6	-2
4hbz	4-Hydroxybenzoate	cytosol	C7H5O3	-1
4hbz	4-Hydroxybenzoate	mitochondrion	C7H5O3	-1
4hglusa	L-4-Hydroxyglutamate semialdehyde	mitochondrion	C5H9NO4	0
4hpro-LT	trans-4-Hydroxy-L-proline	cytosol	C5H9NO3	0
4hpro-LT	trans-4-Hydroxy-L-proline	mitochondrion	C5H9NO3	0
4hthr	4-Hydroxy-L-threonine	cytosol	C4H9NO4	0
4mhetz	4-Methyl-5-(2-hydroxyethyl)-thiazole	cytosol	C6H9NOS	0
4mlacac	4-Maleylacetoacetate	cytosol	C8H6O6	-2
4mop	4-Methyl-2-oxopentanoate	cytosol	C6H9O3	-1
4mop	4-Methyl-2-oxopentanoate	mitochondrion	C6H9O3	-1
4mpetz	4-Methyl-5-(2-phosphoethyl)-thiazole	cytosol	C6H8NO4PS	-2

4mzym	4-methylzymosterol	cytosol	C28H46O	0
4mzym_int1	4-Methylzymosterol intermediate 1	cytosol	C29H46O3	0
4mzym_int2	4-Methylzymosterol intermediate 2	cytosol	C28H44O	0
4pasp	4-Phospho-L-aspartate	cytosol	C4H6NO7P	-2
4ppan	D-4'-Phosphopantothenate	cytosol	C9H15NO8P	-3
4ppcys	N-((R)-4-Phosphopantothenoyl)-L-cysteine	cytosol	C12H20N2O9PS	-3
4r5au	4-(1-D-Ribitylamino)-5-aminouracil	cytosol	C9H16N4O6	0
5aizc	5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxylate	cytosol	C9H11N3O9P	-3
5aop	5-Amino-4-oxopentanoate	cytosol	C5H9NO3	0
5aop	5-Amino-4-oxopentanoate	extracellular	C5H9NO3	0
5aop	5-Amino-4-oxopentanoate	mitochondrion	C5H9NO3	0
5aprbu	5-Amino-6-(5'-phosphoribitylamino)uracil	cytosol	C9H15N4O9P	-2
5apru	5-Amino-6-(5'-phosphoribosylamino)uracil	cytosol	C9H13N4O9P	-2
5dpmev	(R)-5-Diphosphomevalonate	cytosol	C6H10O10P2	-4
5fthf	5-Formyltetrahydrofolate	cytosol	C20H21N7O7	-2
5fthf	5-Formyltetrahydrofolate	mitochondrion	C20H21N7O7	-2
5mta	5-Methylthioadenosine	cytosol	C11H15N5O3S	0
5mthf	5-Methyltetrahydrofolate	cytosol	C20H24N7O6	-1
5mthf	5-Methyltetrahydrofolate	mitochondrion	C20H24N7O6	-1
5pmev	(R)-5-Phosphomevalonate	cytosol	C6H10O7P	-3
6dg	D-Gal-alpha-1->6D-Glucose	cytosol	C12H22O11	0
6pgc	6-Phospho-D-gluconate	cytosol	C6H10O10P	-3
6pgl	6-phospho-D-glucono-1,5-lactone	cytosol	C6H9O9P	-2
6pgl	6-phospho-D-glucono-1,5-lactone	endoplasmic reticulum	C6H9O9P	-2
8aonn	8-Amino-7-oxononanoate	cytosol	C9H17NO3	0
8aonn	8-Amino-7-oxononanoate	extracellular	C9H17NO3	0
ACP	acyl carrier protein	cytosol	C11H21N2O7PRS	-1
ACP	acyl carrier protein	mitochondrion	C11H21N2O7PRS	-1
Dara14lac	D-Arabinono-1,4-lactone	cytosol	C5H8O5	0
L2aadp	L-2-Aminoadipate	cytosol	C6H10NO4	-1
L2aadp6sa	L-2-Aminoadipate 6-semialdehyde	cytosol	C6H11NO3	0
Lfmkynr	L-Formylkynurenine	cytosol	C11H12N2O4	0
Lkynr	L-Kynurenine	cytosol	C10H12N2O3	0
N1aspmd	N1-Acetylspermidine	cytosol	C9H23N3O	2
N1sprm	N1-Acetylspermine	cytosol	C12H31N4O	3
NPmehis	N(pai)-Methyl-L-histidine	cytosol	C7H11N3O2	0
Sfglutth	S-Formylglutathione	cytosol	C11H16N3O7S	-1
Ssq23epx	(S)-Squalene-2,3-epoxide	cytosol	C30H50O	0
Ssq23epx	(S)-Squalene-2,3-epoxide	endoplasmic reticulum	C30H50O	0
aacoa	Acetoacetyl-CoA	cytosol	C25H36N7O18P3S	-4
aacoa	Acetoacetyl-CoA	mitochondrion	C25H36N7O18P3S	-4
abt	L-Arabinitol	cytosol	C5H12O5	0
abt	L-Arabinitol	extracellular	C5H12O5	0
ac	Acetate	cytosol	C2H3O2	-1
ac	Acetate	extracellular	C2H3O2	-1
ac	Acetate	mitochondrion	C2H3O2	-1
ac	Acetate	peroxisome	C2H3O2	-1
acACP	Acetyl-ACP	cytosol	C13H23N2O8PRS	-1
acACP	Acetyl-ACP	mitochondrion	C13H23N2O8PRS	-1
acac	Acetoacetate	cytosol	C4H5O3	-1
acald	Acetaldehyde	cytosol	C2H4O	0
acald	Acetaldehyde	extracellular	C2H4O	0
acald	Acetaldehyde	mitochondrion	C2H4O	0
accoa	Acetyl-CoA	cytosol	C23H34N7O17P3S	-4
accoa	Acetyl-CoA	mitochondrion	C23H34N7O17P3S	-4
accoa	Acetyl-CoA	nucleus	C23H34N7O17P3S	-4
accoa	Acetyl-CoA	peroxisome	C23H34N7O17P3S	-4
acg5p	N-Acetyl-L-glutamyl 5-phosphate	mitochondrion	C7H9NO8P	-3
acg5sa	N-Acetyl-L-glutamate 5-semialdehyde	mitochondrion	C7H10NO4	-1
acgam1p	N-Acetyl-D-glucosamine 1-phosphate	cytosol	C8H14NO9P	-2
acgam6p	N-Acetyl-D-glucosamine 6-phosphate	cytosol	C8H14NO9P	-2
acglu	N-Acetyl-L-glutamate	mitochondrion	C7H9NO5	-2
achms	O-Acetyl-L-homoserine	cytosol	C6H11NO4	0
acoa	Acyl-CoA	peroxisome	C22H31N7O17P3RS	-4
acorn	N2-Acetyl-L-ornithine	mitochondrion	C7H14N2O3	0
acrn	O-Acetylcarnitine	cytosol	C9H17NO4	0
acrn	O-Acetylcarnitine	mitochondrion	C9H17NO4	0

acrn	O-Acetylcarnitine	peroxisome	C9H17NO4	0
acser	O-Acetyl-L-serine	cytosol	C5H9NO4	0
acybut	gamma-Amino-gamma-cyanobutanoate	cytosol	C5H8N2O2	0
ade	Adenine	cytosol	C5H5N5	0
ade	Adenine	extracellular	C5H5N5	0
ade	Adenine	mitochondrion	C5H5N5	0
adn	Adenosine	cytosol	C10H13N5O4	0
adn	Adenosine	extracellular	C10H13N5O4	0
adn	Adenosine	mitochondrion	C10H13N5O4	0
adp	ADP	cytosol	C10H12N5O10P2	-3
adp	ADP	Golgi apparatus	C10H12N5O10P2	-3
adp	ADP	mitochondrion	C10H12N5O10P2	-3
adp	ADP	nucleus	C10H12N5O10P2	-3
adp	ADP	vacuole	C10H12N5O10P2	-3
adp	ADP	peroxisome	C10H12N5O10P2	-3
adprib	ADPribose	cytosol	C15H21N5O14P2	-2
adprib	ADPribose	mitochondrion	C15H21N5O14P2	-2
ahcys	S-Adenosyl-L-homocysteine	cytosol	C14H20N6O5S	0
ahcys	S-Adenosyl-L-homocysteine	mitochondrion	C14H20N6O5S	0
ahcys	S-Adenosyl-L-homocysteine	nucleus	C14H20N6O5S	0
ahdt	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)dihydropteridine triphosphate	cytosol	C9H13N5O13P3	-3
aicar	5-Amino-1-(5-Phospho-D-ribosyl)imidazole-4-carboxamide	cytosol	C9H13N4O8P	-2
air	5-amino-1-(5-phospho-D-ribosyl)imidazole	cytosol	C8H12N3O7P	-2
akg	2-Oxoglutarate	cytosol	C5H4O5	-2
akg	2-Oxoglutarate	extracellular	C5H4O5	-2
akg	2-Oxoglutarate	mitochondrion	C5H4O5	-2
akg	2-Oxoglutarate	nucleus	C5H4O5	-2
akg	2-Oxoglutarate	peroxisome	C5H4O5	-2
ala-B	beta-Alanine	cytosol	C3H7NO2	0
ala-L	L-Alanine	cytosol	C3H7NO2	0
ala-L	L-Alanine	extracellular	C3H7NO2	0
ala-L	L-Alanine	mitochondrion	C3H7NO2	0
alac-S	(S)-2-Acetolactate	mitochondrion	C5H7O4	-1
alatrna	L-Alanyl-tRNA(Ala)	cytosol	C3H6NOR	1
allphn	Allophanate	cytosol	C2H3N2O3	-1
alltn	Allantoin	cytosol	C4H6N4O3	0
alltn	Allantoin	extracellular	C4H6N4O3	0
alltt	Allantoate	cytosol	C4H7N4O4	-1
alltt	Allantoate	extracellular	C4H7N4O4	-1
alpam	S-aminomethyldihydrolipoamide	mitochondrion	C9H21N2OS2	1
alpro	S-Aminomethyldihydrolipoylprotein	mitochondrion	CH6NS2X	1
am6sa	2-Aminomuconate 6-semialdehyde	cytosol	C6H7NO3	0
amet	S-Adenosyl-L-methionine	cytosol	C15H23N6O5S	1
amet	S-Adenosyl-L-methionine	extracellular	C15H23N6O5S	1
amet	S-Adenosyl-L-methionine	mitochondrion	C15H23N6O5S	1
amet	S-Adenosyl-L-methionine	nucleus	C15H23N6O5S	1
ametam	S-Adenosylmethioninamine	cytosol	C14H24N6O3S	2
amob	S-Adenosyl-4-methylthio-2-oxobutanoate	cytosol	C15H19N5O6S	0
amp	AMP	cytosol	C10H12N5O7P	-2
amp	AMP	mitochondrion	C10H12N5O7P	-2
amp	AMP	peroxisome	C10H12N5O7P	-2
amuco	2-Aminomuconate	cytosol	C6H6NO4	-1
anth	Anthranilate	cytosol	C7H6NO2	-1
ap4a	P1,P4-Bis(5'-adenosyl) tetraphosphate	cytosol	C20H24N10O19P4	-4
ap4g	P1-(5'-adenosyl),P4-(5'-guanosyl) tetraphosphate	cytosol	C20H24N10O20P4	-4
apep	Nalpha-Acetylpeptide	cytosol	C6H7N2O4R2	-1
aproa	3-Aminopropanal	cytosol	C3H8NO	1
aprop	alpha-Aminopropiononitrile	cytosol	C3H7N2	1
aprut	N-Acetylputrescine	cytosol	C6H15N2O	1
aps	Adenosine 5'-phosphosulfate	cytosol	C10H12N5O10PS	-2
arab-D	D-Arabinose	cytosol	C5H10O5	0
arab-D	D-Arabinose	extracellular	C5H10O5	0
arab-L	L-Arabinose	cytosol	C5H10O5	0
arab-L	L-Arabinose	extracellular	C5H10O5	0
arg-L	L-Arginine	cytosol	C6H15N4O2	1
arg-L	L-Arginine	extracellular	C6H15N4O2	1

	arg-L	L-Arginine	mitochondrion	C6H15N4O2	1
	argsuc	N(omega)-(L-Arginino)succinate	cytosol	C10H17N4O6	-1
	argtrna	L-Arginyl-tRNA(Arg)	cytosol	C6H14N4OR	2
	argtrna	L-Arginyl-tRNA(Arg)	mitochondrion	C6H14N4OR	2
	asn-L	L-Asparagine	cytosol	C4H8N2O3	0
	asn-L	L-Asparagine	extracellular	C4H8N2O3	0
	asn-L	L-Asparagine	mitochondrion	C4H8N2O3	0
	asntrna	L-Asparaginyl-tRNA(Asn)	cytosol	C4H7N2O2R	1
	asntrna	L-Asparaginyl-tRNA(Asn)	mitochondrion	C4H7N2O2R	1
	asp-L	L-Aspartate	cytosol	C4H6NO4	-1
	asp-L	L-Aspartate	extracellular	C4H6NO4	-1
	asp-L	L-Aspartate	mitochondrion	C4H6NO4	-1
	asp-L	L-Aspartate	nucleus	C4H6NO4	-1
	asp-L	L-Aspartate	peroxisome	C4H6NO4	-1
	aspsa	L-Aspartate 4-semialdehyde	cytosol	C4H7NO3	0
	asptrna	L-Aspartyl-tRNA(Asp)	cytosol	C4H5NO3R	0
	asptrna	L-Aspartyl-tRNA(Asp)	mitochondrion	C4H5NO3R	0
	atp	ATP	cytosol	C10H12N5O13P3	-4
	atp	ATP	Golgi apparatus	C10H12N5O13P3	-4
	atp	ATP	mitochondrion	C10H12N5O13P3	-4
	atp	ATP	nucleus	C10H12N5O13P3	-4
	atp	ATP	vacuole	C10H12N5O13P3	-4
	atp	ATP	peroxisome	C10H12N5O13P3	-4
	b124tc	But-1-ene-1,2,4-tricarboxylate	mitochondrion	C7H5O6	-3
	btn	Biotin	cytosol	C10H15N2O3S	-1
	btn	Biotin	extracellular	C10H15N2O3S	-1
	camp	cAMP	cytosol	C10H11N5O6P	-1
	caphis	2-(3-Carboxy-3-aminopropyl)-L-histidine	cytosol	C10H16N4O4	0
	cbasp	N-Carbamoyl-L-aspartate	cytosol	C5H6N2O5	-2
	cbasp	N-Carbamoyl-L-aspartate	nucleus	C5H6N2O5	-2
	cbp	Carbamoyl phosphate	cytosol	CH2NO5P	-2
	cbp	Carbamoyl phosphate	nucleus	CH2NO5P	-2
	cdp	CDP	cytosol	C9H12N3O11P2	-3
	cdp	CDP	nucleus	C9H12N3O11P2	-3
	cdpchol	CDPcholine	cytosol	C14H25N4O11P2	-1
*	cdpdag_SC	CDPdiacylglycerol, yeast-specific	cytosol	C4440H7744N300O1500P200	-200
*	cdpdag_SC	CDPdiacylglycerol, yeast-specific	mitochondrion	C4440H7744N300O1500P200	-200
	cdpea	CDPethanolamine	cytosol	C11H19N4O11P2	-1
	cer1_24	Ceramide-1 (Sphinganine:n-C24:0)	cytosol	C42H85NO3	0
	cer1_26	Ceramide-1 (Sphinganine:n-C26:0)	cytosol	C44H89NO3	0
	cer2'_24	Ceramide-2' (Sphinganine:n-C24:0OH)	cytosol	C42H85NO4	0
	cer2'_26	Ceramide-2' (Sphinganine:n-C26:0OH)	cytosol	C44H89NO4	0
	cer2_24	Ceramide-2 (Phytosphingosine:n-C24:0)	cytosol	C42H85NO4	0
	cer2_26	Ceramide-2 (Phytosphingosine:n-C26:0)	cytosol	C44H89NO4	0
	cer3_24	Ceramide-3 (Phytosphingosine:n-C24:0OH)	cytosol	C42H85NO5	0
	cer3_26	Ceramide-3 (Phytosphingosine:n-C26:0OH)	cytosol	C44H89NO5	0
	cgly	Cys-Gly	cytosol	C5H10N2O3S	0
	ch4s	Methanethiol	cytosol	CH4S	0
	chitin	Chitin	cytosol	C8H13NO5	0
	chitos	Chitosan	cytosol	C6H11NO4	0
	chol	Choline	cytosol	C5H14NO	1
	chol	Choline	extracellular	C5H14NO	1
	cholp	Choline phosphate	cytosol	C5H13NO4P	-1
	chor	Chorismate	cytosol	C10H8O6	-2
	cit	Citrate	cytosol	C6H5O7	-3
	cit	Citrate	extracellular	C6H5O7	-3
	cit	Citrate	mitochondrion	C6H5O7	-3
	cit	Citrate	peroxisome	C6H5O7	-3
	citr-L	L-Citrulline	cytosol	C6H13N3O3	0
*	clpn_SC	Cardiolipin, yeast-specific	mitochondrion	C7380H13688O1700P200	-200
	cmaphis	2-[3-Carboxy-3-(methylammonio)propyl]-L-histidine	cytosol	C11H18N4O4	0
	cmp	CMP	cytosol	C9H12N3O8P	-2
	cmp	CMP	mitochondrion	C9H12N3O8P	-2
	cmusa	2-Amino-3-carboxymuconate semialdehyde	cytosol	C7H6NO5	-1

co2	CO2	cytosol	CO2	0
co2	CO2	extracellular	CO2	0
co2	CO2	Golgi apparatus	CO2	0
co2	CO2	mitochondrion	CO2	0
co2	CO2	nucleus	CO2	0
co2	CO2	vacuole	CO2	0
co2	CO2	peroxisome	CO2	0
coa	Coenzyme A	cytosol	C21H32N7O16P3S	-4
coa	Coenzyme A	mitochondrion	C21H32N7O16P3S	-4
coa	Coenzyme A	nucleus	C21H32N7O16P3S	-4
coa	Coenzyme A	peroxisome	C21H32N7O16P3S	-4
cpppg3	Coproporphyrinogen III	cytosol	C36H40N4O8	-4
crn	L-Carnitine	cytosol	C7H15NO3	0
crn	L-Carnitine	extracellular	C7H15NO3	0
crn	L-Carnitine	mitochondrion	C7H15NO3	0
crn	L-Carnitine	peroxisome	C7H15NO3	0
csn	Cytosine	cytosol	C4H5N3O	0
csn	Cytosine	extracellular	C4H5N3O	0
ctp	CTP	cytosol	C9H12N3O14P3	-4
ctp	CTP	mitochondrion	C9H12N3O14P3	-4
cys-L	L-Cysteine	cytosol	C3H7NO2S	0
cys-L	L-Cysteine	extracellular	C3H7NO2S	0
cyst-L	L-Cystathionine	cytosol	C7H14N2O4S	0
cyst-L	L-Cystathionine	peroxisome	C7H14N2O4S	0
cystrna	L-Cysteinyl-tRNA(Cys)	cytosol	C3H6NOSR	1
cytd	Cytidine	cytosol	C9H13N3O5	0
cytd	Cytidine	extracellular	C9H13N3O5	0
dad-2	Deoxyadenosine	cytosol	C10H13N5O3	0
dad-2	Deoxyadenosine	extracellular	C10H13N5O3	0
dadp	dADP	cytosol	C10H12N5O9P2	-3
dadp	dADP	nucleus	C10H12N5O9P2	-3
* dagpy_SC	diacylglycerol pyrophosphate, yeast-specific	cytosol	C3540H6544O1100P200	-300
damp	dAMP	cytosol	C10H12N5O6P	-2
dann	7,8-Diaminononanoate	cytosol	C9H21N2O2	1
dann	7,8-Diaminononanoate	extracellular	C9H21N2O2	1
datp	dATP	cytosol	C10H12N5O12P3	-4
db4p	3,4-dihydroxy-2-butanone 4-phosphate	cytosol	C4H7O6P	-2
dc2coa	trans-Dec-2-enoyl-CoA	peroxisome	C31H48N7O17P3S	-4
dca	Decanoate (n-C10:0)	cytosol	C10H19O2	-1
dca	Decanoate (n-C10:0)	peroxisome	C10H19O2	-1
dcaACP	Decanoyl-ACP (n-C10:0ACP)	mitochondrion	C21H39N2O8PRS	-1
dcacoa	Decanoyl-CoA (n-C10:0CoA)	cytosol	C31H50N7O17P3S	-4
dcacoa	Decanoyl-CoA (n-C10:0CoA)	peroxisome	C31H50N7O17P3S	-4
dcamp	N6-(1,2-Dicarboxyethyl)-AMP	cytosol	C14H14N5O11P	-4
dcdp	dCDP	cytosol	C9H12N3O10P2	-3
dcdp	dCDP	nucleus	C9H12N3O10P2	-3
dcmp	dCMP	cytosol	C9H12N3O7P	-2
dctp	dCTP	cytosol	C9H12N3O13P3	-4
dcyt	Deoxycytidine	cytosol	C9H13N3O4	0
dcyt	Deoxycytidine	extracellular	C9H13N3O4	0
dd2coa	trans-Dodec-2-enoyl-CoA	peroxisome	C33H52N7O17P3S	-4
ddca	Dodecanoate (n-C12:0)	cytosol	C12H23O2	-1
ddca	Dodecanoate (n-C12:0)	peroxisome	C12H23O2	-1
ddcaACP	Dodecanoyl-ACP (n-C12:0ACP)	cytosol	C23H43N2O8PRS	-1
ddcaACP	Dodecanoyl-ACP (n-C12:0ACP)	mitochondrion	C23H43N2O8PRS	-1
ddcacoa	Dodecanoyl-CoA (n-C12:0CoA)	cytosol	C33H54N7O17P3S	-4
ddcacoa	Dodecanoyl-CoA (n-C12:0CoA)	peroxisome	C33H54N7O17P3S	-4
dgdp	dGDP	cytosol	C10H12N5O10P2	-3
dgdp	dGDP	nucleus	C10H12N5O10P2	-3
dgmp	dGMP	cytosol	C10H12N5O7P	-2
dgsn	Deoxyguanosine	cytosol	C10H13N5O4	0
dgsn	Deoxyguanosine	extracellular	C10H13N5O4	0
dgtp	dGTP	cytosol	C10H12N5O13P3	-4
dha	Dihydroxyacetone	cytosol	C3H6O3	0
dhap	Dihydroxyacetone phosphate	cytosol	C3H5O6P	-2
dhap	Dihydroxyacetone phosphate	mitochondrion	C3H5O6P	-2
dhf	7,8-Dihydrofolate	cytosol	C19H20N7O6	-1
dhf	7,8-Dihydrofolate	mitochondrion	C19H20N7O6	-1

dhlam	Dihydrolipoamide	mitochondrion	C8H17NOS2	0
dhlpro	Dihydrolipolprotein	mitochondrion	H2S2X	0
dhnpt	2-Amino-4-hydroxy-6-(D-erythro-1,2,3-trihydroxypropyl)-7,8-dihydropteridine	cytosol	C9H14N5O4	1
dhnpt	2-Amino-4-hydroxy-6-(D-erythro-1,2,3-trihydroxypropyl)-7,8-dihydropteridine	mitochondrion	C9H14N5O4	1
dhor-S	(S)-Dihydroorotate	cytosol	C5H5N2O4	-1
dhor-S	(S)-Dihydroorotate	nucleus	C5H5N2O4	-1
dhpmp	Dihydroneopterin monophosphate	cytosol	C9H13N5O7P	-1
dhpt	Dihydropteroate	cytosol	C14H13N6O3	-1
dhpt	Dihydropteroate	mitochondrion	C14H13N6O3	-1
din	Deoxyinosine	cytosol	C10H12N4O4	0
din	Deoxyinosine	extracellular	C10H12N4O4	0
dmlz	6,7-Dimethyl-8-(1-D-ribityl)lumazine	cytosol	C13H18N4O6	0
dmpp	Dimethylallyl diphosphate	cytosol	C5H9O7P2	-3
dnad	Deamino-NAD+	cytosol	C21H24N6O15P2	-2
dnad	Deamino-NAD+	mitochondrion	C21H24N6O15P2	-2
dolichol	Dolichol	cytosol	C15H28O	0
dolmanp	Dolichyl phosphate D-mannose	endoplasmic reticulum	C21H38O9P	-1
dolp	Dolichol phosphate	cytosol	C15H27O4P	-2
dolp	Dolichol phosphate	endoplasmic reticulum	C15H27O4P	-2
dpcoa	Dephospho-CoA	cytosol	C21H33N7O13P2S	-2
dpcoa	Dephospho-CoA	mitochondrion	C21H33N7O13P2S	-2
drib	Deoxyribose	cytosol	C5H10O4	0
dtbt	Dethiobiotin	cytosol	C10H17N2O3	-1
dtdp	dTDP	cytosol	C10H13N2O11P2	-3
dtmp	dTMP	cytosol	C10H13N2O8P	-2
dttp	dTTP	cytosol	C10H13N2O14P3	-4
dttp	dTTP	extracellular	C10H13N2O14P3	-4
dudp	dUDP	cytosol	C9H11N2O11P2	-3
dudp	dUDP	nucleus	C9H11N2O11P2	-3
dump	dUMP	cytosol	C9H11N2O8P	-2
dump	dUMP	nucleus	C9H11N2O8P	-2
duri	Deoxyuridine	cytosol	C9H12N2O5	0
duri	Deoxyuridine	extracellular	C9H12N2O5	0
dutp	dUTP	cytosol	C9H11N2O14P3	-4
e4hglu	L-erythro-4-Hydroxyglutamate	cytosol	C5H8NO5	-1
e4hglu	L-erythro-4-Hydroxyglutamate	mitochondrion	C5H8NO5	-1
e4hglu	L-erythro-4-Hydroxyglutamate	peroxisome	C5H8NO5	-1
e4p	D-Erythrose 4-phosphate	cytosol	C4H7O7P	-2
e4p	D-Erythrose 4-phosphate	mitochondrion	C4H7O7P	-2
eig3p	D-erythro-1-(Imidazol-4-yl)glycerol 3-phosphate	cytosol	C6H9N2O6P	-2
epist	episterol	cytosol	C28H46O	0
epm	Epimelibiose	cytosol	C12H22O11	0
ergst	Ergosterol	cytosol	C28H44O	0
ergst	Ergosterol	extracellular	C28H44O	0
ergst	Ergosterol	endoplasmic reticulum	C28H44O	0
ergtetrol	Ergosta-5,7,22,24,(28)-tetraen-3beta-ol	cytosol	C28H42O	0
ergtetrol	Ergosta-5,7,22,24,(28)-tetraen-3beta-ol	endoplasmic reticulum	C28H42O	0
ergtrol	ergosta-5,7,24(28)-trienol	cytosol	C28H44O	0
etha	Ethanolamine	cytosol	C2H8NO	1
ethamp	Ethanolamine phosphate	cytosol	C2H7NO4P	-1
etoh	Ethanol	cytosol	C2H6O	0
etoh	Ethanol	extracellular	C2H6O	0
etoh	Ethanol	mitochondrion	C2H6O	0
f1p	D-Fructose 1-phosphate	cytosol	C6H11O9P	-2
f26bp	D-Fructose 2,6-bisphosphate	cytosol	C6H10O12P2	-4
f6p	D-Fructose 6-phosphate	cytosol	C6H11O9P	-2
f6p-B	beta-D-Fructose 6-phosphate	cytosol	C6H11O9P	-2
fad	FAD	cytosol	C27H31N9O15P2	-2
fad	FAD	mitochondrion	C27H31N9O15P2	-2
fadh2	FADH2	mitochondrion	C27H33N9O15P2	-2
fald	Formaldehyde	cytosol	CH2O	0
fdp	D-Fructose 1,6-bisphosphate	cytosol	C6H10O12P2	-4
fe2	Fe2+	mitochondrion	Fe	2
fecost	fecosterol	cytosol	C28H46O	0
fgam	N2-Formyl-N1-(5-phospho-D-ribosyl)glycinamide	cytosol	C8H13N2O9P	-2
ficytc	Ferricytochrome c	mitochondrion	C42H52FeN8O6S2	1

fmettrna	N-Formylmethionyl-tRNA	mitochondrion	C6H9NO2SR	0
fmn	FMN	cytosol	C17H19N4O9P	-2
fmn	FMN	extracellular	C17H19N4O9P	-2
fmn	FMN	mitochondrion	C17H19N4O9P	-2
focytc	Ferrocytochrome c	mitochondrion	C42H53FeN8O6S2	1
for	Formate	cytosol	CH1O2	-1
for	Formate	extracellular	CH1O2	-1
for	Formate	mitochondrion	CH1O2	-1
fpram	2-(Formamido)-N1-(5-phospho-D-ribosyl)acetamidine	cytosol	C8H15N3O8P	-1
fprica	5-Formamido-1-(5-phospho-D-ribosyl)imidazole-4-carboxamide	cytosol	C10H13N4O9P	-2
frdp	Farnesyl diphosphate	cytosol	C15H25O7P2	-3
fru	D-Fructose	cytosol	C6H12O6	0
fru	D-Fructose	extracellular	C6H12O6	0
fum	Fumarate	cytosol	C4H2O4	-2
fum	Fumarate	extracellular	C4H2O4	-2
fum	Fumarate	mitochondrion	C4H2O4	-2
g1p	D-Glucose 1-phosphate	cytosol	C6H11O9P	-2
g3p	Glyceraldehyde 3-phosphate	cytosol	C3H5O6P	-2
g6p	D-Glucose 6-phosphate	cytosol	C6H11O9P	-2
g6p	D-Glucose 6-phosphate	endoplasmic reticulum	C6H11O9P	-2
g6p-B	beta-D-glucose 6-phosphate	cytosol	C6H11O9P	-2
gal	D-Galactose	cytosol	C6H12O6	0
gal	D-Galactose	extracellular	C6H12O6	0
gal1p	alpha-D-Galactose 1-phosphate	cytosol	C6H11O9P	-2
gam1p	D-Glucosamine 1-phosphate	cytosol	C6H13NO8P	-1
gam6p	D-Glucosamine 6-phosphate	cytosol	C6H13NO8P	-1
gam6p	D-Glucosamine 6-phosphate	extracellular	C6H13NO8P	-1
gar	N1-(5-Phospho-D-ribosyl)glycinamide	cytosol	C7H14N2O8P	-1
gcald	Glycolaldehyde	cytosol	C2H4O2	0
gcald	Glycolaldehyde	extracellular	C2H4O2	0
gcald	Glycolaldehyde	mitochondrion	C2H4O2	0
gdp	GDP	cytosol	C10H12N5O11P2	-3
gdp	GDP	Golgi apparatus	C10H12N5O11P2	-3
gdp	GDP	mitochondrion	C10H12N5O11P2	-3
gdp	GDP	nucleus	C10H12N5O11P2	-3
gdpmann	GDP-D-mannose	cytosol	C16H23N5O16P2	-2
gdpmann	GDP-D-mannose	Golgi apparatus	C16H23N5O16P2	-2
ggl	Galactosylglycerol	cytosol	C9H18O8	0
glc-D	D-Glucose	cytosol	C6H12O6	0
glc-D	D-Glucose	extracellular	C6H12O6	0
glc-D	D-Glucose	vacuole	C6H12O6	0
gln-L	L-Glutamine	cytosol	C5H10N2O3	0
gln-L	L-Glutamine	extracellular	C5H10N2O3	0
gln-L	L-Glutamine	nucleus	C5H10N2O3	0
glntrna	L-Glutaminyl-tRNA(Gln)	cytosol	C5H9N2O2R	1
glp	Glycylpeptide	cytosol	C4H7N2O3R	0
glu-L	L-Glutamate	cytosol	C5H8NO4	-1
glu-L	L-Glutamate	extracellular	C5H8NO4	-1
glu-L	L-Glutamate	mitochondrion	C5H8NO4	-1
glu-L	L-Glutamate	nucleus	C5H8NO4	-1
glu-L	L-Glutamate	peroxisome	C5H8NO4	-1
glu5p	L-Glutamate 5-phosphate	cytosol	C5H8NO7P	-2
glu5sa	L-Glutamate 5-semialdehyde	cytosol	C5H9NO3	0
glu5sa	L-Glutamate 5-semialdehyde	mitochondrion	C5H9NO3	0
gluala	5-L-Glutamyl-L-alanine	cytosol	C8H13N2O5	-1
glucys	gamma-L-Glutamyl-L-cysteine	cytosol	C8H13N2O5S	-1
glutrna	L-Glutamyl-tRNA(Glu)	cytosol	C5H7NO3R	0
glutrna	L-Glutamyl-tRNA(Glu)	mitochondrion	C5H7NO3R	0
glx	Glyoxylate	cytosol	C2H1O3	-1
glx	Glyoxylate	peroxisome	C2H1O3	-1
gly	Glycine	cytosol	C2H5NO2	0
gly	Glycine	extracellular	C2H5NO2	0
gly	Glycine	mitochondrion	C2H5NO2	0
glyald	D-Glyceraldehyde	cytosol	C3H6O3	0
glyc	Glycerol	cytosol	C3H8O3	0
glyc	Glycerol	extracellular	C3H8O3	0

glyc3p	Glycerol 3-phosphate	cytosol	C3H7O6P	-2
glyc3p	Glycerol 3-phosphate	mitochondrion	C3H7O6P	-2
glycogen	glycogen	cytosol	C6H10O5	0
glytrna	Glycyl-tRNA(Gly)	cytosol	C2H4NOR	1
gmp	GMP	cytosol	C10H12N5O8P	-2
gmp	GMP	Golgi apparatus	C10H12N5O8P	-2
gp4g	P1,P4-Bis(5'-guanosyl) tetraphosphate	cytosol	C20H24N10O21P4	-4
grdp	Geranyl diphosphate	cytosol	C10H17O7P2	-3
gsn	Guanosine	cytosol	C10H13N5O5	0
gsn	Guanosine	extracellular	C10H13N5O5	0
gsn	Guanosine	mitochondrion	C10H13N5O5	0
gthox	Oxidized glutathione	cytosol	C20H30N6O12S2	-2
gthox	Oxidized glutathione	extracellular	C20H30N6O12S2	-2
gthrd	Reduced glutathione	cytosol	C10H16N3O6S	-1
gthrd	Reduced glutathione	mitochondrion	C10H16N3O6S	-1
gtp	GTP	cytosol	C10H12N5O14P3	-4
gtp	GTP	mitochondrion	C10H12N5O14P3	-4
gua	Guanine	cytosol	C5H5N5O	0
gua	Guanine	extracellular	C5H5N5O	0
gua	Guanine	mitochondrion	C5H5N5O	0
h	H+	cytosol	H	1
h	H+	extracellular	H	1
h	H+	Golgi apparatus	H	1
h	H+	mitochondrion	H	1
h	H+	nucleus	H	1
h	H+	endoplasmic reticulum	H	1
h	H+	vacuole	H	1
h	H+	peroxisome	H	1
h2o	H2O	cytosol	H2O	0
h2o	H2O	extracellular	H2O	0
h2o	H2O	Golgi apparatus	H2O	0
h2o	H2O	mitochondrion	H2O	0
h2o	H2O	nucleus	H2O	0
h2o	H2O	endoplasmic reticulum	H2O	0
h2o	H2O	vacuole	H2O	0
h2o	H2O	peroxisome	H2O	0
h2o2	Hydrogen peroxide	cytosol	H2O2	0
h2o2	Hydrogen peroxide	peroxisome	H2O2	0
h2s	Hydrogen sulfide	cytosol	H2S	0
hLkynr	3-Hydroxy-L-kynurenine	cytosol	C10H12N2O4	0
hcit	2-Hydroxybutane-1,2,4-tricarboxylate	mitochondrion	C7H7O7	-3
hcit	2-Hydroxybutane-1,2,4-tricarboxylate	nucleus	C7H7O7	-3
hco3	Bicarbonate	cytosol	CHO3	-1
hco3	Bicarbonate	mitochondrion	CHO3	-1
hco3	Bicarbonate	nucleus	CHO3	-1
hcys-L	L-Homocysteine	cytosol	C4H9NO2S	0
hcys-L	L-Homocysteine	peroxisome	C4H9NO2S	0
hdca	Hexadecanoate (n-C16:0)	cytosol	C16H31O2	-1
hdca	Hexadecanoate (n-C16:0)	extracellular	C16H31O2	-1
hdca	Hexadecanoate (n-C16:0)	peroxisome	C16H31O2	-1
hdcea	hexadecenoate (n-C16:1)	cytosol	C16H29O2	-1
hdcea	hexadecenoate (n-C16:1)	extracellular	C16H29O2	-1
hdcea	hexadecenoate (n-C16:1)	peroxisome	C16H29O2	-1
hdcoa	Hexadecenoyl-CoA (n-C16:1CoA)	cytosol	C37H60N7O17P3S	-4
hdcoa	Hexadecenoyl-CoA (n-C16:1CoA)	peroxisome	C37H60N7O17P3S	-4
hdd2coa	trans-Hexadec-2-enoyl-CoA	peroxisome	C37H60N7O17P3S	-4
hdeACP	Hexadecenoyl-ACP (n-C16:1ACP)	cytosol	C27H49N2O8PRS	-1
hdeACP	Hexadecenoyl-ACP (n-C16:1ACP)	mitochondrion	C27H49N2O8PRS	-1
hexc	hexacosanoate (n-C26:0)	cytosol	C26H51O2	-1
hexc	hexacosanoate (n-C26:0)	peroxisome	C26H51O2	-1
hexccoa	Hexacosanoyl-CoA (n-C26:0CoA)	cytosol	C47H82N7O17P3S	-4
hexccoa	Hexacosanoyl-CoA (n-C26:0CoA)	peroxisome	C47H82N7O17P3S	-4
hgentis	Homogentisate	cytosol	C8H7O4	-1
hicit	Homoisocitrate	mitochondrion	C7H7O7	-3
his-L	L-Histidine	cytosol	C6H9N3O2	0
his-L	L-Histidine	extracellular	C6H9N3O2	0
his-L	L-Histidine	mitochondrion	C6H9N3O2	0
hisp	L-Histidinol phosphate	cytosol	C6H11N3O4P	-1

histd	L-Histidinol	cytosol	C6H12N3O	1
histrna	L-Histidyl-tRNA(His)	cytosol	C6H8N3OR	1
histrna	L-Histidyl-tRNA(His)	mitochondrion	C6H8N3OR	1
hmbil	Hydroxymethylbilane	cytosol	C40H38N4O17	-8
hmgcoa	Hydroxymethylglutaryl-CoA	cytosol	C27H39N7O20P3S	-5
hmgcoa	Hydroxymethylglutaryl-CoA	mitochondrion	C27H39N7O20P3S	-5
hom-L	L-Homoserine	cytosol	C4H9NO3	0
hpglu	Tetrahydropteroyltri-L-glutamate	cytosol	C24H34N8O12	0
hxan	Hypoxanthine	cytosol	C5H4N4O	0
hxan	Hypoxanthine	extracellular	C5H4N4O	0
hxc2coa	trans-Hexacos-2-enoyl-CoA	peroxisome	C47H80N7O17P3S	-4
hxdcal	Hexadecanal	cytosol	C16H32O	0
iad	Indole-3-acetamide	cytosol	C10H10N2O	0
iasp	Iminoaspartate	cytosol	C4H4NO4	-1
icit	Isocitrate	cytosol	C6H5O7	-3
icit	Isocitrate	mitochondrion	C6H5O7	-3
icit	Isocitrate	peroxisome	C6H5O7	-3
id3acald	Indole-3-acetaldehyde	cytosol	C10H9NO	0
id3acald	Indole-3-acetaldehyde	mitochondrion	C10H9NO	0
idp	IDP	cytosol	C10H11N4O11P2	-3
idp	IDP	mitochondrion	C10H11N4O11P2	-3
ile-L	L-Isoleucine	cytosol	C6H13NO2	0
ile-L	L-Isoleucine	extracellular	C6H13NO2	0
ile-L	L-Isoleucine	mitochondrion	C6H13NO2	0
iletrna	L-Isoleucyl-tRNA(Ile)	cytosol	C6H12NOR	1
iletrna	L-Isoleucyl-tRNA(Ile)	mitochondrion	C6H12NOR	1
imacp	3-(Imidazol-4-yl)-2-oxopropyl phosphate	cytosol	C6H7N2O5P	-2
imp	IMP	cytosol	C10H11N4O8P	-2
ind3ac	Indole-3-acetate	cytosol	C10H8NO2	-1
ind3ac	Indole-3-acetate	mitochondrion	C10H8NO2	-1
ind3acnl	Indole-3-acetonitrile	cytosol	C10H8N2	0
indpyr	Indolepyruvate	cytosol	C11H8NO3	-1
inost	myo-Inositol	cytosol	C6H12O6	0
inost	myo-Inositol	extracellular	C6H12O6	0
ins	Inosine	cytosol	C10H12N4O5	0
ins	Inosine	extracellular	C10H12N4O5	0
* ipc124_SC	Inositol phosphorylceramide, ceramide-1 (24C), yeast-specific	cytosol	C4800H9500N100O1100P100	-100
* ipc126_SC	Inositol phosphorylceramide, ceramide-1 (26C), yeast-specific	cytosol	C5000H9900N100O1100P100	-100
* ipc224_SC	Inositol phosphorylceramide, ceramide-2 (24C), yeast-specific	cytosol	C4800H9500N100O1200P100	-100
* ipc226_SC	Inositol phosphorylceramide, ceramide-2 (26C), yeast-specific	cytosol	C5000H9900N100O1200P100	-100
* ipc324_SC	Inositol phosphorylceramide, ceramide-3 (24C), yeast-specific	cytosol	C4800H9500N100O1300P100	-100
* ipc326_SC	Inositol phosphorylceramide, ceramide-3 (26C), yeast-specific	cytosol	C5000H9900N100O1300P100	-100
ipdp	Isopentenyl diphosphate	cytosol	C5H9O7P2	-3
itaccoa	Itaconyl-CoA	mitochondrion	C26H35N7O19P3S	-5
itacon	Itaconate	mitochondrion	C5H4O4	-2
itp	ITP	cytosol	C10H11N4O14P3	-4
itp	ITP	mitochondrion	C10H11N4O14P3	-4
k	K+	cytosol	K	1
k	K+	extracellular	K	1
lac-D	D-Lactate	cytosol	C3H5O3	-1
lac-D	D-Lactate	mitochondrion	C3H5O3	-1
lac-L	L-Lactate	cytosol	C3H5O3	-1
lac-L	L-Lactate	extracellular	C3H5O3	-1
lac-L	L-Lactate	mitochondrion	C3H5O3	-1
lald-L	L-Lactaldehyde	mitochondrion	C3H6O2	0
lanost	Lanosterol	cytosol	C30H50O	0
leu-L	L-Leucine	cytosol	C6H13NO2	0
leu-L	L-Leucine	extracellular	C6H13NO2	0
leu-L	L-Leucine	mitochondrion	C6H13NO2	0
leutrna	L-Leucyl-tRNA(Leu)	cytosol	C6H12NOR	1
leutrna	L-Leucyl-tRNA(Leu)	mitochondrion	C6H12NOR	1
lgt-S	(R)-S-Lactoylglutathione	cytosol	C13H20N3O8S	-1

lgt-S	(R)-S-Lactoylglutathione	mitochondrion	C13H20N3O8S	-1
lpam	Lipoamide	mitochondrion	C8H15NOS2	0
lpro	Lipoylprotein	mitochondrion	S2X	0
lys-L	L-Lysine	cytosol	C6H15N2O2	1
lys-L	L-Lysine	extracellular	C6H15N2O2	1
lys-L	L-Lysine	mitochondrion	C6H15N2O2	1
lystrna	L-Lysine-tRNA (Lys)	cytosol	C6H14N2OR	2
lystrna	L-Lysine-tRNA (Lys)	mitochondrion	C6H14N2OR	2
m1macchitppdol	alpha-D-mannosyl-beta-D-mannosyl-diacylchitobiosyldiphosphodolichol	Golgi apparatus	C43H74N2O27P2	-2
m2macchitppdol	(alpha-D-mannosyl)2-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol	Golgi apparatus	C49H84N2O32P2	-2
m3macchitppdol	(alpha-D-mannosyl)3-beta-D-mannosyl-diacetylchitodiphosphodolichol	Golgi apparatus	C55H94N2O37P2	-2
m4macchitppdol	(alpha-D-Mannosyl)4-beta-D-mannosyl-diacetylchitobiosyldiphosphodolichol	Golgi apparatus	C61H104N2O42P2	-2
macchitppdol	beta-D-Mannosyldiacetylchitobiosyldiphosphodolichol	Golgi apparatus	C37H64N2O22P2	-2
mal-L	L-Malate	cytosol	C4H4O5	-2
mal-L	L-Malate	extracellular	C4H4O5	-2
mal-L	L-Malate	mitochondrion	C4H4O5	-2
mal-L	L-Malate	peroxisome	C4H4O5	-2
malACP	Malonyl-[acyl-carrier protein]	cytosol	C14H22N2O10PRS	-2
malACP	Malonyl-[acyl-carrier protein]	mitochondrion	C14H22N2O10PRS	-2
malcoa	Malonyl-CoA	cytosol	C24H33N7O19P3S	-5
malcoa	Malonyl-CoA	mitochondrion	C24H33N7O19P3S	-5
malt	Maltose	cytosol	C12H22O11	0
malt	Maltose	extracellular	C12H22O11	0
man	D-Mannose	cytosol	C6H12O6	0
man	D-Mannose	extracellular	C6H12O6	0
man1p	D-Mannose 1-phosphate	cytosol	C6H11O9P	-2
man6p	D-Mannose 6-phosphate	cytosol	C6H11O9P	-2
mannan	Mannan	cytosol	C6H10O5	0
mannan	Mannan	endoplasmic reticulum	C6H10O5	0
melib	Melibiose	cytosol	C12H22O11	0
melib	Melibiose	extracellular	C12H22O11	0
melt	melibiitol	cytosol	C12H24O11	0
met-L	L-Methionine	cytosol	C5H11NO2S	0
met-L	L-Methionine	extracellular	C5H11NO2S	0
met-L	L-Methionine	mitochondrion	C5H11NO2S	0
methf	5,10-Methenyltetrahydrofolate	cytosol	C20H20N7O6	-1
methf	5,10-Methenyltetrahydrofolate	mitochondrion	C20H20N7O6	-1
mettrna	L-Methionyl-tRNA (Met)	cytosol	C5H10NOSR	1
mettrna	L-Methionyl-tRNA (Met)	mitochondrion	C5H10NOSR	1
mev-R	(R)-Mevalonate	cytosol	C6H11O4	-1
mhpglu	5-Methyltetrahydropteroyltri-L-glutamate	cytosol	C25H36N8O12	0
mi145tp-D	1D-myo-Inositol 1,4,5-trisphosphate	cytosol	C6H9O15P3	-6
mi1p-D	1D-myo-Inositol 1-phosphate	cytosol	C6H11O9P	-2
* mip2c124_SC	mannose-(inositol-P)2-ceramide, ceramide-1 (24C), yeast-specific	cytosol	C6000H11500N100O2400P200	-200
* mip2c126_SC	mannose-(inositol-P)2-ceramide, ceramide-1 (26C), yeast-specific	cytosol	C6200H11900N100O2400P200	-200
* mip2c224_SC	mannose-(inositol-P)2-ceramide, ceramide-2 (24C), yeast-specific	cytosol	C6000H11500N100O2500P200	-200
* mip2c226_SC	mannose-(inositol-P)2-ceramide, ceramide-2 (26C), yeast-specific	cytosol	C6200H11900N100O2500P200	-200
* mip2c324_SC	mannose-(inositol-P)2-ceramide, ceramide-3 (24C), yeast-specific	cytosol	C6000H11500N100O2600P200	-200
* mip2c326_SC	mannose-(inositol-P)2-ceramide, ceramide-3 (26C), yeast-specific	cytosol	C6200H11900N100O2600P200	-200
* mipc124_SC	mannose-inositol phosphorylceramide, ceramide-1 (24C), yeast-specific	cytosol	C5400H10500N100O1600P100	-100
* mipc126_SC	mannose-inositol phosphorylceramide, ceramide-1 (26C), yeast-specific	cytosol	C5600H10900N100O1600P100	-100
* mipc224_SC	mannose-inositol phosphorylceramide, ceramide-2 (24C), yeast-specific	cytosol	C5400H10500N100O1700P100	-100
* mipc226_SC	mannose-inositol phosphorylceramide, ceramide-2 (26C), yeast-specific	cytosol	C5600H10900N100O1700P100	-100

* mipc324_SC	mannose-inositol phosphorylceramide, ceramide-3 (24C), yeast-specific	cytosol	C5400H10500N100O1800P100	-100
* mipc326_SC	mannose-inositol phosphorylceramide, ceramide-3 (26C)	cytosol	C5600H10900N100O1800P100	-100
mlthf	5,10-Methylenetetrahydrofolate	cytosol	C20H22N7O6	-1
mlthf	5,10-Methylenetetrahydrofolate	mitochondrion	C20H22N7O6	-1
mmet	S-Methyl-L-methionine	cytosol	C6H14NO2S	1
mmet	S-Methyl-L-methionine	extracellular	C6H14NO2S	1
mnl1p	D-Mannitol 1-phosphate	cytosol	C6H13O9P	-2
mthgxl	Methylglyoxal	cytosol	C3H4O2	0
myrsACP	Myristoyl-ACP (n-C14:0ACP)	cytosol	C25H47N2O8PRS	-1
myrsACP	Myristoyl-ACP (n-C14:0ACP)	mitochondrion	C25H47N2O8PRS	-1
n4abutn	N4-Acetylaminobutanal	cytosol	C6H11NO2	0
na1	Sodium	cytosol	Na	1
na1	Sodium	extracellular	Na	1
nac	Nicotinate	cytosol	C6H4NO2	-1
nac	Nicotinate	mitochondrion	C6H4NO2	-1
nad	Nicotinamide adenine dinucleotide	cytosol	C21H26N7O14P2	-1
nad	Nicotinamide adenine dinucleotide	mitochondrion	C21H26N7O14P2	-1
nad	Nicotinamide adenine dinucleotide	peroxisome	C21H26N7O14P2	-1
nadh	Nicotinamide adenine dinucleotide - reduced	cytosol	C21H27N7O14P2	-2
nadh	Nicotinamide adenine dinucleotide - reduced	mitochondrion	C21H27N7O14P2	-2
nadh	Nicotinamide adenine dinucleotide - reduced	peroxisome	C21H27N7O14P2	-2
nadp	Nicotinamide adenine dinucleotide phosphate	cytosol	C21H25N7O17P3	-3
nadp	Nicotinamide adenine dinucleotide phosphate	mitochondrion	C21H25N7O17P3	-3
nadp	Nicotinamide adenine dinucleotide phosphate	endoplasmic reticulum	C21H25N7O17P3	-3
nadp	Nicotinamide adenine dinucleotide phosphate	peroxisome	C21H25N7O17P3	-3
nadph	Nicotinamide adenine dinucleotide phosphate - reduced	cytosol	C21H26N7O17P3	-4
nadph	Nicotinamide adenine dinucleotide phosphate - reduced	mitochondrion	C21H26N7O17P3	-4
nadph	Nicotinamide adenine dinucleotide phosphate - reduced	endoplasmic reticulum	C21H26N7O17P3	-4
nadph	Nicotinamide adenine dinucleotide phosphate - reduced	peroxisome	C21H26N7O17P3	-4
ncam	Nicotinamide	cytosol	C6H6N2O	0
ncam	Nicotinamide	mitochondrion	C6H6N2O	0
nh4	Ammonium	cytosol	H4N	1
nh4	Ammonium	extracellular	H4N	1
nh4	Ammonium	mitochondrion	H4N	1
nh4	Ammonium	peroxisome	H4N	1
nicrnt	Nicotinate D-ribonucleotide	cytosol	C11H12NO9P	-2
nicrnt	Nicotinate D-ribonucleotide	mitochondrion	C11H12NO9P	-2
nmn	NMN	cytosol	C11H14N2O8P	-1
nmn	NMN	extracellular	C11H14N2O8P	-1
nmn	NMN	mitochondrion	C11H14N2O8P	-1
nmn	NMN	peroxisome	C11H14N2O8P	-1
o2	O2	cytosol	O2	0
o2	O2	extracellular	O2	0
o2	O2	mitochondrion	O2	0
o2	O2	endoplasmic reticulum	O2	0
o2	O2	peroxisome	O2	0
oaa	Oxaloacetate	cytosol	C4H2O5	-2
oaa	Oxaloacetate	mitochondrion	C4H2O5	-2
oaa	Oxaloacetate	peroxisome	C4H2O5	-2
ocACP	Octanoyl-ACP (n-C8:0ACP)	mitochondrion	C19H35N2O8PRS	-1
occoa	Octanoyl-CoA (n-C8:0CoA)	cytosol	C29H46N7O17P3S	-4
occoa	Octanoyl-CoA (n-C8:0CoA)	peroxisome	C29H46N7O17P3S	-4
ocdca	octadecanoate (n-C18:0)	cytosol	C18H35O2	-1
ocdca	octadecanoate (n-C18:0)	extracellular	C18H35O2	-1
ocdcaACP	Octadecanoyl-ACP (n-C18:0ACP)	cytosol	C29H55N2O8PRS	-1
ocdcaACP	Octadecanoyl-ACP (n-C18:0ACP)	mitochondrion	C29H55N2O8PRS	-1
ocdcea	octadecenoate (n-C18:1)	cytosol	C18H33O2	-1
ocdcea	octadecenoate (n-C18:1)	extracellular	C18H33O2	-1
ocdcya	octadecynoate (n-C18:2)	cytosol	C18H31O2	-1
ocdcya	octadecynoate (n-C18:2)	extracellular	C18H31O2	-1
ocdcyaACP	Octadecynoyl-ACP (n-C18:2ACP)	cytosol	C29H51N2O8PRS	-1
ocdcyaACP	Octadecynoyl-ACP (n-C18:2ACP)	mitochondrion	C29H51N2O8PRS	-1

ocdycacoa	Octadecynoyl-CoA (n-C18:2CoA)	cytosol	C39H62N7O17P3S	-4
ocdycacoa	Octadecynoyl-CoA (n-C18:2CoA)	peroxisome	C39H62N7O17P3S	-4
octa	octanoate (n-C8:0)	cytosol	C8H15O2	-1
octa	octanoate (n-C8:0)	peroxisome	C8H15O2	-1
octdp_5	all-trans-Octaprenyl diphosphate (5 repeating units)	cytosol	C30H49O7P2	-3
octdp_5	all-trans-Octaprenyl diphosphate (5 repeating units)	mitochondrion	C30H49O7P2	-3
octeACP	Octadecenoyl-ACP (n-C18:1ACP)	cytosol	C29H53N2O8PRS	-1
octeACP	Octadecenoyl-ACP (n-C18:1ACP)	mitochondrion	C29H53N2O8PRS	-1
od2coa	trans-Octadec-2-enoyl-CoA	peroxisome	C39H64N7O17P3S	-4
odecoa	Octadecenoyl-CoA (n-C18:1CoA)	cytosol	C39H64N7O17P3S	-4
odecoa	Octadecenoyl-CoA (n-C18:1CoA)	peroxisome	C39H64N7O17P3S	-4
oh1	hydroxide ion	cytosol	HO	-1
oh1	hydroxide ion	mitochondrion	HO	-1
ohpb	2-Oxo-3-hydroxy-4-phosphobutanoate	cytosol	C4H4O8P	-3
orn	Ornithine	cytosol	C5H13N2O2	1
orn	Ornithine	extracellular	C5H13N2O2	1
orn	Ornithine	mitochondrion	C5H13N2O2	1
orot	Orotate	cytosol	C5H3N2O4	-1
orot5p	Orotidine 5'-phosphate	cytosol	C10H10N2O11P	-3
oxag	Oxaloglutarate	cytosol	C7H5O7	-3
oxag	Oxaloglutarate	mitochondrion	C7H5O7	-3
* pa_SC	Phosphatidate, yeast-specific	cytosol	C3540H6544O800P100	-200
* pa_SC	Phosphatidate, yeast-specific	mitochondrion	C3540H6544O800P100	-200
pac	Phenylacetic acid	cytosol	C8H7O2	-1
pacald	Phenylacetaldehyde	cytosol	C8H8O	0
pad	2-Phenylacetamide	cytosol	C8H9NO	0
palmACP	Palmitoyl-ACP (n-C16:0ACP)	cytosol	C27H51N2O8PRS	-1
palmACP	Palmitoyl-ACP (n-C16:0ACP)	mitochondrion	C27H51N2O8PRS	-1
pan4p	Pantetheine 4'-phosphate	cytosol	C11H21N2O7PS	-2
pan4p	Pantetheine 4'-phosphate	mitochondrion	C11H21N2O7PS	-2
pant-R	(R)-Pantoate	cytosol	C6H11O4	-1
pant-R	(R)-Pantoate	mitochondrion	C6H11O4	-1
pap	Adenosine 3',5'-bisphosphate	cytosol	C10H11N5O10P2	-4
pap	Adenosine 3',5'-bisphosphate	extracellular	C10H11N5O10P2	-4
pap	Adenosine 3',5'-bisphosphate	mitochondrion	C10H11N5O10P2	-4
paps	3'-Phosphoadenylyl sulfate	cytosol	C10H11N5O13P2S	-4
* pc_SC	Phosphatidylcholine, yeast-specific	cytosol	C4040H7844N100O800P100	0
pdx5p	Pyridoxine 5'-phosphate	cytosol	C8H10NO6P	-2
* pe_SC	phosphatidylethanolamine, yeast-specific	cytosol	C3740H7244N100O800P100	0
* pe_SC	phosphatidylethanolamine, yeast-specific	Golgi apparatus	C3740H7244N100O800P100	0
* pe_SC	phosphatidylethanolamine, yeast-specific	mitochondrion	C3740H7244N100O800P100	0
* pe_SC	phosphatidylethanolamine, yeast-specific	vacuole	C3740H7244N100O800P100	0
pep	Phosphoenolpyruvate	cytosol	C3H2O6P	-3
pep	Phosphoenolpyruvate	mitochondrion	C3H2O6P	-3
pepd	peptide	cytosol	C2H4NO2RC2H2NOR	0
pepd	peptide	extracellular	C2H4NO2RC2H2NOR	0
* pg_SC	Phosphatidylglycerol, yeast-specific	mitochondrion	C3840H7244O1000P100	-100
* pgp_SC	Phosphatidylglycerophosphate, yeast-specific	mitochondrion	C3840H7144O1300P200	-300
phe-L	L-Phenylalanine	cytosol	C9H11NO2	0
phe-L	L-Phenylalanine	extracellular	C9H11NO2	0
phe-L	L-Phenylalanine	mitochondrion	C9H11NO2	0
pheme	Protoheme	mitochondrion	C34H30FeN4O4	-2
phetrna	L-Phenylalanyl-tRNA(Phe)	cytosol	C9H10NOR	1
phetrna	L-Phenylalanyl-tRNA(Phe)	mitochondrion	C9H10NOR	1
phom	O-Phospho-L-homoserine	cytosol	C4H8NO6P	-2
phpyr	Phenylpyruvate	cytosol	C9H7O3	-1
phthr	O-Phospho-4-hydroxy-L-threonine	cytosol	C4H8NO7P	-2
pi	Phosphate	cytosol	HO4P	-2
pi	Phosphate	extracellular	HO4P	-2
pi	Phosphate	Golgi apparatus	HO4P	-2
pi	Phosphate	mitochondrion	HO4P	-2

pi	Phosphate	nucleus	HO4P	-2
pi	Phosphate	vacuole	HO4P	-2
pi	Phosphate	peroxisome	HO4P	-2
pmtcoa	Palmitoyl-CoA (n-C16:0CoA)	cytosol	C37H62N7O17P3S	-4
pmtcoa	Palmitoyl-CoA (n-C16:0CoA)	peroxisome	C37H62N7O17P3S	-4
pnto-R	(R)-Pantothenate	cytosol	C9H16NO5	-1
pnto-R	(R)-Pantothenate	extracellular	C9H16NO5	-1
ppbng	Porphobilinogen	cytosol	C10H13N2O4	-1
ppcoa	Propanoyl-CoA	cytosol	C24H36N7O17P3S	-4
pphn	Prephenate	cytosol	C10H8O6	-2
ppi	Diphosphate	cytosol	HO7P2	-3
ppi	Diphosphate	mitochondrion	HO7P2	-3
ppi	Diphosphate	peroxisome	HO7P2	-3
ppp9	Protoporphyrin	mitochondrion	C34H32N4O4	-2
pppg9	Protoporphyrinogen IX	cytosol	C34H38N4O4	-2
pppg9	Protoporphyrinogen IX	mitochondrion	C34H38N4O4	-2
pram	5-Phospho-beta-D-ribosylamine	cytosol	C5H11NO7P	-1
pran	N-(5-Phospho-D-ribosyl)anthranilate	cytosol	C12H13NO9P	-3
prbamp	1-(5-Phosphoribosyl)-AMP	cytosol	C15H19N5O14P2	-4
prbatp	1-(5-Phosphoribosyl)-ATP	cytosol	C15H19N5O20P4	-6
prfp	1-(5-Phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide	cytosol	C15H21N5O15P2	-4
prlp	5-[(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-carboxamide	cytosol	C15H21N5O15P2	-4
pro-L	L-Proline	cytosol	C5H9NO2	0
pro-L	L-Proline	extracellular	C5H9NO2	0
pro-L	L-Proline	mitochondrion	C5H9NO2	0
protrna	L-Prolyl-tRNA(Pro)	cytosol	C5H8NOR	1
prpp	5-Phospho-alpha-D-ribose 1-diphosphate	cytosol	C5H8O14P3	-5
prpp	5-Phospho-alpha-D-ribose 1-diphosphate	mitochondrion	C5H8O14P3	-5
* ps_SC	phosphatidylserine, yeast-specific	cytosol	C3840H7144N100O1000P100	-100
* ps_SC	phosphatidylserine, yeast-specific	Golgi apparatus	C3840H7144N100O1000P100	-100
* ps_SC	phosphatidylserine, yeast-specific	mitochondrion	C3840H7144N100O1000P100	-100
* ps_SC	phosphatidylserine, yeast-specific	vacuole	C3840H7144N100O1000P100	-100
psd5p	Pseudouridine 5'-phosphate	cytosol	C9H11N2O9P	-2
pser-L	O-Phospho-L-serine	cytosol	C3H6NO6P	-2
psph1p	Phytosphingosine 1-phosphate	cytosol	C18H39NO6P	-1
psphings	Phytosphingosine	cytosol	C18H40NO3	1
* ptd134bp_SC	phosphatidyl-1D-myo-inositol 3,4-bisphosphate, yeast-specific	cytosol	C4140H7444O1900P300	-500
* ptd145bp_SC	1-Phosphatidyl-D-myo-inositol 4,5-bisphosphate, yeast-specific	cytosol	C4140H7444O1900P300	-500
* ptd1ino_SC	phosphatidyl-1D-myo-inositol, yeast-specific	cytosol	C4140H7644O1300P100	-100
* ptd1ino_SC	phosphatidyl-1D-myo-inositol, yeast-specific	nucleus	C4140H7644O1300P100	-100
* ptd2meeta_SC	Phosphatidyl-N-dimethylethanolamine	cytosol	C3940H7644N100O800P100	0
* ptd3ino_SC	phosphatidyl-1D-myo-3-inositol, yeast-specific	cytosol	C4140H7544O1600P200	-300
* ptd4ino_SC	phosphatidyl-1D-myo-4-inositol, yeast specific	cytosol	C4140H7544O1600P200	-300
* ptd4ino_SC	phosphatidyl-1D-myo-4-inositol, yeast specific	nucleus	C4140H7544O1600P200	-300
* ptdmeeta_SC	Phosphatidyl-N-methylethanolamine, yeast-specific	cytosol	C3840H7444N100O800P100	0
ptrc	Putrescine	cytosol	C4H14N2	2
ptrc	Putrescine	extracellular	C4H14N2	2
pyam5p	Pyridoxamine 5'-phosphate	cytosol	C8H12N2O5P	-1
pydam	Pyridoxamine	cytosol	C8H13N2O2	1
pydx	Pyridoxal	cytosol	C8H9NO3	0
pydx5p	Pyridoxal 5'-phosphate	cytosol	C8H8NO6P	-2
pydxn	Pyridoxine	cytosol	C8H11NO3	0
pyr	Pyruvate	cytosol	C3H3O3	-1
pyr	Pyruvate	extracellular	C3H3O3	-1
pyr	Pyruvate	mitochondrion	C3H3O3	-1
pyr	Pyruvate	peroxisome	C3H3O3	-1

q6	Ubiquinone-6	mitochondrion	C39H58O4	0
q6h2	Ubiquinol-6	mitochondrion	C39H60O4	0
quln	Quinolinate	cytosol	C7H3NO4	-2
quln	Quinolinate	mitochondrion	C7H3NO4	-2
r1p	alpha-D-Ribose 1-phosphate	cytosol	C5H9O8P	-2
r1p	alpha-D-Ribose 1-phosphate	mitochondrion	C5H9O8P	-2
r5p	alpha-D-Ribose 5-phosphate	cytosol	C5H9O8P	-2
raffin	Raffinose	cytosol	C18H32O16	0
rib-D	D-Ribose	cytosol	C5H10O5	0
rib-D	D-Ribose	extracellular	C5H10O5	0
ribflv	Riboflavin	cytosol	C17H20N4O6	0
ribflv	Riboflavin	extracellular	C17H20N4O6	0
ribflv	Riboflavin	mitochondrion	C17H20N4O6	0
ru5p-D	D-Ribulose 5-phosphate	cytosol	C5H9O8P	-2
s	Sulfur	cytosol	S	0
s17bp	Sedoheptulose 1,7-bisphosphate	cytosol	C7H12O13P2	-4
s7p	Sedoheptulose 7-phosphate	cytosol	C7H13O10P	-2
saccrp-L	L-Saccharopine	cytosol	C11H19N2O6	-1
sbt-D	D-Sorbitol	cytosol	C6H14O6	0
sbt-D	D-Sorbitol	extracellular	C6H14O6	0
sbt-L	L-Sorbitol	cytosol	C6H14O6	0
sbt-L	L-Sorbitol	extracellular	C6H14O6	0
sdhlam	S-Succinyldihydrolipoamide	mitochondrion	C12H20NO4S2	-1
ser-L	L-Serine	cytosol	C3H7NO3	0
ser-L	L-Serine	extracellular	C3H7NO3	0
ser-L	L-Serine	mitochondrion	C3H7NO3	0
sertrna	L-Seryl-tRNA(Ser)	cytosol	C3H6NO2R	1
shcl	Sirohydrochlorin	cytosol	C42H41N4O16	-7
skm	Shikimate	cytosol	C7H9O5	-1
skm5p	Shikimate 5-phosphate	cytosol	C7H8O8P	-3
so3	Sulfite	cytosol	O3S	-2
so4	Sulfate	cytosol	O4S	-2
so4	Sulfate	extracellular	O4S	-2
sph1p	Sphinganine 1-phosphate	cytosol	C18H39NO5P	-1
sphgn	Sphinganine	cytosol	C18H40NO2	1
spmd	Spermidine	cytosol	C7H22N3	3
spmd	Spermidine	extracellular	C7H22N3	3
sprm	Spermine	cytosol	C10H30N4	4
sprm	Spermine	extracellular	C10H30N4	4
sql	Squalene	cytosol	C30H50	0
sql	Squalene	endoplasmic reticulum	C30H50	0
srb-L	L-Sorbose	cytosol	C6H12O6	0
srb-L	L-Sorbose	extracellular	C6H12O6	0
stcoa	Stearoyl-CoA (n-C18:0CoA)	cytosol	C39H66N7O17P3S	-4
stcoa	Stearoyl-CoA (n-C18:0CoA)	peroxisome	C39H66N7O17P3S	-4
succ	Succinate	cytosol	C4H4O4	-2
succ	Succinate	extracellular	C4H4O4	-2
succ	Succinate	mitochondrion	C4H4O4	-2
succoa	Succinyl-CoA	mitochondrion	C25H35N7O19P3S	-5
suchms	O-Succinyl-L-homoserine	cytosol	C8H12NO6	-1
sucr	Sucrose	cytosol	C12H22O11	0
sucr	Sucrose	extracellular	C12H22O11	0
sucsal	Succinic semialdehyde	cytosol	C4H5O3	-1
tag6p-D	D-Tagatose 6-phosphate	cytosol	C6H11O9P	-2
tagdp-D	D-Tagatose 1,6-biphosphate	cytosol	C6H10O12P2	-4
td2coa	trans-Tetradec-2-enoyl-CoA	peroxisome	C35H56N7O17P3S	-4
tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	cytosol	C35H58N7O17P3S	-4
tdcoa	Tetradecanoyl-CoA (n-C14:0CoA)	peroxisome	C35H58N7O17P3S	-4
tdeACP	Tetradecenoyl-ACP (n-C14:1ACP)	cytosol	C25H45N2O8PRS	-1
tdeACP	Tetradecenoyl-ACP (n-C14:1ACP)	mitochondrion	C25H45N2O8PRS	-1
tdecoa	Tetradecenoyl-CoA (n-C14:1CoA)	cytosol	C35H56N7O17P3S	-4
tdecoa	Tetradecenoyl-CoA (n-C14:1CoA)	peroxisome	C35H56N7O17P3S	-4
tglp	N-Tetradecanoylglycylpeptide	cytosol	C18H32N2O4R	0
thf	5,6,7,8-Tetrahydrofolate	cytosol	C19H22N7O6	-1
thf	5,6,7,8-Tetrahydrofolate	mitochondrion	C19H22N7O6	-1
thfglu	Tetrahydrofolyl-[Glu](2)	cytosol	C24H28N8O9	-2
thm	Thiamin	cytosol	C12H17N4OS	1
thm	Thiamin	extracellular	C12H17N4OS	1

thmmp	Thiamin monophosphate	cytosol	C12H16N4O4PS	-1
thmmp	Thiamin monophosphate	extracellular	C12H16N4O4PS	-1
thmpp	Thiamine diphosphate	cytosol	C12H16N4O7P2S	-2
thmpp	Thiamine diphosphate	extracellular	C12H16N4O7P2S	-2
thmtp	Thiamin triphosphate	cytosol	C12H16N4O10P3S	-3
thr-L	L-Threonine	cytosol	C4H9NO3	0
thr-L	L-Threonine	extracellular	C4H9NO3	0
thr-L	L-Threonine	mitochondrion	C4H9NO3	0
thrtrna	L-Threonyl-tRNA(Thr)	cytosol	C4H8NO2R	1
thrtrna	L-Threonyl-tRNA(Thr)	mitochondrion	C4H8NO2R	1
thym	Thymine	cytosol	C5H6N2O2	0
thym	Thymine	extracellular	C5H6N2O2	0
thymd	Thymidine	cytosol	C10H14N2O5	0
thymd	Thymidine	extracellular	C10H14N2O5	0
trdox	Oxidized thioredoxin	cytosol	X	0
trdox	Oxidized thioredoxin	mitochondrion	X	0
trdox	Oxidized thioredoxin	nucleus	X	0
trdrd	Reduced thioredoxin	cytosol	XH2	0
trdrd	Reduced thioredoxin	mitochondrion	XH2	0
trdrd	Reduced thioredoxin	nucleus	XH2	0
tre	Trehalose	cytosol	C12H22O11	0
tre	Trehalose	extracellular	C12H22O11	0
tre	Trehalose	vacuole	C12H22O11	0
tre6p	alpha,alpha'-Trehalose 6-phosphate	cytosol	C12H21O14P	-2
* triglyc_SC	triglyceride, yeast-specific	cytosol	C5160H9566O600	0
trnaala	tRNA(Ala)	cytosol	R	0
trnaarg	tRNA(Arg)	cytosol	R	0
trnaarg	tRNA(Arg)	mitochondrion	R	0
trnaasn	tRNA(Asn)	cytosol	R	0
trnaasn	tRNA(Asn)	mitochondrion	R	0
trnaasp	tRNA(Asp)	cytosol	R	0
trnaasp	tRNA(Asp)	mitochondrion	R	0
trnacys	tRNA(Cys)	cytosol	R	0
trnagln	tRNA(Gln)	cytosol	R	0
trnaglu	tRNA (Glu)	cytosol	R	0
trnaglu	tRNA (Glu)	mitochondrion	R	0
trnagly	tRNA(Gly)	cytosol	R	0
trnahis	tRNA(His)	cytosol	R	0
trnahis	tRNA(His)	mitochondrion	R	0
trnaile	tRNA(Ile)	cytosol	R	0
trnaile	tRNA(Ile)	mitochondrion	R	0
trnaleu	tRNA(Leu)	cytosol	R	0
trnaleu	tRNA(Leu)	mitochondrion	R	0
trnalys	tRNA(Lys)	cytosol	R	0
trnalys	tRNA(Lys)	mitochondrion	R	0
trnamet	tRNA(Met)	cytosol	R	0
trnamet	tRNA(Met)	mitochondrion	R	0
trnaphe	tRNA(Phe)	cytosol	R	0
trnaphe	tRNA(Phe)	mitochondrion	R	0
trnapro	tRNA(Pro)	cytosol	R	0
trnaser	tRNA(Ser)	cytosol	R	0
trnathr	tRNA(Thr)	cytosol	R	0
trnathr	tRNA(Thr)	mitochondrion	R	0
trnatrp	tRNA(Trp)	cytosol	R	0
trnatrp	tRNA(Trp)	mitochondrion	R	0
trnatyr	tRNA(Tyr)	cytosol	R	0
trnatyr	tRNA(Tyr)	mitochondrion	R	0
trnaval	tRNA(Val)	cytosol	R	0
trnaval	tRNA(Val)	mitochondrion	R	0
trp-L	L-Tryptophan	cytosol	C11H12N2O2	0
trp-L	L-Tryptophan	extracellular	C11H12N2O2	0
trp-L	L-Tryptophan	mitochondrion	C11H12N2O2	0
trptrna	L-Tryptophanyl-tRNA(Trp)	cytosol	C11H11N2OR	1
trptrna	L-Tryptophanyl-tRNA(Trp)	mitochondrion	C11H11N2OR	1
ttc	tetracosanoate (n-C24:0)	cytosol	C24H47O2	-1
ttc	tetracosanoate (n-C24:0)	peroxisome	C24H47O2	-1
ttccoa	tetracosanoyl-CoA (n-C24:0CoA)	cytosol	C45H78N7O17P3S	-4
ttccoa	tetracosanoyl-CoA (n-C24:0CoA)	peroxisome	C45H78N7O17P3S	-4

ttdca	tetradecanoate (n-C14:0)	cytosol	C14H27O2	-1
ttdca	tetradecanoate (n-C14:0)	extracellular	C14H27O2	-1
ttdca	tetradecanoate (n-C14:0)	peroxisome	C14H27O2	-1
ttdcea	tetradecenoate (n-C14:1)	cytosol	C14H25O2	-1
ttdcea	tetradecenoate (n-C14:1)	peroxisome	C14H25O2	-1
tyr-L	L-Tyrosine	cytosol	C9H11NO3	0
tyr-L	L-Tyrosine	extracellular	C9H11NO3	0
tyr-L	L-Tyrosine	mitochondrion	C9H11NO3	0
tyr-L	L-Tyrosine	peroxisome	C9H11NO3	0
tyrtrna	L-Tyrosyl-tRNA(Tyr)	cytosol	C9H10NO2R	1
tyrtrna	L-Tyrosyl-tRNA(Tyr)	mitochondrion	C9H10NO2R	1
udp	UDP	cytosol	C9H11N2O12P2	-3
udp	UDP	nucleus	C9H11N2O12P2	-3
udpacgal	UDP-N-acetyl-D-galactosamine	cytosol	C17H25N3O17P2	-2
udpg	UDPglucose	cytosol	C15H22N2O17P2	-2
udpgal	UDPgalactose	cytosol	C15H22N2O17P2	-2
ump	UMP	cytosol	C9H11N2O9P	-2
ump	UMP	nucleus	C9H11N2O9P	-2
uppg3	Uroporphyrinogen III	cytosol	C40H36N4O16	-8
ura	Uracil	cytosol	C4H4N2O2	0
ura	Uracil	extracellular	C4H4N2O2	0
urdglyc	(-)-Ureidoglycolate	cytosol	C3H5N2O4	-1
urea	Urea	cytosol	CH4N2O	0
urea	Urea	extracellular	CH4N2O	0
uri	Uridine	cytosol	C9H12N2O6	0
uri	Uridine	extracellular	C9H12N2O6	0
utp	UTP	cytosol	C9H11N2O15P3	-4
val-L	L-Valine	cytosol	C5H11NO2	0
val-L	L-Valine	extracellular	C5H11NO2	0
val-L	L-Valine	mitochondrion	C5H11NO2	0
valtrna	L-Valyl-tRNA(Val)	cytosol	C5H10NOR	1
valtrna	L-Valyl-tRNA(Val)	mitochondrion	C5H10NOR	1
xan	Xanthine	cytosol	C5H4N4O2	0
xan	Xanthine	extracellular	C5H4N4O2	0
xmp	Xanthosine 5'-phosphate	cytosol	C10H11N4O9P	-2
xtsn	Xanthosine	cytosol	C10H12N4O6	0
xtsn	Xanthosine	extracellular	C10H12N4O6	0
xu5p-D	D-Xylulose 5-phosphate	cytosol	C5H9O8P	-2
xyl-D	D-Xylose	cytosol	C5H10O5	0
xyl-D	D-Xylose	extracellular	C5H10O5	0
xylt	Xylitol	cytosol	C5H12O5	0
xylt	Xylitol	extracellular	C5H12O5	0
xylu-D	D-Xylulose	cytosol	C5H10O5	0
zym_int1	zymosterol intermediate 1	cytosol	C28H44O3	0
zym_int2	zymosterol intermediate 2	cytosol	C27H42O	0
zymst	zymosterol	cytosol	C27H44O	0
zymst	zymosterol	extracellular	C27H44O	0

* Metabolite represents 100 copies of this compound. For reactions involving this metabolite, the stoichiometric coefficients have been appropriately scaled (*e.g.* , 1/100 or 2/100).

Key to deletion results

ORF	ORF name
Name	Gene name
Annotation	Gene annotation (from SGD)
Ess sim	Essential (YPD) simulation
Ess call	Essential call (FP/TN)
Slow sim	Slow growth simulation
Slow exp	Slow growth experimental [Giaever02]
Slow call	Slow growth call (FP/TN)
MMD sim	Glucose minimal media simulation
MMD exp	MMD experimental (1=normal growth, 0=retarded growth)
MMD ave	MMD average of experimental scores
MMD call	MMD call (FP/FN/TP/TN)
YPGal sim	YP galactose simulation
YPGal exp	YPGal experimental (1=normal growth, 0=retarded growth)
YPGal ave	YPGal average of experimental scores
YPGal call	YPGal call (FP/FN/TP/TN)
YPD sim	YPD simulation
YPD exp	YPD experimental
YPD call	YPD call (FP/FN/TP/TN)
YPDGE sim	YPDGE simulation
YPDGE exp	YPDGE experimental
YPDGE call	YPDGE call (FP/FN/TP/TN)
YPG sim	YPG simulation
YPG exp	YPG experimental
YPG call	YPG call (FP/FN/TP/TN)
YPE sim	YPE simulation
YPE exp	YPE experimental
YPE call	YPE call (FP/FN/TP/TN)
YPL sim	YPL simulation
YPL exp	YPL experimental
YPL call	YPL call (FP/FN/TP/TN)
Class	Primary source for false prediction(s)
Explanation	Detailed explanation for false prediction(s)
Forster et al	Result in Forster et al. study - only false predictions are listed

Abbreviations for sources for false predictions

Acc	Accumulation of a toxic intermediate
Bio	Problems with in silico biomass constitution
Den	Dead end in the in silico model
Dis	Discrepancy in experimental data
Iso	Problems with in silico gene-protein-reaction associations
Med	Problems with in silico media composition
Mod	Problems with in silico model structure
Oth	Involvement of the gene in non-metabolic processes
Reg	Missing transcriptional regulation
Unk	Unknown source for false prediction

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YMR056C	AAC1	ADP/ATP translocator	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.06	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YNL141W	AAH1	Adenine aminohydrolase (adenine deaminase)	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.07	TP	1.08	1	TP	1.1	1	TP	1.11	1	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YKL106W	AAT1	Aspartate aminotransferase	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.05	TP	1.08	0.98	TP	1.1	0.97	TP	1.09	0.87	TP	1.11	0.82	TP	1.1	0.84	TP	NA	NA	NA
YLR027C	AAT2	Aspartate aminotransferase	NA	NA	NA	NA	NA	1	1	0.96	TP	1	1	0	TP	1.08	0.93	TP	1.1	0.83	FP	1.08	0.74	FP	1.11	0.65	FP	1.1	0.87	TP	Unk	The model correctly predicts that the effect of the deletion is larger on non-fermentable carbon sources, but the predicted change in growth rate is too small for the slow growth criterion. The model does not predict higher growth of lactate than on other non-fermentable carbon sources though.	NA
YNR033W	ABZ1	Aminodeoxychorismate synthase	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YGR037C	ACB1	Acyl-CoA-binding protein (ACBP)/diazepam binding inhibitor (DBI)/endozepine (EP)	NA	NA	NA	NA	NA	0	1	0.23	FN	0	1	-0.04	FN	0	0.93	FN	0	0.97	FN	0	0.94	FN	0	0.95	FN	0	0.94	FN	Unk	Product of ACB1 is part of FAS complex; involved in termination of fatty acid synthesis and transport of newly synthesized acyl-CoA esters from the fatty acid synthetase to acyl-CoA-consuming processes, may also transport medium- and long-chain acyl CoA esters [MIPS]; since enzymatic mechanism is unknown and transport function is not well defined, may want to remove from FAS complex.	NA
YNR016C	ACC1	Acetyl CoA carboxylase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YBL015W	ACH1	Acetyl CoA hydrolase	NA	NA	NA	NA	NA	1	1	-0.01	TP	0.99	1	-0.05	TP	1.08	1.03	TP	1.1	1.05	TP	1.1	1.04	TP	0.96	1.06	TP	1.11	1.06	TP	NA	NA	NA
YLR304C	ACO1	Aconitase	NA	NA	1	3.6	FP	1	1	0.02	TP	1	1	-0.04	TP	1.08	0.86	FP	1.1	0.75	FP	1.11	0.59	FP	1.12	0.52	FP	1.11	0.6	FP	Iso	YJL200C codes for an isozyme for Aco1p, but Aco1p is probably the major isoform.	NA
YKL192C	ACP1	Acyl carrier protein	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Acp1p used in synthesis of fatty-acyl ACPs, which are not required in the model.	NA
YAL054C	ACS1	Acetyl CoA synthetase	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	-0.03	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	0.98	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YLR153C	ACS2	Acetyl CoA synthetase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	FP
YAR015W	ADE1	Phosphoribosyl amino imidazolesuccinocarbozamide synthetase	NA	NA	NA	NA	NA	0	1	0.02	FN	1	1	0	TP	1.08	0.97	TP	1.1	0.93	TP	1.11	0.99	TP	1.12	0.97	TP	1.11	0.95	TP	Med	Should be an adenine auxotroph [SGD] - should not grow normally on minimal media.	NA
YNL220W	ADE12	Adenylosuccinate synthetase	NA	NA	1	4.5	FP	0	1	-0.01	TN	1	1	0	TP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Med	FP for rich media - TN for MMD. There appears to be an extra component in the in silico rich medium.	NA
YLR359W	ADE13	Adenylosuccinate lyase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Med	Null mutant is an adenine auxotroph [MIPS]. The deletion is lethal if adenine is removed from the rich media.	NA
YLR028C	ADE16	5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase/IMP cyclohydrolase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.01	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.05	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YMR120C	ADE17	5-aminoimidazole-4-carboxamide ribonucleotide (AICAR) transformylase/IMP cyclohydrolase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.02	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YGR204W	ADE3	C1-tetrahydrofolate synthase	NA	NA	NA	NA	NA	0	1	2.08	TN	0.99	1	0	TP	1.07	1.01	TP	1.09	0.99	TP	1.06	0.99	TP	1.12	1	TP	1.06	1	TP	NA	Weak false negative	FN
YMR300C	ADE4	Phosphoribosylpyrophosphate amidotransferase	NA	NA	NA	NA	NA	0	0	4.2	TN	1	1	-0.06	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YGL234W	ADE5,	Aminoimidazole ribotide synthetase|glycinamide ribotide synthetase	NA	NA	NA	NA	NA	0	1	0.95	FN	1	1	-0.03	TP	1.08	0.99	TP	1.1	0.99	TP	1.11	1	TP	1.12	1	TP	1.11	0.99	TP	Med	Should be an adenine auxotroph [SGD] - should not grow normally on minimal media.	NA
YGR061C	ADE6	5'-phosphoribosylformyl glycinamidine synthetase	NA	NA	NA	NA	NA	0	0	5.08	TN	1	1	-0.02	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YDR408C	ADE8	Glycinamide ribotide transformylase	NA	NA	NA	NA	NA	0	1	1.1	TN	1	1	0	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.02	TP	NA	Weak false negative	NA
YOL086C	ADH1	Alcohol dehydrogenase	NA	NA	1	10.1	FP	1	1	0	TP	1	1	0	TP	1.08	0.76	FP	1.1	0.87	TP	1.11	1.12	TP	1.12	1.09	TP	1.11	1.15	TP	Reg	Most likely a regulatory effect as this may be the only isozyme (out of five) active under severely glucose repressed conditions.	NA
YMR303C	ADH2	Alcohol dehydrogenase II	NA	NA	NA	NA	NA	1	1	0.13	TP	1	1	-0.04	TP	1.08	1	TP	1.1	1	TP	1.11	1.01	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA
YMR083W	ADH3	Alcohol dehydrogenase isoenzyme III	NA	NA	NA	NA	NA	1	1	1.2	TP	1	1	-0.01	TP	1.08	0.98	TP	1.1	0.97	TP	1.11	0.97	TP	1.12	0.93	TP	1.11	0.95	TP	NA	NA	NA
YGL256W	ADH4	Alcohol dehydrogenase isoenzyme IV	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.07	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YBR145W	ADH5	Alcohol dehydrogenase isoenzyme V	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.04	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YDR226W	ADK1	Adenylate kinase	NA	NA	0	9.7	TN	0	1	0	TN	0	1	-0.03	TN	0	0.7	TN	0	0.75	TN	0	0.74	TN	0	0.72	TN	0	0.76	TN	NA	NA	FN
YER170W	ADK2	Adenylate kinase|mitochondrial GTP:AMP phosphotransferase	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0.02	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YJR105W	ADO1	Adenosine kinase	NA	NA	NA	NA	NA	1	1	0.73	TP	1	1	0	TP	1.08	0.79	FP	1.1	0.8	FP	1.11	0.94	TP	1.12	0.92	TP	1.11	0.94	TP	Unk	There is an alternative pathway involving Pnp1p that can substitute for the function of this adenosine kinase. This activity of Pnp1p does not seem to have been established conclusively in the literature.	NA
YCL025C	AGP1	Amino acid permease	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YFL055W	AGP3	The acronym may be misleading. AGP3 has not been shown to be a general amino acid permease with broad substrate specificity	NA	NA	NA	NA	NA	1	1	0.12	TP	1	1	-0.02	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	0.99	TP	1.12	1.03	TP	1.11	1.01	TP	NA	NA	NA
YOR335C	ALA1	Cytoplasmic alanyl-tRNA synthetase gene	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model.	NA
YMR170C	ALD2	Aldeyhde dehydrogenase	NA	NA	NA	NA	NA	1	1	0.08	TP	1	1	-0.04	TP	1.08	0.99	TP	1.1	1	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YMR169C	ALD3	Aldehyde dehydrogenase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YOR374W	ALD4	Aldehyde dehydrogenase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.08	TP	1.08	1	TP	1.1	1	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	0.98	TP	NA	NA	NA
YER073W	ALD5	Aldehyde dehydrogenase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.07	TP	1.12	1.07	TP	1.11	1.06	TP	NA	NA	NA
YPL061W	ALD6	Aldehyde dehydrogenase	NA	NA	NA	NA	NA	1	1	0.1	TP	1	1	-0.04	TP	1.07	0.86	FP	1.08	0.91	TP	1.11	1	TP	1.06	0.93	TP	1.11	0.98	TP	Unk	The model uses a mitochondrial acetaldehyde dehydrogenase in the deletion strain. In vivo this activity cannot fully compensate for the cytoplasmic activity.	NA
YNL270C	ALP1	Basic amino acid permease	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.07	TP	1.08	1	TP	1.1	0.99	TP	1.11	1.01	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA
YML035C	AMD1	AMP deaminase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.01	TP	1.08	1.02	TP	1.1	1	TP	1.11	0.99	TP	1.12	1.02	TP	1.11	0.99	TP	NA	NA	NA
YDR242W	AMD2	Amidase (putative)	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.01	TP	1.11	1	TP	1.12	1.03	TP	1.11	1.01	TP	NA	NA	NA
YPR128C	ANT1	Adenine nucleotide transporter	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	0.99	TP	1.11	0.99	TP	1.12	1	TP	1.11	1.01	TP	NA	NA	NA
YCL050C	APA1	Diadenosine 5',5'''-P1,P4-tetraphosphate phosphorylase I	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.07	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.06	TP	1.12	1.07	TP	1.11	1.06	TP	NA	NA	NA
YDR530C	APA2	5',5'''-P-1,P-4-tetraphosphate phosphorylase II	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.06	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.06	TP	1.11	1.04	TP	NA	NA	NA
YML022W	APT1	Adenine phosphoribosyltransferase	NA	NA	NA	NA	NA	1	1	1.41	TP	1	1	0	TP	1.08	0.96	TP	1.1	0.95	TP	1.11	0.96	TP	1.12	0.96	TP	1.11	0.96	TP	NA	NA	NA
YDR441C	APT2	Similar to adenine phosphoribosyltransferase; appears to be a nonfunctional pseudogene	NA	NA	NA	NA	NA	1	1	0.11	TP	1	1	-0.02	TP	1.08	0.99	TP	1.1	1	TP	1.11	0.97	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YBR149W	ARA1	D-arabinose dehydrogenase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.03	TP	1.08	0.99	TP	1.1	0.99	TP	1.11	1	TP	1.12	0.98	TP	1.11	0.98	TP	NA	NA	NA
YOL058W	ARG1	Argininosuccinate synthetase	NA	NA	NA	NA	NA	0	1	5.51	TN	1	1	-0.07	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.01	TP	1.1	1.02	TP	NA	Weak false negative	NA
YJL071W	ARG2	Acetylglutamate synthase	NA	NA	NA	NA	NA	1	1	3.27	TP	1	1	-0.06	TP	1.08	1	TP	1.1	1.04	TP	1.11	1.05	TP	1.12	1.06	TP	1.11	1.05	TP	NA	NA	NA
YJL088W	ARG3	Ornithine carbamoyltransferase	NA	NA	NA	NA	NA	0	1	2.1	TN	1	1	-0.01	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.05	TP	1.12	1.04	TP	1.1	1.04	TP	NA	Weak false negative	NA
YHR018C	ARG4	Argininosuccinate lyase	NA	NA	NA	NA	NA	0	1	6.58	TN	1	1	0	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.04	TP	1.1	1.03	TP	NA	Weak false negative	NA
YER069W	ARG5,	N-acetyl-gamma-glutamyl-phosphate reductase and acetylglutamate kinase	NA	NA	NA	NA	NA	0	1	2.36	TN	1	1	-0.06	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.01	TP	1.11	1.01	TP	NA	Weak false negative	NA
YDR127W	ARO1	3-dehydroquinate dehydratase (3-dehydroquinase)|3-dehydroquinate synthase|epsp synthase|pentafunctional arom polypeptide|shikimate 5-dehydrogenase|shikimate kinase	NA	NA	1	10.5	FP	0	1	-0.03	TN	1	1	-0.03	TP	1.08	0.99	TP	1.1	0.99	TP	1.11	1.02	TP	1.12	1.04	TP	1.11	1.02	TP	Med	FP for rich media - TN for MMD. There appears to be an extra component in the in silico rich medium.	NA
YDR380W	ARO10	NA	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.02	TP	1.08	1.04	TP	1.1	1.05	TP	1.11	1.04	TP	1.12	1.09	TP	1.11	1.07	TP	NA	NA	NA
YGL148W	ARO2	Chorismate synthase	NA	NA	NA	NA	NA	0	1	5.13	TN	1	1	-0.03	TP	1.08	0.98	TP	1.1	1	TP	1.11	1.03	TP	1.12	1.04	TP	1.11	1.05	TP	NA	Weak false negative	NA
YDR035W	ARO3	DAHP synthase; a.k.a. phospho-2-dehydro-3-deoxyheptonate aldolase, phenylalanine-inhibited; phospho-2-keto-3-deoxyheptonate aldolase; 2-dehydro-3-deoxyphosphoheptonate aldolase; 3 deoxy-D-arabine-heptulosonate-7-phosphate synthase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.06	TP	1.11	1.05	TP	NA	NA	NA
YBR249C	ARO4	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase isoenzyme	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0.01	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.04	TP	1.11	1.04	TP	NA	NA	NA
YPR060C	ARO7	Chorismate mutase	NA	NA	NA	NA	NA	0	0	3.64	TN	1	1	-0.02	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.06	TP	1.11	1.05	TP	NA	NA	NA
YGL202W	ARO8	Aromatic amino acid aminotransferase	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	-0.01	TP	1.08	1.01	TP	1.1	1	TP	1.11	0.99	TP	1.12	1.02	TP	1.11	1	TP	NA	NA	NA
YHR137W	ARO9	Aromatic amino acid aminotransferase II	NA	NA	NA	NA	NA	0	1	0.18	FN	1	1	-0.02	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.01	TP	1.11	1.01	TP	Iso	ARO8 should be able to complement ARO9 deletion on minimal media, but the gpr association might be wrong [Urrestarazu98].	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YDL100C	ARR4	Provides low levels of resistance to arsenicals	NA	NA	NA	NA	NA	1	1	0.4	TP	1	1	-0.01	TP	1.08	0.97	TP	1.1	0.96	TP	1.11	0.93	TP	1.12	0.91	TP	1.11	0.92	TP	NA	NA	NA
YPR145W	ASN1	Asparagine synthetase	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	-0.02	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YGR124W	ASN2	Asparagine synthetase	NA	NA	NA	NA	NA	1	1	0.07	TP	1	1	0.03	TP	1.08	1.01	TP	1.1	1	TP	1.11	1	TP	1.12	0.99	TP	1.11	0.99	TP	NA	NA	NA
YDR321W	ASP1	Asparaginase I|intracellular isozyme	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0.01	TP	1.08	1	TP	1.1	0.99	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	0.99	TP	NA	NA	NA
YPR026W	ATH1	Acid trehalase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0.04	TP	1.08	1.02	TP	1.1	1.01	TP	1.11	1	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YBL099W	ATP1	F1F0-ATPase alpha subunit	NA	NA	0.91	4	TN	0.91	1	0	TP	0.82	1	-0.03	TP	0.98	0.91	TP	0.24	0.81	TN	0.14	0.56	TN	0.16	0.49	TN	0.05	0.54	TN	NA	NA	NA
YLR295C	ATP14	ATP synthase subunit h	NA	NA	0.91	4.7	TN	0.91	1	0	TP	0.82	1	-0.01	TP	0.98	0.73	FP	0.24	0.59	TN	0.14	0.56	TN	0.16	0.52	TN	0.05	0.5	TN	Oth	Mitochondrial maintenance not required in the model in primarily fermentative conditions.	NA
YPL271W	ATP15	ATP synthase epsilon subunit|nuclear encoded	NA	NA	0.91	9.5	TN	0.91	1	-0.03	TP	0.82	1	-0.03	TP	0.98	0.72	FP	0.24	0.69	TN	0.14	0.58	TN	0.16	0.54	TN	0.05	0.57	TN	Oth	Mitochondrial maintenance not required in the model in primarily fermentative conditions.	NA
YDL004W	ATP16	ATP synthase delta subunit	0.91	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	In silico slow growth.	NA
YDR377W	ATP17	ATP synthase subunit f	NA	NA	0.91	3.3	TN	0.91	1	-0.03	TP	0.82	1	-0.04	TP	0.98	0.83	FP	0.24	0.78	TN	0.14	0.66	TN	0.16	0.66	TN	0.05	0.69	TN	Oth	Mitochondrial maintenance not required in the model in primarily fermentative conditions.	NA
YML081CA	ATP18	ATP synthase associated protein	NA	NA	NA	NA	NA	0.91	1	-0.02	TP	0.82	1	0.15	TP	0.98	1.03	TP	0.24	0.96	FN	0.14	0.65	TN	0.16	0.63	TN	0.05	0.65	TN	Med	This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium.	NA
YJR121W	ATP2	F(1)F(0)-ATPase complex beta subunit	NA	NA	NA	NA	NA	0.91	1	0	TP	0.82	1	-0.02	TP	0.98	0.86	FP	0.24	0.82	TN	0.14	0.51	TN	0.16	0.55	TN	0.05	0.53	TN	Med	This is close enough to count as a correct prediction. With small changes in uptake rates this would be true negative.	NA
YPR020W	ATP20	ATP synthase subunit g homolog	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.02	TP	1.08	1	TP	1.1	0.98	TP	1.11	0.94	TP	1.12	0.95	TP	1.11	0.94	TP	NA	NA	NA
YPL078C	ATP4	F(1)F(0)-ATPase complex subunit b	NA	NA	0.91	4.1	TN	0.91	1	0.19	TP	0.82	1	0.15	TP	0.98	0.83	FP	0.24	0.77	TN	0.14	0.52	TN	0.16	0.51	TN	0.05	0.54	TN	Oth	Mitochondrial maintenance not required in the model in primarily fermentative conditions.	NA
YDR298C	ATP5	ATP synthase subunit 5|oligomycin sensitivity-conferring protein	NA	NA	0.91	7.7	TN	0.91	1	-0.03	TP	0.82	1	-0.02	TP	0.98	0.75	FP	0.24	0.66	TN	0.14	0.53	TN	0.16	0.53	TN	0.05	0.57	TN	Oth	Mitochondrial maintenance not required in the model in primarily fermentative conditions.	NA
YKL016C	ATP7	ATP synthase d subunit	NA	NA	0.91	3.7	TN	0.91	1	-0.03	TP	0.82	1	0.02	TP	0.98	0.76	FP	0.24	0.64	TN	0.14	0.48	TN	0.16	0.44	TN	0.05	0.59	TN	Oth	Mitochondrial maintenance not required in the model in primarily fermentative conditions.	NA
YKL004W	AUR1	Involved in phospholipid metabolism	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Sphingolipid synthesis not required in the model	FP
YOR011W	AUS1	ATP-binding cassette (ABC) family	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.02	TP	1.11	1.03	TP	NA	NA	NA
YBR068C	BAP2	Amino acid permease for leucine, valine, and isoleucine (putative)	NA	NA	NA	NA	NA	1	1	0.81	TP	1	1	-0.06	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YDR046C	BAP3	Valine transporter	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.04	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.06	TP	1.11	1.05	TP	NA	NA	NA
YJR148W	BAT2	Branched-chain amino acid transaminase	NA	NA	NA	NA	NA	0	1	-0.04	FN	1	1	-0.01	TP	0.69	1.03	FN	1.1	1.04	TP	1.11	1.04	TP	1.12	1.06	TP	1.11	1.05	TP	Iso	BAT2 single deletion should not be lethal as there is a mitochondrial isozyme (BAT1) - double deletion should be lethal. Bat1p currently does not catalyze valine transamination so this functionality should probably be added [Kispal96].	NA
YPR176C	BET2	Geranylgeranyltransferase type II beta subunit	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Quinone biosynthesis is not required in the model.	FP
YJL031C	BET4	Geranylgeranyltransferase type II alpha subunit (PGGTase-II, alpha subunit)	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Quinone biosynthesis is not required in the model.	NA
YGR282C	BGL2	Cell wall endo-beta-1,3-glucanase	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	0.03	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.04	TP	NA	NA	NA
YGR286C	BIO2	Biotin synthase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.02	TP	1.08	1.01	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	0.99	TP	1.11	0.99	TP	NA	NA	NA
YNR058W	BIO3	7,8-diamino-pelargonic acid aminotransferase (DAPA) aminotransferase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.02	TP	1.08	1.04	TP	1.1	1.04	TP	1.11	1.02	TP	1.12	1.06	TP	1.11	1.04	TP	NA	NA	NA
YNR057C	BIO4	Dethiobiotin synthetase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.01	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YNR056C	BIO5	Transmembrane regulator of KAPA/DAPA transport	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0.08	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YJR025C	BNA1	3-hydroxyanthranilic acid dioxygenase	NA	NA	NA	NA	NA	1	1	-0.06	TP	1	1	-0.01	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YJR078W	BNA2	Tryptophan 2,3-dioxygenase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.02	TP	1.08	1.01	TP	1.1	1.05	TP	1.11	1.05	TP	1.12	1.08	TP	1.11	1.06	TP	NA	NA	NA
YBL098W	BNA4	Kynurenine 3-mono oxygenase	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	0.02	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YLR231C	BNA5	Kynureninase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.01	TP	1.08	1.03	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.06	TP	1.11	1.04	TP	NA	NA	NA
YFR047C	BNA6	Quinolinate phosphoribosyl transferase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1	TP	1.11	0.99	TP	1.12	1.01	TP	1.11	1	TP	NA	NA	NA
YCR032W	BPH1	Beige protein homologue 1	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.07	TP	1.08	1.02	TP	1.05	1.06	TP	1.11	1.05	TP	1.1	1.07	TP	1.11	1.07	TP	NA	NA	NA
YEL063C	CAN1	Arginine permease	NA	NA	NA	NA	NA	1	1	0.1	TP	1	1	-0.03	TP	1.08	0.99	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YPL111W	CAR1	Arginase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1.02	TP	0.99	1	TP	1.11	0.98	TP	1.03	0.97	TP	NA	NA	NA
YLR438W	CAR2	Ornithine aminotransferase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0.11	TP	1.08	1.02	TP	1.1	1.03	TP	1.01	0.98	TP	1.11	1	TP	1.05	0.98	TP	NA	NA	NA
YML042W	CAT2	Carnitine O-acetyltransferase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.06	TP	1.11	1.04	TP	NA	NA	NA
YLR307W	CDA1	Chitin deacetylase	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	0.06	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.03	TP	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YLR308W	CDA2	Chitin deacetylase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	0.23	TP	1.08	1.02	TP	1.1	1	TP	1.11	1	TP	1.12	0.98	TP	1.11	1	TP	NA	NA	NA
YAL038W	CDC19	Pyruvate kinase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Reg	Model has Pyk2p as an isozyme. Pyk2p may only be expressed under conditions of very low glycolytic flux [MIPS]	FP
YOR074C	CDC21	Thymidylate synthase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Essential for nuclear and mitochondrial biosynthesis, which are not required in our model.	NA
YGL155W	CDC43	Protein geranylgeranyltransferase type 1 polypeptide subunit	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Quinone biosynthesis is not required in the model.	NA
YPL160W	CDC60	Leucine--tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YJR057W	CDC8	Thymidylate kinase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Essential for DNA synthesis, which is not required in our model.	FP
YBR029C	CDS1	Phosphatidate cytidylyltransferase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YER061C	CEM1	Beta-keto-acyl synthase homolog	NA	NA	NA	NA	NA	1	1	0.55	TP	1	1	0.05	TP	1.08	0.81	FP	1.1	0.77	FP	1.11	0.57	FP	1.12	0.54	FP	1.11	0.54	FP	Oth	Cem1p is involved in the synthesis of a specialized molecule related to fatty acids, which is essential for mitochondrial function.	NA
YCL064C	CHA1	Catabolic serine (threonine) dehydratase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.04	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YGR157W	CHO2	Phosphatidyl-ethanolamine N-methyltransferase	NA	NA	NA	NA	NA	0	1	-0.03	FN	0	1	-0.01	FN	0	1.01	FN	0	1	FN	0	0.97	FN	0	0.98	FN	0	0.99	FN	Bio	Catalyzes 1st step in pathway from PE to PC. Opi3p can also catalyze this step, but it is very inefficient; mutant cells are viable and not auxotrophic for choline or other phospholipid intermediates; membranes of mutants contain 10% PC and 40-50% PE (WT is 40-45% PC and 15-20% PE); this deletion is lethal in silico since we require fixed amounts of these specific phospholipids in our biomass (in vivo there is flexibility as to which phospholipids are used).	FN
YNL192W	CHS1	Chitin synthase 1	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.03	TP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YBR038W	CHS2	Chitin synthase 2	1	FP	NA	NA	NA	1	1	0	TP	1	1	-0.03	TP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Dis	Gene is listed as essential, but there is data for MMD and YPGal. In any case chitin synthesis is not required in the model.	NA
YBR023C	CHS3	Chitin synthase 3	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1	TP	1.11	1.01	TP	1.12	0.99	TP	1.11	1.01	TP	NA	NA	NA
YNR001C	CIT1	Citrate synthase	NA	NA	NA	NA	NA	1	1	0.19	TP	1	1	-0.02	TP	1.08	0.99	TP	1.1	0.96	TP	1.11	0.79	TP	1.12	0.92	TP	1.11	0.81	TP	NA	NA	NA
YCR005C	CIT2	Citrate synthase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.07	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YPR001W	CIT3	Citrate synthase	NA	NA	NA	NA	NA	1	1	0.21	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YLR133W	CKI1	Choline kinase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0	TP	1.08	0.99	TP	1.1	1.01	TP	1.11	1.04	TP	1.12	1.08	TP	1.11	1.05	TP	NA	NA	NA
YBR003W	COQ1	Hexaprenyl pyrophosphate synthetase	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0.09	TP	1.08	0.95	TP	1.1	0.83	FP	1.11	0.48	FP	1.12	0.45	FP	1.11	0.58	FP	Bio	Quinone biosynthesis is not required in the model.	NA
YNR041C	COQ2	Para hydroxybenzoate: polyprenyl transferase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0.11	TP	1.08	0.95	TP	1.1	0.91	TP	1.11	0.56	FP	1.12	0.54	FP	1.11	0.52	FP	Bio	Quinone biosynthesis is not required in the model.	NA
YOL096C	COQ3	3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase	NA	NA	1	4.3	FP	1	1	0.21	TP	1	1	0.06	TP	1.08	0.85	FP	1.1	0.78	FP	1.11	0.51	FP	1.12	0.49	FP	1.11	0.57	FP	Bio	Quinone biosynthesis is not required in the model.	NA
YML110C	COQ5	C-methyltransferase (putative)	NA	NA	1	4.7	FP	1	1	-0.04	TP	1	1	-0.02	TP	1.08	0.77	FP	1.1	0.64	FP	1.11	0.53	FP	1.12	0.52	FP	1.11	0.49	FP	Bio	Quinone biosynthesis is not required in the model	NA
YGR255C	COQ6	Monooxygenase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0.11	TP	1.08	0.87	FP	1.1	0.8	FP	1.11	0.5	FP	1.12	0.52	FP	1.11	0.58	FP	Bio	Quinone biosynthesis is not required in the model	NA
YBL045C	COR1	Coenzyme QH2 cytochrome c reductase 44 kDa core protein subunit	NA	NA	0.9	4	TN	0.89	1	-0.03	TP	0.82	1	-0.03	TP	0.98	0.82	FP	0.24	0.77	TN	0.14	0.5	TN	0.08	0.47	TN	0.17	0.54	TN	Oth	Mitochondrial maintenance not required in the model in primarily fermentative conditions.	NA
YPL172C	COX10	Farnesyl transferase (putative)	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0.4	TP	1.08	0.97	TP	1.1	0.94	TP	1.11	0.59	FP	1.12	0.54	FP	1.11	0.61	FP	Bio	Quinone biosynthesis is not required in the model	NA
YLR038C	COX12	Cytochrome c oxidase subunit VIb	NA	NA	NA	NA	NA	0.89	1	0.31	TP	0.82	1	0.02	TP	0.98	0.98	TP	0.24	0.91	FN	0.14	0.55	TN	0.08	0.5	TN	0.05	0.57	TN	Med	This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium.	NA
YNL052W	COX5A	Cytochrome c oxidase chain Va	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0.17	TP	1.08	1.02	TP	1.1	0.94	TP	1.11	0.65	FP	1.12	0.61	FP	1.11	0.68	FP	Iso	COX5A is the dominant isoform - COX5B cannot fully compensate [SGD].	NA
YIL111W	COX5B	Cytochrome c oxidase chain Vb	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.05	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YHR051W	COX6	Cytochrome c oxidase subunit	NA	NA	NA	NA	NA	0.89	1	-0.04	TP	0.82	1	-0.01	TP	0.98	0.82	FP	0.24	0.73	TN	0.14	0.62	TN	0.08	0.61	TN	0.05	0.63	TN	Med	Higher oxygen uptake rate or lower glucose uptake rate will make this deleterious in the model.	NA
YMR256C	COX7	Cytochrome c oxidase subunit VII	NA	NA	0.9	3.6	TN	0.89	1	-0.03	TP	0.82	1	0	TP	0.98	0.8	FP	0.24	0.74	TN	0.14	0.71	TN	0.08	0.69	TN	0.05	0.69	TN	Oth	Mitochondrial maintenance not required in the model in primarily fermentative conditions.	NA
YLR395C	COX8	Cytochrome c oxidase chain VIII	NA	NA	NA	NA	NA	0.89	1	-0.04	TP	0.82	1	-0.03	TP	0.98	1.01	TP	0.24	0.99	FN	0.14	0.91	FN	0.08	0.91	FN	0.05	0.94	FN	Dis	Null mutant is viable, but should be deficient in cellular respiration and cytochrome C oxidase activity [SGD] so there should be a growth defect on non-fermentable carbon sources.	NA
YDL067C	COX9	Cytochrome c oxidase subunit VIIa	NA	NA	NA	NA	NA	0.89	1	0.14	TP	0.82	1	0.05	TP	0.98	0.82	FP	0.24	0.75	TN	0.14	0.53	TN	0.08	0.5	TN	0.05	0.52	TN	Med	Higher oxygen uptake rate or lower glucose uptake rate will make this deleterious in the model.	NA
YOR303W	CPA1	Arginine specific|carbamoyl phosphate synthetase	NA	NA	NA	NA	NA	0	1	6.82	TN	1	1	-0.1	TP	1.08	1.02	TP	1.1	0.98	TP	1.11	0.98	TP	1.12	0.98	TP	1.1	0.98	TP	NA	Weak false negative	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YJR109C	CPA2	Carbamyl phosphate synthetase	NA	NA	NA	NA	NA	0	1	8.21	TN	1	1	0.07	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.04	TP	1.1	1.04	TP	NA	Weak false negative	NA
YNL130C	CPT1	Sn-1,2-diacylglycerol cholinephosphotransferase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.04	TP	1.08	1	TP	1.1	1	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	0.99	TP	NA	NA	NA
YOR100C	CRC1	Carnitine transporter	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YDL142C	CRD1	Cardiolipin synthase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.02	TP	1.08	0.98	TP	1.1	0.99	TP	1.11	0.93	TP	1.12	0.85	TP	1.11	0.93	TP	NA	NA	NA
YBR036C	CSG2	Required for mannosylation of inositolphosphorylceramide (IPC)	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.01	TP	1.11	0.98	TP	1.12	0.99	TP	1.11	1.01	TP	NA	NA	NA
YDR256C	CTA1	Catalase A	NA	NA	NA	NA	NA	1	1	0.28	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.01	TP	1.11	0.99	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YBR291C	CTP1	Citrate tranporter	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	0.21	TP	1.08	0.99	TP	1.1	0.98	TP	1.11	0.96	TP	0.79	0.93	FN	1.08	0.93	TP	Med	Lower oxygen uptake rate would correct this false negative prediction.	NA
YGR088W	CTT1	Catalase T	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.07	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YEL027W	CUP5	17 kDa|VO sector subunit|dicyclohexylcarbodiimide binding subunit|proteolipid|vacuolar ATP synthase proteolipid C|vacuolar ATPase V0 domain subunit c (dicyclohexylcarbodiimide binding subunit) (17 kDa)	NA	NA	1	17.9	FP	1	1	-0.01	TP	1	1	0	TP	1.08	0.72	FP	1.1	0.62	FP	1.11	0.53	FP	1.12	0.58	FP	1.11	0.58	FP	Oth	The cup5 null mutant is viable but lacks vacuolar (H)-ATPase activity, and is defective in vacuolar acidification, vacuole biogenesis, vacuolar protein targeting, and endocytosis [SGD]. The slow growth phenotype could be due to problems in pH balancing.	NA
YML054C	CYB2	L-lactate cytochrome c oxidoreductase|cytochrome b2	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.06	TP	1.12	1.08	TP	0.64	1.07	FN	Med	Lower oxygen uptake rate would correct this false negative prediction.	NA
YJL005W	CYR1	Adenylate cyclase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	cAMP synthesis not required in model as its primarily used as a signaling molecule.	FP
YAL012W	CYS3	Cystathionine gamma-lyase	NA	NA	NA	NA	NA	1	1	0.29	TP	1	1	0.63	TP	1.08	0.94	TP	1.1	0.9	TP	1.11	0.67	FP	1.12	0.77	FP	1.11	0.88	TP	Med	This reaction is not used in complete media, because cysteine is available. Should only be a cysteine auxotroph [SGD].	NA
YGR155W	CYS4	Cystathionine beta-synthase	NA	NA	1	3.7	FP	1	1	0.11	TP	1	1	0.17	TP	1.08	0.91	TP	1.1	0.9	TP	1.11	0.71	FP	1.12	0.72	FP	1.11	0.83	TP	Oth	CYS4 null mutant is deficient in vacuolar ATPase activity and vacuolar acidification [MIPS]. The false positives could be due to pH balancing, which is not accounted for in the model.	NA
YOR065W	CYT1	Cytochrome c1	NA	NA	NA	NA	NA	0.89	1	0.02	TP	0.82	1	0.23	TP	0.98	0.96	TP	0.24	0.92	FN	0.14	0.62	TN	0.08	0.57	TN	0.17	0.61	TN	Med	This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium.	NA
YML070W	DAK1	Dihydroxyacetone kinase (putative)	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	0	TP	1.08	0.99	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YFL053W	DAK2	Dihydroxyacetone kinase	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	-0.06	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YIR027C	DAL1	Allantoinase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YIR029W	DAL2	Allantoicase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.05	TP	1.08	1.03	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.07	TP	1.11	1.05	TP	NA	NA	NA
YIR032C	DAL3	Ureidoglycolate hydrolase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0	TP	1.08	1.02	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	0.99	TP	1.11	0.99	TP	NA	NA	NA
YIR028W	DAL4	Allantoin permease	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	0.05	TP	1.08	1.02	TP	1.1	1	TP	1.11	0.99	TP	1.12	1.01	TP	1.11	1	TP	NA	NA	NA
YJR152W	DAL5	Allantoate permease	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.01	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.04	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YIR031C	DAL7	Malate synthase 2	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0	TP	1.08	1.02	TP	1.1	0.98	TP	1.11	0.98	TP	1.12	0.98	TP	1.11	0.98	TP	NA	NA	NA
YHR019C	DED81	Asparaginyl-tRNA synthetase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	FP
YFL001W	DEG1	Similar to rRNA methyltransferase (Caenorhabditis elegans) and hypothetical 28K protein (alkaline endoglucanase gene 5' region) from Bacillus sp.	NA	NA	1	3.5	FP	1	1	-0.02	TP	1	1	-0.02	TP	1.08	0.86	FP	1.1	0.79	FP	1.11	0.8	TP	1.12	0.8	TP	1.11	0.81	TP	Oth	Pseudouridine biosynthesis not required in the model.	NA
YOR236W	DFR1	Dihydrofolate reductase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Acc	Folate biosynthesis is not required in rich media. Lethality may be due to toxicity of DHP [Bayly02].	FP
YHR011W	DIA4	Protein similar to bacterial seryl-tRNA synthases	NA	NA	1	6.5	FP	1	1	-0.04	TP	1	1	0.19	TP	1.08	0.74	FP	1.1	0.65	FP	1.11	0.54	FP	1.12	0.44	FP	1.11	0.49	FP	Oth	Protein synthesis not included in the model.	NA
YLR348C	DIC1	Dicarboxylate transport protein	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.03	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YPL266W	DIM1	Dimethyladenosine transferase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Quinone biosynthesis is not required in the model	FP
YPL265W	DIP5	Dicarboxylic amino acid permease	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0.03	TP	1.08	0.99	TP	1.1	0.96	TP	1.11	0.87	TP	1.12	0.81	TP	1.11	0.88	TP	NA	NA	NA
YDL174C	DLD1	D-lactate ferricytochrome c oxidoreductase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.04	TP	1.11	1.04	TP	NA	NA	NA
YLR172C	DPH5	Diphthamide biosynthesis	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.02	TP	1.08	0.99	TP	1.1	0.99	TP	1.11	1	TP	1.12	1.02	TP	1.11	1	TP	NA	NA	NA
YDR294C	DPL1	Dihydrosphingosine phosphate lyase (also known as sphingosine phosphate lyase)	NA	NA	NA	NA	NA	1	1	0.06	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YPR183W	DPM1	Dolichol phosphate mannose synthase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YDR284C	DPP1	Diacylglycerol pyrophosphate phosphatase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	FN

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YLL018C	DPS1	Aspartyl-tRNA synthetase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YBR208C	DUR1,	Urea amidolyase (contains urea carboxylase and allophanate hydrolase)	NA	NA	NA	NA	NA	1	1	0.11	TP	1	1	0.02	TP	1.08	1	TP	1.1	0.98	TP	1.11	0.96	TP	1.12	0.97	TP	1.11	0.98	TP	NA	NA	NA
YHL016C	DUR3	Urea active transport protein	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.02	TP	1.07	1.03	TP	1.11	1.04	TP	1.07	1.02	TP	NA	NA	NA
YBR252W	DUT1	DUTP pyrophosphatase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Converts dUTP to dUMP preventing uracil incorporation into DNA [MIPS]. Since we do not include DNA replication in our model, this function is unnecessary.	FP
YHR068W	DYS1	Deoxyhypusine synthase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Dys1p catalyzes first two steps in hypusine biosynthesis. Hypusine is required in our model.	FP
YJR137C	ECM17	Sulfite reductase (putative)	NA	NA	NA	NA	NA	1	1	2.28	TP	1	1	0.06	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YBR176W	ECM31	ExtraCellular Mutant	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.06	TP	1.11	1.04	TP	NA	NA	NA
YLR299W	ECM38	Gamma-glutamyltransferase homolog	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0.07	TP	1.08	1.01	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	0.98	TP	1.11	0.98	TP	NA	NA	NA
YMR062C	ECM40	Acetylornithine acetyltransferase	NA	NA	NA	NA	NA	0	1	2.04	TN	1	1	-0.01	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1	TP	1.12	1.01	TP	1.11	1.01	TP	NA	Weak false negative	NA
YDR147W	EKI1	Ethanolamine kinase	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0	TP	1.08	1.02	TP	1.1	1	TP	1.11	1	TP	1.12	0.98	TP	1.11	1	TP	NA	NA	NA
YGR254W	ENO1	Enolase I	NA	NA	NA	NA	NA	1	1	-0.06	TP	1	1	-0.07	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YHR123W	EPT1	Sn-1,2-diacylglycerol ethanolamine- and cholinephosphotranferase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YGR175C	ERG1	Squalene monooxygenase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YPL028W	ERG10	Acetoacetyl CoA thiolase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	FP
YHR007C	ERG11	Cytochrome P450 lanosterol 14a-demethylase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YMR208W	ERG12	Mevalonate kinase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YML126C	ERG13	3-hydroxy-3-methylglutaryl coenzyme A synthase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0	0.96	FN	0	0.91	FN	0	0.92	FN	0	0.9	FN	0	0.9	FN	Dis	Deletion of ERG13 is lethal [Daum98]. Discrepancy between the two experimental studies.	FP
YMR202W	ERG2	C-8 sterol isomerase	NA	NA	1	3.2	FP	1	1	0.54	TP	1	1	0.16	TP	1.08	0.92	TP	1.1	0.76	FP	1.11	0.86	TP	1.12	0.75	FP	1.11	0.73	FP	Mod	Ergosterol can be synthesized by the model from zymosterol, which bypasses the reaction catalyzed by the ERG2 gene product. This bypass is probably incorrect.	NA
YJL167W	ERG20	Farnesyl diphosphate synthetase (FPP synthetase)	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YNL280C	ERG24	Sterol C-14 reductase	NA	NA	0	7	TN	0	1	0.11	TN	0	1	0	TN	0	0.79	TN	0	0.62	TN	0	0.7	TN	0	0.55	TN	0	0.68	TN	NA	NA	NA
YGR060W	ERG25	C-4 sterol methyl oxidase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YGL001C	ERG26	C-3 sterol dehydrogenase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YLR100W	ERG27	3-keto sterol reductase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YLR056W	ERG3	C-5 sterol desaturase	NA	NA	1	5.5	FP	1	1	0.06	TP	1	1	-0.04	TP	1.08	0.92	TP	1.1	0.9	TP	1.11	0.82	TP	1.12	0.84	TP	1.11	0.92	TP	Mod	Ergosterol can be synthesized by the model from zymosterol, which bypasses the reaction catalyzed by the ERG3 gene product. This bypass is probably incorrect.	FN
YGL012W	ERG4	Sterol C-24 reductase	NA	NA	NA	NA	NA	0	1	0.03	FN	0	1	0	FN	0	0.96	FN	0	0.96	FN	0	0.93	FN	0	1.01	FN	0	0.95	FN	Bio	Erg4p catalyzes the last step in the synthesis of ergosterol. when it is deleted, the precursor accounts for 90% of the cell's sterol composition, suggesting that Erg4p is the only enzyme that can catalyze this reaction; ergosterol is completely replaced by its precursor in the plasma membrane of erg4 mutants; the mutant is viable, but there are distinct defects relating to drug sensitivity [Zweytick00]; thus, this FN is a result of our biomass function, which requires ergosterol.	FN
YMR015C	ERG5	Cytochrome P450|involved in C-22 denaturation of the ergosterol side-chain	NA	NA	NA	NA	NA	1	1	0.14	TP	1	1	-0.1	TP	1.08	1	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.03	TP	1.11	1.04	TP	NA	NA	FN
YML008C	ERG6	Ergosterol synthesis	NA	NA	1	3.2	FP	1	1	0.36	TP	1	1	0.02	TP	1.08	0.84	FP	1.1	0.81	FP	1.11	0.82	TP	1.12	0.78	TP	1.11	0.72	FP	Mod	Ergosterol can be synthesized by the model from zymosterol, which bypasses the reaction catalyzed by the ERG6 gene product. This bypass is probably incorrect.	FN
YHR072W	ERG7	2,3-oxidosqualene-lanosterol cyclase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YMR220W	ERG8	48 kDa phosphomevalonate kinase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YHR190W	ERG9	Squalene synthetase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YLR300W	EXG1	Exo-1,3-beta-glucanase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YDR261C	EXG2	Exo-1,3-beta-glucanase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.02	TP	1.08	1	TP	1.1	1	TP	1.11	1	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YOR317W	FAA1	Long chain fatty acyl:CoA synthetase	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YIL009W	FAA3	Acyl-CoA synthase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.01	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.03	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YMR246W	FAA4	Long chain fatty acyl:CoA synthetase|long-chain fatty acid:CoA ligase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.04	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YFR019W	FAB1	1-phosphatidylinositol-3-phosphate 5-kinase	NA	NA	1	8.3	FP	1	1	0	TP	1	1	-0.03	TP	1.08	0.63	FP	1.1	0.73	FP	1.11	0.55	FP	1.12	0.5	FP	1.11	0.54	FP	Oth	Mutation causes pleiotropic effects on nuclear migration and orientation, and separation of mitotic chromosomes (forms aploid and binucleate cells).Mutant has defects in vacuolar function and morphology [SGD].	NA
YDL045C	FAD1	FAD synthetase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Riboflavin biosynthesis is not required in the model	FP
YKL182W	FAS1	Acetyl transferase|dehydratase|enoyl reductase|malonyl/palmityl transferase|pentafunctional enzyme	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YPL231W	FAS2	Fatty acid synthase alpha subuni	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YBR041W	FAT1	Fatty acid transporter	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.01	TP	1.08	1.01	TP	1.1	1	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YER183C	FAU1	5,10-methenyltetrahydrofolate synthetase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.02	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YKL060C	FBA1	Aldolase	0.19	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	In silico slow growth.	NA
YLR377C	FBP1	Fructose-1,6-bisphosphatase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0	TP	1.08	1	TP	1.1	1	TP	1.11	0.85	TP	0.41	0.84	FN	0.89	0.88	TP	Med	Lower oxygen uptake rate would correct this false negative prediction.	NA
YJL155C	FBP26	Fructose-2,6-bisphosphatase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	0.96	TP	1.12	0.91	TP	1.11	0.92	TP	NA	NA	NA
YPR062W	FCY1	Cytosine deaminase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.07	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YER056C	FCY2	Purine-cytosine permease	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.04	TP	1.08	0.97	TP	1.1	1	TP	1.11	1.04	TP	1.12	1.02	TP	1.11	1.03	TP	NA	NA	NA
YER060W	FCY21	Purine-cytosine permease	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.01	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.04	TP	1.12	1.02	TP	1.11	1.03	TP	NA	NA	NA
YER060WA	FCY22	Purine-cytosine permease	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	0.01	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.04	TP	1.11	1.04	TP	NA	NA	NA
YCR034W	FEN1	1,3-beta-glucan synthase subunit (putative)|ELO1 homolog	NA	NA	NA	NA	NA	0	1	0.36	FN	0	1	-0.05	FN	0	0.93	FN	0	0.94	FN	0	0.92	FN	0	0.81	FN	0	0.94	FN	Bio	Involved in synthesis of 1,3-beta-glucan, probable beta-1,3-glucan synthase subunit - unknown whether it is a catalytic subunit or GTP-binding subunit. Membranes of mutant cells have 90% less beta-1,3-glucan synthase activity - could an alternate subunit exist? This is lethal in silico because beta-1,3-glucan is required in biomass.	NA
YCR028C	FEN2	Plasma Membrane H+-Pantothenate Symporter	NA	NA	1	3.1	FP	1	1	0.11	TP	1	1	0	TP	1.08	0.8	FP	1.1	0.8	FP	1.11	0.83	TP	1.12	0.77	FP	1.11	0.72	FP	Oth	Pantothenate is necessary for CoA biosynthesis, which is not required by the model.	NA
YLR342W	FKS1	1,3-beta-D-glucan synthase	NA	NA	1	4.5	FP	1	1	-0.01	TP	1	1	0	TP	1.08	0.62	FP	1.1	0.74	FP	1.11	0.84	TP	1.12	0.84	TP	1.11	0.87	TP	Iso	There are three alternate isozymes in the model, but FKS1 deletion experimentally disrupts the enzymatic function significantly.	NA
YMR306W	FKS3	Protein with similarity to Gls1p and Gls2p (GB:Z49212)	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA
YIL134W	FLX1	FAD carrier protein	NA	NA	1	3.4	FP	1	1	-0.02	TP	1	1	-0.01	TP	1.08	0.99	TP	1.1	1.03	TP	1.11	1.07	TP	1.12	1.03	TP	1.11	0.99	TP	Dis	There is no evidence of significant deleterious phenotype. Experimentally flx1 strain has low FMN/FAD ratio [MIPS]. The two studies also show conflicting results.	NA
YDR236C	FMN1	Riboflavin kinase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Riboflavin biosynthesis is not required in the model	FP
YBL013W	FMT1	Methionyl-tRNA transformylase	NA	NA	NA	NA	NA	1	1	0.42	TP	1	1	-0.03	TP	1.08	1.03	TP	1.1	1.04	TP	1.11	0.95	TP	1.12	0.97	TP	1.11	0.94	TP	NA	NA	NA
YNL256W	FOL1	Dihydro-6-hydroxymethylpterin pyrophosphokinase|dihydroneopterin aldolase|dihydropteroate synthetase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Acc	Folate biosynthesis is not required in rich media. Lethality may be due to toxicity of DHP [Bayly02].	FP
YGR267C	FOL2	GTP-cyclohydrolase I	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Acc	Folate biosynthesis is not required in rich media. Lethality may be due to toxicity of DHP [Bayly02].	FP
YMR113W	FOL3	Dihydrofolate synthetase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Acc	Folate biosynthesis is not required in rich media. Lethality may be due to toxicity of DHP [Bayly02].	FP
YKR009C	FOX2	Multifunctional beta-oxidation protein	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.07	TP	1.08	1.03	TP	1.1	1.05	TP	1.11	1.04	TP	1.12	1.07	TP	1.11	1.06	TP	NA	NA	NA
YLL043W	FPS1	Glycerol channel proteir	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.04	TP	1.08	0.99	TP	1.08	1.02	TP	0.9	1.05	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YLR060W	FRS1	Phenylalanine-tRNA ligase subuni	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YFL022C	FRS2	Phenylalanine-tRNA ligase subuni	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YBL042C	FUI1	Uridine permease	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.01	TP	1.08	0.94	TP	1.1	0.89	TP	1.11	0.88	TP	1.12	0.82	TP	1.11	0.94	TP	NA	NA	NA
YPL262W	FUM1	Fumarase (fumarate hydralase)	NA	NA	NA	NA	NA	1	1	0.7	TP	1	1	0.04	TP	1.08	0.97	TP	1.08	0.96	TP	0.96	0.73	FP	0.59	0.82	FN	0.95	0.71	FP	Unk	The model predicts a reduced growth rate, but the drop is not that large.	NA
YMR250W	GAD1	Glutamate decarboxylase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.08	TP	1.12	1.08	TP	1.11	1.07	TP	NA	NA	NA
YBR020W	GAL1	Galactokinase	NA	NA	NA	NA	NA	1	1	-0.01	TP	0.18	1	2.08	TN	1.08	0.99	TP	1.1	0.97	TP	1.11	0.99	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA
YBR019C	GAL10	UDP-glucose 4-epimerase	NA	NA	NA	NA	NA	1	1	-0.01	TP	0.18	0	3.14	TN	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	0.99	TP	1.11	0.99	TP	NA	NA	NA
YLR081W	GAL2	Galactose permease	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	0	1.52	FP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.04	TP	Iso	Gal2p is the high-affinity galactose transporter, which is known to be a major player in gal transport. Deletion of GAL2 drastically reduces growth on galactose [Douglas64]. Model includes other isozymes (HXT genes) that are not nearly as efficient for gal transport so disabling their gal transport ability should result correct prediction.	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YBR018C	GAL7	Galactose-1-phosphate uridyl transferase	NA	NA	NA	NA	NA	1	1	-0.02	TP	0.18	0	5.37	TN	1.08	1.01	TP	1.1	1.01	TP	1.11	1	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YKR039W	GAP1	General amino acid permease	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YDR019C	GCV1	Glycine decarboxylase complex T subunit	NA	NA	NA	NA	NA	1	1	-0.03	TP	0.99	1	-0.03	TP	1.07	1.03	TP	1.09	1.05	TP	1.03	1.05	TP	0.87	1.08	TP	1.04	1.06	TP	NA	NA	NA
YMR189W	GCV2	Glycine cleavage system P subunit|glycine decarboxylase complex P subunit|glycine synthase P subunit	NA	NA	NA	NA	NA	1	1	0.02	TP	0.99	1	-0.04	TP	1.07	0.99	TP	1.09	1.01	TP	1.03	1.03	TP	0.87	1.02	TP	1.04	1.02	TP	NA	NA	NA
YAL044C	GCV3	Glycine cleavage system H-protein subunit	NA	NA	NA	NA	NA	1	1	0	TP	0.99	1	-0.01	TP	1.07	0.76	FP	1.09	0.77	FP	1.03	0.6	FP	0.87	0.58	FP	1.04	0.55	FP	Dis	Should not be deleterious except when glycine is the only nitrogen source [Nagarajan97]. Could also be due to complicated gene-protein-reaction associations.	NA
YEL042W	GDA1	Guanosine diphosphatase of Golgi membrane	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.06	TP	1.08	0.97	TP	1.1	0.97	TP	1.11	1.02	TP	1.12	0.99	TP	1.11	0.98	TP	NA	NA	NA
YOR375C	GDH1	NADP-specific glutamate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.39	TP	1	1	-0.02	TP	1.08	1	TP	1.1	1.01	TP	1.11	1	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YDL215C	GDH2	NAD-dependent glutamate dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.06	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YAL062W	GDH3	NADP-linked glutamate dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.02	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.05	TP	1.12	1.06	TP	1.11	1.05	TP	NA	NA	NA
YKL104C	GFA1	Glucoseamine-6-phosphate synthase|glutamine_fructose-6-phosphate amidotransferase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Essential for synthesis of cell wall precursors (leading to chitin biosynthesis), which are not required in the model.	FP
YCR098C	GIT1	Permease involved in the uptake of glycerophosphoinositol (GroPIns)	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.02	TP	1.08	0.97	TP	1.1	0.94	TP	1.11	0.97	TP	1.12	0.94	TP	1.11	0.97	TP	NA	NA	NA
YEL011W	GLC3	1,4-glucan-6-(1,4-glucano)-transferase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.03	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YCL040W	GLK1	Glucokinase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.02	TP	1.11	1.03	TP	NA	NA	NA
YPR035W	GLN1	Glutamine synthetase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Med	Null mutants are glutamine auxotrophs [MIPS]. The deletion is lethal if glutamine is removed from the media.	NA
YOR168W	GLN4	Glutamine-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1.08	1.03	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.06	TP	1.11	1.03	TP	Oth	Protein synthesis not required in the model	NA
YML004C	GLO1	Lactoylglutathione lyase (glyoxalase I)	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0	TP	1.08	1.03	TP	1.1	1.06	TP	1.11	1.07	TP	1.12	1.07	TP	1.11	1.07	TP	NA	NA	NA
YDR272W	GLO2	Glyoxylase-II	NA	NA	NA	NA	NA	1	1	0.07	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YOR040W	GLO4	Glyoxylase-II	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.07	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YPL091W	GLR1	Glutathione oxidoreductase|EC 1.6.4.2	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.03	TP	1.08	1	TP	1.1	1.01	TP	1.11	1	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YDL171C	GLT1	Glutamate synthase (NADH)	NA	NA	NA	NA	NA	1	1	0.29	TP	1	1	-0.07	TP	1.08	1.02	TP	1.1	1.01	TP	1.11	1	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YEL046C	GLY1	Threonine aldolase	NA	NA	1	5.5	FP	1	1	0.03	TP	1	1	0	TP	1.08	0.71	FP	1.1	0.7	FP	1.11	0.83	TP	1.12	0.77	FP	1.11	0.85	TP	Dis	Should be a glycine auxotroph when grown on glucose so that the deletion strain should grow normally in complex media [Monschau97].	NA
YFL017C	GNA1	Glucosamine-phosphate N-acetyltransferase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	N-Acetylglucosamine synthesis is not required in the model.	NA
YHR183W	GND1	6-phosphogluconate dehydrogenase, decarboxylating; converts 6-phosphogluconate + NADP to ribulose-5-phosphate + NADPH + CO2	NA	NA	1	5	FP	1	1	-0.01	TP	1	1	-0.04	TP	1.08	0.65	FP	1.1	0.82	FP	1.11	0.83	TP	1.12	0.99	TP	1.11	0.95	TP	Iso	This is the major isozyme (80% of activity) [MIPS].	NA
YGR256W	GND2	6-phosphogluconate dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0.03	TP	1.08	1.02	TP	1.1	1	TP	1.11	0.99	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YDR508C	GNP1	High affinity glutamine permease	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.05	TP	1.08	1.03	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.08	TP	1.11	1.04	TP	NA	NA	NA
YDL022W	GPD1	Glycerol-3-phosphate dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.05	TP	1.08	1.03	TP	1.1	1.06	TP	1.11	1.05	TP	1.12	1.08	TP	1.11	1.06	TP	NA	NA	NA
YOL059W	GPD2	Glycerol-3-phosphate dehydrogenase (NAD+)	NA	NA	NA	NA	NA	1	1	0.24	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YPR160W	GPH1	Glycogen phosphorylase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.02	TP	1.08	1.03	TP	1.1	1	TP	1.11	1	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YKL152C	GPM1	Phosphoglycerate mutase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Essential for sporulation, which is not required in our model.	FP
YDL021W	GPM2	Similar to GPM1 (phosphoglycerate mutase); converts 3-phosphoglycerate to 2-phosphoglycerate in glycolysis	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.06	TP	1.12	1.07	TP	1.11	1.07	TP	NA	NA	NA
YOL056W	GPM3	Phosphoglycerate mutase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.03	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YKL026C	GPX1	Glutathione peroxidase paralogue	NA	NA	NA	NA	NA	1	1	0.13	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	0.99	TP	1.12	1.01	TP	1.11	1	TP	NA	NA	NA
YBR244W	GPX2	Glutathione peroxidase paralogue	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0.05	TP	1.08	0.98	TP	1.1	0.94	TP	1.11	0.96	TP	1.12	0.98	TP	1.11	1.01	TP	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YHR104W	GRE3	Aldose reductase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.01	TP	1.08	0.99	TP	1.1	1	TP	1.11	1	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YBR121C	GRS1	Glycine-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YGR032W	GSC2	1,3-beta-D-glucan synthase catalytic component	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YJL101C	GSH1	Gamma-glutamylcysteine synthetase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0.2	TP	1.08	0.99	TP	1.1	1	TP	1.11	0.93	TP	1.12	0.94	TP	1.11	0.94	TP	NA	NA	NA
YOL049W	GSH2	Glutathione synthetase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA
YFR015C	GSY1	Glycogen synthase (UDP-glucose-starch glucosyltransferase)	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.02	TP	1.08	1.03	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.07	TP	1.11	1.04	TP	NA	NA	NA
YLR258W	GSY2	Glycogen synthase (UDP-glucose-starch glucosyltransferase)	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.07	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.05	TP	NA	NA	NA
YDR454C	GUK1	Guanylate kinase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YHL032C	GUT1	Converts glycerol to glycerol-3-phosphate|glyerol kinase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.08	TP	1.08	1	TP	1.08	1.02	TP	0.9	0.98	TP	1.12	1	TP	1.11	1.01	TP	NA	NA	NA
YIL155C	GUT2	Glycerol-3-phosphate dehydrogenase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.07	TP	1.08	1	TP	1.08	0.99	TP	0.9	0.93	TP	1.12	0.96	TP	1.11	0.99	TP	NA	NA	NA
YDR232W	HEM1	5-aminolevulinate synthase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Heme biosynthesis not required in the model	FP
YDR047W	HEM12	Uroporphyrinogen decarboxylase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Heme biosynthesis not required in the model	FP
YDR044W	HEM13	Coproporphyrinogen III oxidase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Heme biosynthesis not required in the model	FP
YER014W	HEM14	Protoporphyrinogen oxidase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1.08	0.82	FP	1.1	0.84	FP	1.11	0.85	TP	1.12	0.68	FP	1.11	0.74	FP	Acc	Heme is not required in the model. May also result in heme precursor accumulation in vivo [SGD].	NA
YOR176W	HEM15	Ferrochelatase (protoheme ferrolyase)	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1.08	1.04	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.03	TP	1.11	1.04	TP	Dis	Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates.	FP
YGL040C	HEM2	Delta-aminolevulinate dehydratase (porphobilinogen synthase)	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Heme biosynthesis not required in the model.	FP
YDL205C	HEM3	Phorphobilinogen deaminase (uroporphyrinogen synthase)	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1.08	1.04	TP	1.1	1.04	TP	1.11	1.05	TP	1.12	1.06	TP	1.11	1.03	TP	Dis	Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates.	FP
YOR278W	HEM4	Uroporphyrinogen III synthase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Heme biosynthesis not required in the model	FP
YGR191W	HIP1	Histidine permease	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Used as a histidine transporter in our model, but there are isozymes for this function. Lethality may be due to the role of Hip1p in Mg2+ transport.	FP
YER055C	HIS1	ATP phosphoribosyltransferase	NA	NA	NA	NA	NA	1	1	0.29	TP	1	1	-0.04	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1	TP	1.11	1.02	TP	NA	NA	NA
YFR025C	HIS2	Histidinolphosphatase	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	0.02	TP	1.08	1	TP	1.1	0.99	TP	1.11	1	TP	1.12	1.01	TP	1.11	1	TP	NA	NA	NA
YOR202W	HIS3	Imidazoleglycerol-phosphate dehydratase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.08	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YCL030C	HIS4	Histidinol dehydrogenase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.04	TP	1.11	1.04	TP	NA	NA	NA
YIL116W	HIS5	Histidinol-phosphate aminotransferase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.04	TP	1.12	1.02	TP	1.11	1.04	TP	NA	NA	NA
YIL020C	HIS6	Phosphoribosyl-5-amino-1-phosphoribosyl-4-imidazolecarboxiamide isomerase	NA	NA	NA	NA	NA	1	1	0.09	TP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YBR248C	HIS7	Glutamine amidotransferase:cyclase|imidazole glycerol phosphate synthase (synonym)	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	0.13	TP	1.08	1	TP	1.1	1	TP	1.11	1.01	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA
YML075C	HMG1	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme	NA	NA	NA	NA	NA	1	1	0.06	TP	1	1	-0.02	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	0.99	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YLR450W	HMG2	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0	TP	1.08	0.99	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	0.98	TP	1.11	0.98	TP	NA	NA	NA
YBR034C	HMT1	Arginine methyltransferase|mono-and asymmetrically dimethylating enzyme	NA	NA	NA	NA	NA	1	1	0.06	TP	1	1	0.04	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YGL077C	HNM1	Transporter (permease) for choline and nitrogen mustard; share homology with UGA4	NA	NA	NA	NA	NA	1	1	0.31	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	0.99	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YDR305C	HNT2	Fhit homolog, member of the histidine triad superfamily of nucleotide binding-proteins	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	0.97	TP	1.11	0.98	TP	NA	NA	NA
YDR158W	HOM2	Aspartic beta semi-aldehyde dehydrogenase	NA	NA	NA	NA	NA	1	0	10.74	FP	1	1	0	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.06	TP	1.11	1.06	TP	Unk	Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this pathway, but neither of these reactions can be removed from the model.	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YER052C	HOM3	Aspartate kinase (L-aspartate 4-P-transferase) (EC 2.7.2.4)	NA	NA	NA	NA	NA	1	0	4.46	FP	1	1	0.04	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.02	TP	1.11	1.05	TP	Unk	Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this pathway, but neither of these reactions can be removed from the model.	NA
YJR139C	HOM6	L-homoserine:NADP oxidoreductase|homoserine dehydrogenase	NA	NA	NA	NA	NA	1	0	9.11	FP	1	1	-0.03	TP	1.08	0.98	TP	1.1	0.98	TP	1.11	0.96	TP	1.12	0.91	TP	1.11	0.97	TP	Unk	Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this pathway, but neither of these reactions can be removed from the model.	NA
YER062C	HOR2	DL-glycerol-3-phosphatase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1	TP	1.11	1.01	TP	1.12	0.99	TP	1.11	1.01	TP	NA	NA	NA
YDR399W	HPT1	Hypoxanthine guanine phosphoribosyltransferase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0	TP	1.08	0.99	TP	1.1	0.99	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YPR033C	HTS1	Histidine-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	FP
YFR053C	HXK1	Hexokinase I (PI) (also called hexokinase A)	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.05	TP	1.08	1.03	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YGL253W	HXK2	Hexokinase II (PII) (also called hexokinase B)	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	0	TP	1.08	0.95	TP	1.1	1.02	TP	1.11	1.07	TP	1.12	1.07	TP	1.11	1.07	TP	NA	NA	NA
YHR094C	HXT1	Hexose transporter	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1	TP	1.11	1	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA
YFL011W	HXT10	High affinity hexose transporter	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.03	TP	1.08	1.02	TP	1.1	0.97	TP	1.11	0.98	TP	1.12	0.97	TP	1.11	0.97	TP	NA	NA	NA
YNL318C	HXT14	Hexose transporter	NA	NA	NA	NA	NA	1	1	0.1	TP	1	1	-0.06	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YNR072W	HXT17	Hexose transporter	NA	NA	NA	NA	NA	1	1	0.08	TP	1	1	-0.04	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YMR011W	HXT2	High affinity hexose transporter-2	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.06	TP	1.11	1.07	TP	1.12	1.07	TP	1.11	1.07	TP	NA	NA	NA
YDR345C	HXT3	Low affinity glucose transporter	NA	NA	NA	NA	NA	1	1	-0.06	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.04	TP	1.12	1.07	TP	1.11	1.06	TP	NA	NA	NA
YHR092C	HXT4	High affinity glucose transporter	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.06	TP	1.12	1.06	TP	1.11	1.05	TP	NA	NA	NA
YHR096C	HXT5	Hexose transporter	NA	NA	NA	NA	NA	1	1	0.85	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YJL214W	HXT8	Hexose permease	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA
YIR037W	HYR1	Glutathione-peroxidase (putative)	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	0	TP	1.08	1	TP	1.1	0.97	TP	1.11	0.98	TP	1.12	0.96	TP	1.11	0.97	TP	NA	NA	NA
YER065C	ICL1	Isocitrate lyase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.04	TP	1.08	1	TP	1.1	1	TP	1.11	1.02	TP	0.79	0.99	FN	1.08	1	TP	Med	Lower oxygen uptake rate would correct this false negative prediction.	NA
YPR006C	ICL2	2-methylisocitrate lyase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YNL037C	IDH1	Isocitrate dehydrogenase 1 alpha-4-beta-4 subunit	NA	NA	1	4.7	FP	1	1	-0.06	TP	1	1	0.02	TP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Unk	The model does not utilize this part of the TCA cycle.	NA
YOR136W	IDH2	NAD-dependent isocitrate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.96	TP	1	1	0.17	TP	1.08	0.99	TP	1.1	0.88	TP	1.11	0.68	FP	1.12	0.78	TP	1.11	0.6	FP	Unk	The model does not use the corresponding reaction when grown on glycerol or lactate. In vivo there is a NAD/NADH balancing issue.	NA
YPL117C	IDI1	Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP isomerase)	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YDL066W	IDP1	NADP-dependent isocitrate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.12	TP	1	1	0.03	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.07	TP	1.12	1.05	TP	1.11	1.09	TP	NA	NA	NA
YLR174W	IDP2	NADP-dependent isocitrate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0	TP	1.08	1	TP	1.1	1.01	TP	1.11	0.99	TP	1.12	1	TP	1.11	0.98	TP	NA	NA	NA
YNL009W	IDP3	NADP-dependent isocitrate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.02	TP	1.08	1.04	TP	1.1	1	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YBL076C	ILS1	Isoleucine-tRNA synthetase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YER086W	ILV1	Threonine deaminase	NA	NA	NA	NA	NA	0	0	10.66	TN	1	1	-0.01	TP	0.95	0.99	TP	1.1	0.98	TP	1.11	1.01	TP	1.12	0.96	TP	1.11	0.98	TP	NA	NA	NA
YJR016C	ILV3	Dihydroxyacid dehydratase	0.64	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	In silico slow growth.	FP
YLR355C	ILV5	Acetohydroxyacid reductoisomerase	0.64	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	In silico slow growth.	FP
YCL009C	ILV6	Acetolactate synthase regulatory subunit	NA	NA	NA	NA	NA	0	1	-0.01	FN	1	1	0	TP	0.69	1.01	FN	1.1	1.02	TP	1.11	1.01	TP	1.12	1	TP	1.11	1.01	TP	Iso	Ilv6p is the regulatory subunit of phenylalanine transaminase [SGD]. Null mutant has defective retroinhibition by valine [Cullin96], but apparently this subunit is otherwise non-essential for the enzymatic function.	FP
YLR432W	IMD3	IMP dehydrogenase homolog	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0.05	TP	1.08	1.01	TP	1.1	1	TP	1.11	1	TP	1.12	1.01	TP	1.11	1	TP	NA	NA	NA
YML056C	IMD4	IMP dehydrogenase homolog	NA	NA	NA	NA	NA	1	1	-0.06	TP	1	1	-0.07	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.06	TP	1.12	1.06	TP	1.11	1.05	TP	NA	NA	NA
YHR046C	INM1	Inositol monophosphatase	NA	NA	NA	NA	NA	0	1	0	FN	0	1	-0.01	FN	0	1.01	FN	0	1.04	FN	0	1.08	FN	0	1.1	FN	0	1.08	FN	Iso	YDR287W may code for an isozyme for Inm1p. May not be lethal if inositol is in media.	FN
YJL153C	INO1	L-myo-inositol-1-phosphate synthase	NA	NA	NA	NA	NA	0	1	0.11	FN	0	1	-0.04	FN	0	1.04	FN	0	1.07	FN	0	1.07	FN	0	1.06	FN	0	1.05	FN	Med	Null mutant is viable, but an inositol auxotroph [SGD]. This is consistent with in silico results. Thus, experiments may have some inositol in media.	NA
YBR011C	IPP1	Inorganic pyrophosphatase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YDR072C	IPT1	Inositolphosphotransferase 1	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	0.02	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	0.98	TP	1.12	0.98	TP	1.11	1.01	TP	NA	NA	NA
YPL040C	ISM1	Isoleucine-tRNA ligase	NA	NA	1	5.2	FP	1	1	-0.02	TP	1	1	-0.03	TP	1.08	0.69	FP	1.1	0.66	FP	1.11	0.48	FP	1.12	0.45	FP	1.11	0.56	FP	Oth	Protein synthesis not required in the model	NA
YDR497C	ITR1	Myo-inositol transporter	NA	NA	NA	NA	NA	1	1	0.09	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YOL103W	ITR2	Myo-inositol transporter	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.05	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.01	TP	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YKL217W	JEN1	Carboxylic acid transporter protein homolog	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.05	TP	1.08	1.03	TP	1.1	1.01	TP	1.11	0.99	TP	1.12	1	TP	0.64	1.01	FN	Med	Lower oxygen uptake rate would correct this false negative prediction.	NA
YIL125W	KGD1	Alpha-ketoglutarate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0.03	TP	1.08	0.96	TP	1.1	0.92	TP	1.09	0.6	FP	1.11	0.66	FP	1.1	0.66	FP	Unk	Should definitely have a growth defect on non-fermentable carbon sources. The model just adjusts the flux distribution to utilize more amino acids and dumps acetate.	NA
YDR148C	KGD2	Alpha-ketoglutarate dehydrogenase complex dihydrolipoyl transsuccinylase component	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0.06	TP	1.08	1	TP	1.1	0.95	TP	1.09	0.64	FP	1.11	0.71	FP	1.1	0.6	FP	Unk	Should definitely have a growth defect on non-fermentable carbon sources. The model just adjusts the flux distribution to utilize more amino acids and dumps acetate.	NA
YDR483W	KRE2	Alpha-1,2-mannosyltransferase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0	TP	1.08	1.03	TP	1.1	1.05	TP	1.11	1.04	TP	1.12	1.07	TP	1.11	1.06	TP	NA	NA	NA
YDR037W	KRS1	Lysine-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	FP
YOR099W	KTR1	Type II transmembrane protein	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.03	TP	1.08	1.03	TP	1.1	1.05	TP	1.11	1.04	TP	1.12	1.06	TP	1.11	1.05	TP	NA	NA	NA
YKR061W	KTR2	Mannosyltransferase (putative)|type 2 membrane protein	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	-0.06	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YBR205W	KTR3	Alpha-1,2-mannosyltransferase (putative)	NA	NA	NA	NA	NA	1	1	0.13	TP	1	1	-0.04	TP	1.08	1.02	TP	1.1	1.01	TP	1.11	1	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YBR199W	KTR4	Alpha-1,2-mannosyltransferase (putative)	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	0.06	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YNL029C	KTR5	Mannosyltransferase (putative)	NA	NA	1	4.2	FP	1	1	-0.02	TP	1	1	0	TP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Affects cell wall composition, but should not necessarily have a slow growth phenotype [MIPS].	NA
YPL053C	KTR6	Mannosylphosphate transferase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YNL071W	LAT1	Pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase component (E2)	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.03	TP	1.08	1.02	TP	1.1	0.99	TP	1.11	0.78	FP	1.12	0.89	TP	1.11	0.89	TP	Unk	The model can bypass the PDH complex if necessary.	NA
YMR296C	LCB1	Serine palmitoyltransferase component	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Sphingolipid synthesis not required in the model.	FP
YDR062W	LCB2	Serine palmitoyltransferase component	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Sphingolipid synthesis not required in the model.	FP
YJL134W	LCB3	Dihydrosphingosine-1-phosphate phophatase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.05	TP	1.11	1.06	TP	1.12	1.07	TP	1.11	1.06	TP	NA	NA	NA
YOR171C	LCB4	Sphingoid long chain base (LCB) kinase	NA	NA	NA	NA	NA	1	1	0.23	TP	1	1	-0.07	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YLR260W	LCB5	Sphingoid long chain base (LCB) kinase	NA	NA	1	4.2	FP	1	1	-0.02	TP	1	1	-0.03	TP	1.08	0.7	FP	1.1	0.61	FP	1.11	0.55	FP	1.12	0.48	FP	1.11	0.57	FP	Bio	Sphingolipid synthesis not required in the model.	NA
YGL009C	LEU1	Isopropylmalate isomerase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.03	TP	1.08	1.03	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.07	TP	1.11	1.05	TP	NA	NA	NA
YNL104C	LEU4	Alpha-isopropylmalate synthase (2-isopropylmalate synthase)	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.04	TP	1.11	1.04	TP	NA	NA	NA
YOR108W	LEU9	Alpha-isopropylmalate synthase (2-isopropylmalate synthase)	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.03	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YFL018C	LPD1	Dihydrolipoamide dehydrogenase precursor (mature protein is the E3 component of alpha-ketoacid dehydrogenase complexes)	NA	NA	1	3.7	FP	1	1	0.18	TP	0.97	1	-0.04	TP	1.06	0.76	FP	0.98	0.75	FP	0.94	0.55	FP	0.84	0.53	FP	0.93	0.55	FP	Unk	Should definitely have a growth defect on non-fermentable carbon sources. The model just adjusts the flux distribution to utilize more amino acids and dumps acetate.	NA
YDR503C	LPP1	Lipid phosphate phosphatase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.07	TP	1.11	1.05	TP	NA	NA	NA
YOR142W	LSC1	Alpha subunit of succinyl-CoA ligase (synthetase; ATP-forming), a mitochondrial enzyme of the TCA cycle	NA	NA	NA	NA	NA	1	1	0.08	TP	1	1	-0.02	TP	1.08	1	TP	1.1	1	TP	1.09	0.96	TP	1.11	1	TP	1.1	0.98	TP	NA	NA	NA
YGR244C	LSC2	Beta subunit of succinyl-CoA ligase (synthetase; ATP-forming), a mitochondrial enzyme of the TCA cycle	NA	NA	NA	NA	NA	1	1	0.38	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.03	TP	1.09	0.98	TP	1.11	1.05	TP	1.1	1.01	TP	NA	NA	NA
YNL268W	LYP1	Lysine permease	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.07	TP	1.08	1	TP	1.1	1	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1	TP	NA	NA	NA
YIR034C	LYS1	Saccharopine dehydrogenase	NA	NA	NA	NA	NA	0	0	2.88	TN	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.01	TP	1.11	0.98	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YIL094C	LYS12	Homo-isocitrate dehydrogenase	NA	NA	NA	NA	NA	0	0	5.15	TN	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YDL182W	LYS20	YDL131W (LYS21) homolog|homocitrate synthase	NA	NA	NA	NA	NA	1	1	0.3	TP	1	1	-0.04	TP	1.08	1	TP	1.1	1.01	TP	1.11	1	TP	1.12	0.99	TP	1.11	0.99	TP	NA	NA	NA
YDL131W	LYS21	YDL182W (LYS20) homolog|homocitrate synthase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.03	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.04	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YDR234W	LYS4	Homoaconitase	NA	NA	NA	NA	NA	0	0	1.55	TN	1	1	-0.01	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YGL154C	LYS5	Alpha aminoadipate reductase phosphopantetheinyl transferase	NA	NA	NA	NA	NA	0	0	8.33	TN	1	1	0.01	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.03	TP	NA	NA	NA
YNR050C	LYS9	Seventh step in lysine biosynthesis pathway	NA	NA	NA	NA	NA	0	1	1.27	TN	1	1	-0.02	TP	1.08	0.9	TP	1.1	0.97	TP	1.11	0.97	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YKL029C	MAE1	Malic enzyme	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.05	TP	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YGR289C	MAL11	Alpha-glucoside transporter|hexose transporter|maltose permease	NA	NA	NA	NA	NA	1	1	0.09	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YGR292W	MAL12	Maltase	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.06	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YBR298C	MAL31	Maltose permease	NA	NA	NA	NA	NA	1	1	0.14	TP	1	1	0.16	TP	1.08	0.97	TP	1.1	0.99	TP	1.11	0.96	TP	1.12	0.92	TP	1.11	0.93	TP	NA	NA	NA
YBR299W	MAL32	Maltase	NA	NA	NA	NA	NA	1	1	0.18	TP	1	1	-0.06	TP	1.08	1.03	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.08	TP	1.11	1.06	TP	NA	NA	NA
YOR221C	MCT1	Malonyl-CoA:ACP transferase	NA	NA	NA	NA	NA	1	1	0.08	TP	1	1	-0.03	TP	1.08	0.8	FP	1.1	0.76	FP	1.11	0.49	FP	1.12	0.45	FP	1.11	0.57	FP	Oth	Component of the mitochondrial FAS that supplies phopholipids to the mitochondrial membrane. The model does not account for the formation of the mitochondrial membrane.	NA
YKL085W	MDH1	Malate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1	TP	1.11	0.83	TP	1.12	0.97	TP	1.11	0.86	TP	NA	NA	NA
YOL126C	MDH2	Malate dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.07	TP	1.08	1.04	TP	1.1	1.06	TP	1.11	1.03	TP	1.12	1.06	TP	1.11	1.06	TP	NA	NA	NA
YDL078C	MDH3	Malate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YGR121C	MEP1	Ammonia permease	NA	NA	NA	NA	NA	1	1	0.25	TP	1	1	-0.02	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YNL142W	MEP2	Ammonia transport protein	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.03	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YPR138C	MEP3	NH4+ transporter	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	0.08	TP	1.08	1.01	TP	1.1	0.98	TP	1.11	0.98	TP	1.12	0.97	TP	1.11	0.96	TP	NA	NA	NA
YGR264C	MES1	Methionine-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YKR069W	MET1	Methionine metabolism	NA	NA	NA	NA	NA	1	1	1.55	TP	1	1	-0.04	TP	1.08	1.04	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.06	TP	1.11	1.04	TP	NA	NA	NA
YFR030W	MET10	Assimilatory sulfite reductase subunit	NA	NA	NA	NA	NA	1	1	0.29	TP	1	1	-0.03	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.06	TP	1.11	1.04	TP	NA	NA	NA
YPL023C	MET12	Methylenetetrahydrofolate reductase (mthfr) (putative)	NA	NA	NA	NA	NA	1	1	0.33	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YGL125W	MET13	Methylenetetrahydrofolate reductase (mthfr) (putative)	NA	NA	NA	NA	NA	1	0	3.97	FP	1	1	-0.01	TP	1.08	1	TP	1.1	0.99	TP	1.11	1	TP	1.12	1.02	TP	1.11	1.02	TP	Iso	Met13p is the dominant isozyme, but the model contains an additional isozyme (Met12p).	NA
YKL001C	MET14	Adenylylsulfate kinase	NA	NA	NA	NA	NA	0	1	0.18	FN	1	1	-0.08	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.02	TP	Med	Should not grow as sulfate as only sulfur source [Thomas97]. Maybe minimal media in experimental study has some other sulfur sources.	NA
YPR167C	MET16	3'phosphoadenylylsulfate reductase	NA	NA	NA	NA	NA	0	1	0.64	FN	1	1	-0.04	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1	TP	1.12	1.03	TP	1.11	1.03	TP	Med	Should not grow as sulfate as only sulfur source [Thomas97]. Maybe minimal media in experimental study has some other sulfur sources.	NA
YLR303W	MET17	O-acetylhomoserine (thiol)-lyase	NA	NA	NA	NA	NA	1	0	2.78	FP	1	1	0	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	0.99	TP	1.12	1.01	TP	1.11	1.01	TP	Unk	Homocysteine can be produced in the model using CYSTL (Cys1p) and AHCi (Sah1p) reactions in addition to this pathway, but neither of these reactions can be removed from the model.	NA
YOL064C	MET22	3'(2')5'-bisphosphate nucleotidase	NA	NA	NA	NA	NA	0.99	1	1.33	TP	1	1	0	TP	1.08	0.84	FP	1.1	0.84	FP	1.11	0.81	TP	1.12	0.81	TP	1.11	0.85	TP	Acc	Mutant probably accumulates phosphoadenylyl sulfate (PAPS), which is toxic [Thomas90].	NA
YJR010W	MET3	ATP sulfurylase	NA	NA	NA	NA	NA	1	1	0.96	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1	TP	1.12	0.99	TP	1.11	0.98	TP	NA	NA	NA
YER091C	MET6	Vitamin B12-(cobalamin)-independent isozyme of methionine synthase (also called N5-methyltetrahydrofolate homocysteine methyltransferase or 5-methyltetrahydropteroyl triglutamate homocysteine methyltransferase)	NA	NA	NA	NA	NA	0	0	3.2	TN	0	1	0	FN	0	1	FN	0	1	FN	0	1.01	FN	0	1	FN	0	1	FN	Unk	The in silico met6 strain is incapable of balancing homocysteine, which is a byproduct of phospholipid biosynthesis. For some reason this does not happen in vivo at least not in rich media. There may be another way to drain off excess homocysteine.	FN
YOR241W	MET7	Folylpolyglutamate synthetase	NA	NA	1	7.1	FP	1	1	-0.01	TP	1	1	-0.02	TP	1.08	0.74	FP	1.1	0.73	FP	1.11	0.58	FP	1.12	0.48	FP	1.11	0.51	FP	Den	This is a dead end in the model, but it should be part of the one carbon metabolic conversions. Also the gene product is present in both cytoplam and mitochondia and its deletion causes a petite phenotype as the production of mitochondrial f-Met-tRNA (necessary for mitochondrial translation) is disrupted [DeSouza00].	NA
YLL062C	MHT1	S-Methylmethionine Homocysteine methylTransferase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YJR077C	MIR1	Product of gene unknown	NA	NA	NA	NA	NA	0.96	1	0.24	TP	0.96	1	0.1	TP	1.05	0.98	TP	0.91	0.92	TP	0.92	0.64	FP	0.94	0.61	FP	0.93	0.66	FP	Oth	Mutant implicated in blocking mitochondrial protein import and disrupts mitochondrial function [MIPS]. Model has other ways to transport phosphate into mitochondria.	NA
YBR084W	MIS1	C1-tetrahydrofolate synthase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0	TP	1.08	1.01	TP	1.1	0.99	TP	1.11	0.9	TP	1.12	0.92	TP	1.11	0.91	TP	NA	NA	NA
YNL117W	MLS1	Carbon-catabolite sensitive malate synthase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	0.14	TP	1.08	1.01	TP	1.1	1	TP	1.11	0.93	TP	1.12	0.88	TP	1.11	0.91	TP	NA	NA	NA
YLL061W	MMP1	High affinity S-methylmethionine permease	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.03	TP	1.08	1	TP	1.1	1	TP	1.11	1.01	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YPL104W	MSD1	Aspartyl-tRNA synthetase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0.03	TP	1.08	0.88	FP	1.1	0.77	FP	1.11	0.59	FP	1.12	0.54	FP	1.11	0.57	FP	Oth	Protein synthesis not required in the model	NA
YOL033W	MSE1	Glutamine-tRNA ligase	NA	NA	1	6.3	FP	1	1	-0.03	TP	1	1	-0.02	TP	1.08	0.71	FP	1.1	0.67	FP	1.11	0.55	FP	1.12	0.59	FP	1.11	0.59	FP	Oth	Protein synthesis not required in the model	NA
YPR047W	MSF1	Phenylalanyl-tRNA synthetase alpha subunit	NA	NA	1	3.7	FP	1	1	0.01	TP	1	1	-0.01	TP	1.08	0.79	FP	1.1	0.69	FP	1.11	0.49	FP	1.12	0.45	FP	1.11	0.53	FP	Oth	Protein synthesis not required in the model.	NA
YNL073W	MSK1	Lysine-tRNA ligase	NA	NA	1	4.9	FP	1	1	0	TP	1	1	-0.01	TP	1.08	0.74	FP	1.1	0.7	FP	1.11	0.51	FP	1.12	0.52	FP	1.11	0.58	FP	Oth	Protein synthesis not required in the model	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YGR171C	MSM1	Methionine-tRNA ligase	NA	NA	1	5.9	FP	1	1	0.01	TP	1	1	0	TP	1.08	0.72	FP	1.1	0.65	FP	1.11	0.43	FP	1.12	0.5	FP	1.11	0.56	FP	Oth	Protein synthesis not required in the model	NA
YHR091C	MSR1	Arginyl-tRNA synthetase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.03	TP	1.08	0.71	FP	1.1	0.67	FP	1.11	0.53	FP	1.12	0.52	FP	1.11	0.54	FP	Oth	Protein synthesis not required in the model	NA
YDR208W	MSS4	Phosphatidylinositol 4-phosphate kinase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Phospholipid produced by this reaction leads to a dead end (1D-myo-Inositol 1,4,5-trisphosphate = IP3). This metabolite is used in other cellular processes such as signaling.	FP
YDR268W	MSW1	Tryptophan-tRNA ligase	NA	NA	1	4.3	FP	1	1	-0.02	TP	1	1	0.04	TP	1.08	0.76	FP	1.1	0.65	FP	1.11	0.47	FP	1.12	0.43	FP	1.11	0.53	FP	Oth	Protein synthesis not required in the model	NA
YPL097W	MSY1	Tyrosine-tRNA ligase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.02	TP	1.08	0.74	FP	1.1	0.69	FP	1.11	0.55	FP	1.12	0.48	FP	1.11	0.55	FP	Oth	Protein synthesis not required in the model	NA
YKR080W	MTD1	NAD-dependent 5,10-methylenetetrahydrafolate dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.04	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YGR055W	MUP1	High affinity methionine permease	NA	NA	NA	NA	NA	1	1	0.29	TP	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YHL036W	MUP3	Very low affinity methionine permease	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.07	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YGR007W	MUQ1	Choline phosphate cytidylyltransferase (also called phosphoethanolamine cytidylyltransferase or phosphocholine cytidylyltransferase)	NA	NA	NA	NA	NA	1	1	0.3	TP	1	1	-0.03	TP	1.08	1.03	TP	1.1	1.01	TP	1.11	0.99	TP	1.12	1.02	TP	1.11	1	TP	NA	NA	NA
YNR043W	MVD1	Mevalonate pyrophosphate decarboxylase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YLR382C	NAM2	Leucine-tRNA ligase	NA	NA	1	11.2	FP	1	1	-0.01	TP	1	1	-0.02	TP	1.08	0.69	FP	1.1	0.68	FP	1.11	0.51	FP	1.12	0.56	FP	1.11	0.56	FP	Oth	Protein synthesis not required in the model	NA
YDL040C	NAT1	N-terminal acetyltransferase	NA	NA	1	3.8	FP	1	1	-0.04	TP	1	1	-0.02	TP	1.08	0.89	TP	1.1	0.87	TP	1.11	0.88	TP	1.12	0.8	TP	1.11	0.89	TP	Oth	Protein N-terminal acetylation not required in the model	NA
YGR147C	NAT2	N alpha-acetyltransferase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1.08	0.9	TP	1.1	0.89	TP	1.11	0.96	TP	1.12	0.96	TP	1.11	0.96	TP	Dis	Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates.	FP
YMR145C	NDE1	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.05	TP	1.12	1.05	TP	1.11	1.05	TP	NA	NA	NA
YDL085W	NDE2	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0.26	TP	1	1	-0.07	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YML120C	NDI1	NADH dehydrogenase (ubiquinone)	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.03	TP	1.08	0.98	TP	1.1	0.97	TP	1.11	0.65	FP	1.12	0.93	TP	1.11	0.61	FP	Unk	The model will ferment glycerol or lactate in a ndi1 strain, but the yields are much lower than the wild type strain yield.	NA
YLR138W	NHA1	Putative Na+/H+ antiporter	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.02	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.04	TP	NA	NA	NA
YJL126W	NIT2	Nit protein, nitrilase superfamily member	NA	NA	NA	NA	NA	1	1	0.72	TP	1	1	-0.07	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA
YLR351C	NIT3	Nit protein, nitrilase superfamily member	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.05	TP	1.08	1.03	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.06	TP	1.11	1.05	TP	NA	NA	NA
YLR328W	NMA1	Nicotinamide/nicotinic acid mononucleotide adenylyltransferase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.03	TP	1.08	1.05	TP	1.1	1.05	TP	1.11	1.04	TP	1.12	1.08	TP	1.11	1.06	TP	NA	NA	NA
YGR010W	NMA2	Nicotinamide/nicotinic acid mononucleotide adenylyltransferase	NA	NA	NA	NA	NA	1	1	0.38	TP	1	1	-0.03	TP	1.08	1.03	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YLR195C	NMT1	N-myristoyl transferase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Den	Metabolite produced by this reaction is a dead-end (N-Tetradecanoylglycylpeptide).	FP
YOR209C	NPT1	Nicotinate phosphoribosyltransferase	NA	NA	1	4.8	FP	1	1	0	TP	1	1	0.06	TP	1.08	0.89	TP	1.1	0.9	TP	1.11	0.97	TP	1.12	0.92	TP	1.11	0.95	TP	Oth	Also potentially involved in cromatin silencing through adjusting the NAD/NADH balance.	NA
YGL067W	NPY1	NADH pyrophosphatase 1	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YDR001C	NTH1	Neutral trehalase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.04	TP	1.11	1.04	TP	NA	NA	NA
YBR001C	NTH2	Neutral trehalase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0.05	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YKL120W	OAC1	Oxaloacetate transport protein	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YKL055C	OAR1	3-oxoacyl-[acyl-carrier-protein] reductase	NA	NA	1	5.7	FP	1	1	0.09	TP	1	1	-0.02	TP	1.08	0.75	FP	1.1	0.73	FP	1.11	0.47	FP	1.12	0.45	FP	1.11	0.56	FP	Oth	It has been proposed that the role of the mitochondrial fatty acid synthase is to provide phospholipids for the mitochondrial inner membrane and that the disruption of genes in the FAS (including OAR1) would lead into inability to properly synthesize the inner membrane [Schneider97].	NA
YPL134C	ODC1	Mitochondrial 2-oxodicarboxylate transport protein	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1	TP	1.11	1.01	TP	NA	NA	NA
YOR222W	ODC2	Mitochondrial 2-oxodicarboxylate transport protein	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1	TP	1.11	1.01	TP	NA	NA	NA
YGL055W	OLE1	Delta-9-fatty acid desaturase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YJR073C	OPI3	Unsaturated phospholipid N-methyltransferase	NA	NA	NA	NA	NA	0	1	1.04	TN	0	1	0.16	FN	0	1.01	FN	0	1.01	FN	0	0.97	FN	0	1.03	FN	0	1.03	FN	Unk	The activities catalyzed by this gene are totally lost when it is disrupted, but mutants are viable. The cells accumulate mmPE and membrane is devoid of PC [MIPS]. Surpsingly, mutant were not strict choline auxotrophs (choline req'd for an alternate route to produce PC). Reason why cells are viable is unknown; it has been speculated that a mutation in CHO2 may alter its substrate specificity (CHO2 catalyzes 1st of 3 steps in pathway from PE to PC, OPI3 primarily catalyzes 2nd and 3rd steps, can also catalyze 1st step but is very inefficient).	FN
YOR130C	ORT1	Mitochondrial integral membrane protein, ornithine transporter	NA	NA	NA	NA	NA	0	1	4.31	TN	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.02	TP	NA	Weak false negative	NA
YJR051W	OSM1	Osmotic growth protein	NA	NA	NA	NA	NA	1	1	0.27	TP	1	1	-0.03	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.04	TP	1.11	1.04	TP	NA	NA	NA
YDR538W	PAD1	Phenylacrylic acid decarboxylase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.01	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YIL145C	PAN6	Pantothenate synthase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1	TP	NA	NA	NA
YKR097W	PCK1	Phosphoenolpyruvate carboxylkinase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.04	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.03	TP	0.43	0.93	FN	0.93	1.04	TP	Med	Lower oxygen uptake rate would correct this false negative prediction.	NA
YEL058W	PCM1	Phosphoacetylglucosamine mutase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	N-Acetylglucosamine synthesis is not required in the model.	FP
YGR202C	PCT1	Cholinephosphate cytidylyltransferase|phosphorylcholine transferase	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	0.03	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	0.98	TP	1.12	1.01	TP	1.11	0.99	TP	NA	NA	NA
YER178W	PDA1	Pyruvate dehydrogenase alpha subunit (E1 alpha)	NA	NA	NA	NA	NA	1	1	0.35	TP	1	1	0.28	TP	1.08	1	TP	1.1	0.96	TP	1.11	0.78	FP	1.12	0.79	TP	1.11	0.9	TP	Unk	Pyruvate dehydrogenase (coded by PDA1 & PDB1) is not used by the model when grown on glycerol.	NA
YBR221C	PDB1	Pyruvate dehydrogenase beta subunit (E1 beta)	NA	NA	NA	NA	NA	1	1	0.09	TP	1	1	0	TP	1.08	0.93	TP	1.1	0.91	TP	1.11	0.66	FP	1.12	0.71	FP	1.11	0.8	TP	Unk	Pyruvate dehydrogenase (coded by PDA1 & PDB1) is not used by the model when grown on glycerol or ethanol.	NA
YLR044C	PDC1	Pyruvate decarboxylase	NA	NA	1	3.8	FP	1	1	-0.03	TP	1	1	-0.03	TP	1.08	1	TP	1.1	1	TP	1.11	1	TP	1.12	0.97	TP	1.11	0.99	TP	Iso	There are three alternate isozymes in the model , but PDC1 deletion alone is sufficient to reduce PDC activity significantly enough to result in a slow growth phenotype.	NA
YLR134W	PDC5	Pyruvate decarboxylase	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	0	TP	1.08	1	TP	1.1	1	TP	1.11	1	TP	1.12	1	TP	1.11	0.99	TP	NA	NA	NA
YGR087C	PDC6	Pyruvate decarboxylase isozyme	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YGL248W	PDE1	3',5'-cyclic-nucleotide phosphodiesterase, low affinity	NA	NA	NA	NA	NA	1	1	2.85	TP	1	1	-0.03	TP	1.08	0.99	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	0.97	TP	1.11	0.98	TP	NA	NA	NA
YOR360C	PDE2	High affinity cAMP phosphodiesterase	NA	NA	NA	NA	NA	1	1	0.24	TP	1	1	0.05	TP	1.08	1.06	TP	1.1	1.03	TP	1.11	1	TP	1.12	0.81	TP	1.11	0.99	TP	NA	NA	NA
YBR035C	PDX3	Pyridoxine (pyridoxiamine) phosphate oxidase	NA	NA	NA	NA	NA	1	1	0.71	TP	1	1	-0.05	TP	1.08	0.86	FP	1.1	0.85	FP	1.11	0.74	FP	1.12	0.55	FP	1.11	0.61	FP	Den	The whole pyridoxine metabolism is a dead end in the model.	NA
YBL030C	PET9	ADP/ATP translocator	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.03	TP	Dis	Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates.	FP
YGR240C	PFK1	Phosphofructokinase alpha subunit	NA	NA	0.19	4.8	TN	0.18	1	-0.01	TN	0.19	1	0	TN	0.2	0.89	FN	1.06	0.95	TP	1.1	1.05	TP	1.12	1.08	TP	1.11	1.05	TP	Dis	Slow growth in [Giaever02], but apparently normal growth in [Steinmetz02].	NA
YMR205C	PFK2	Phosphofructokinase beta subunit	NA	NA	0.19	16.7	TN	0.18	1	-0.01	TN	0.19	1	-0.03	TN	0.2	0.7	TN	1.06	0.76	FP	1.1	0.95	TP	1.12	1.01	TP	1.11	0.97	TP	Med	In YPDGE media the max glc uptake in the simulation is too low to cause pfk2 to have a growth defect.	NA
YIL107C	PFK26	6-phosphofructose-2-kinase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0.1	TP	1.08	1	TP	1.1	0.98	TP	1.11	0.99	TP	1.12	0.96	TP	1.11	0.98	TP	NA	NA	NA
YOL136C	PFK27	6-phosphofructo-2-kinase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.08	TP	1.11	1.06	TP	NA	NA	NA
YBR196C	PGI1	Glucose-6-phosphate isomerase	0.54	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	In silico slow growth.	NA
YCR012W	PGK1	3-phosphoglycerate kinase	0.1	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	In silico slow growth.	NA
YKL127W	PGM1	Phosphoglucomutase minor isoform	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YMR105C	PGM2	Phosphoglucomutase	NA	NA	NA	NA	NA	1	1	0.03	TP	1	0	7.28	FP	1.08	1	TP	1.1	1	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	1	TP	Iso	Pgm2p is major isomform of phosphoglucomutase. Maybe the minor isoform (Pgm1p) can't fully compensate for loss of Pgm2p.	NA
YCL004W	PGS1	17 kDa phosphatidylglycerolphosphate synthase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Dis	Should not be absolutely essential [SGD]. Disrupts mitochondrial function somewhat.	FP
YNL316C	PHA2	Prephenate dehydratase	NA	NA	NA	NA	NA	0	0	9.87	TN	1	1	-0.08	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA
YBR092C	PHO3	Acid phosphatase	NA	NA	NA	NA	NA	1	1	-0.07	TP	1	1	-0.07	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YDR481C	PHO8	Repressible alkaline phosphatase	NA	NA	NA	NA	NA	1	1	0.19	TP	1	1	0	TP	1.08	1.03	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YML123C	PHO84	Inorganic phosphate transporter	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.02	TP	1.08	0.96	TP	1.1	0.83	FP	1.11	0.85	TP	1.12	0.82	TP	1.11	0.99	TP	Iso	There are multiple alternative isozymes for the phosphate transporters, but Pho84p may be the dominant one under some conditions.	NA
YCR037C	PHO87	Phosphate permease	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0	TP	1.08	1	TP	1.1	1	TP	1.11	1.01	TP	1.12	1	TP	1.11	1.01	TP	NA	NA	NA
YBR296C	PHO89	Na+/Pi symporter (putative)	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0.02	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1	TP	1.11	0.98	TP	NA	NA	NA
YJL198W	PHO90	Low-affinity phosphate transporter	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	0	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.02	TP	1.11	1.03	TP	NA	NA	NA
YNR013C	PHO91	Low-affinity phosphate transporter	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.03	TP	1.08	1.02	TP	1.1	1	TP	1.11	1	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YNL267W	PIK1	Phosphatidylinositol 4-kinase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Den	Phospholipid produced by this reaction leads to a dead-end (1D-myo-Inositol 1,4,5-trisphosphate). Also Stt4p is an isozyme.	FP
YPR113W	PIS1	Phosphatidylinositol synthase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YPL268W	PLC1	Phosphoinositide-specific phospholipase C	NA	NA	1	14.8	FP	1	1	-0.02	TP	1	1	-0.01	TP	1.08	0.72	FP	1.1	0.7	FP	1.11	0.88	TP	1.12	0.81	TP	1.11	0.89	TP	Oth	Also involved in kinetochore function.	NA
YGL008C	PMA1	Plasma membrane H+-ATPase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Iso	This is the major isoform of the cytosolic ATPase, but in the model a minor isoform can compensate for the function. Deletion of the minor isoform (which contains Pma2p instead of Pma1p) is not lethal experimentally.	FP
YPL036W	PMA2	Plasma membrane ATPase	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.01	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YER003C	PMI40	Mannose-6-phosphate isomerase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YCR024CA	PMP1	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)	NA	NA	NA	NA	NA	0.85	1	0.04	TP	0.23	1	0.01	FN	0.99	1.03	TP	1.03	1.03	TP	1.07	1.02	TP	1.03	1	TP	1.04	1	TP	Med	If oxygen uptake rate on YPGal is increased the pmp1 growth rate increases to that of the wild type.	NA
YEL017CA	PMP2	Proteolipid associated with plasma membrane H(+)-ATPase (Pma1p)	NA	NA	NA	NA	NA	0.85	1	0.33	TP	0.23	1	0	FN	0.99	1.02	TP	1.03	1.03	TP	1.07	1.03	TP	1.03	1.04	TP	1.04	1.03	TP	Med	If oxygen uptake rate on YPGal is increased the pmp2 growth rate increases to that of the wild type.	NA
YDL095W	PMT1	Dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.04	TP	1.08	0.99	TP	1.1	1.02	TP	1.11	0.98	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YAL023C	PMT2	Dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase	NA	NA	1	6.3	FP	1	1	-0.01	TP	1	1	-0.02	TP	1.08	0.94	TP	1.1	0.94	TP	1.11	0.94	TP	1.12	0.96	TP	1.11	0.96	TP	Oth	Mannosyntransferase activity not required in the model.	NA
YOR321W	PMT3	Dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.03	TP	NA	NA	NA
YDL093W	PMT5	Dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase	NA	NA	NA	NA	NA	1	1	-0.06	TP	1	1	-0.06	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.06	TP	1.11	1.03	TP	NA	NA	NA
YGR199W	PMT6	Dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	0.03	TP	1.08	1.01	TP	1.1	0.99	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YGL037C	PNC1	Nicotinamidase|pyrazinamidase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.05	TP	1.08	1.04	TP	1.1	1.06	TP	1.11	1.05	TP	1.12	1.09	TP	1.11	1.07	TP	NA	NA	NA
YLR209C	PNP1	Purine nucleoside phosphorylase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0.04	TP	1.08	1	TP	1.1	1.02	TP	1.05	1	TP	1.1	1.02	TP	1.07	1.01	TP	NA	NA	NA
YPL188W	POS5	Involved in oxidative stress	NA	NA	1	8.3	FP	1	1	0.01	TP	1	1	-0.02	TP	1.08	0.7	FP	1.1	0.82	FP	1.11	0.58	FP	1.12	0.54	FP	1.11	0.6	FP	Mod	Does not grow well under aerobic conditions, because Pos5p is the primary source of NADPH in mitochondria [Outten03]. May need to change the model so that only Pos5p can provide NADPH in mitochondria.	NA
YIL160C	POT1	3-oxoacyl CoA thiolase	NA	NA	NA	NA	NA	1	1	0.69	TP	1	1	-0.03	TP	1.08	1.02	TP	1.1	1	TP	1.11	1.01	TP	1.12	0.95	TP	1.11	0.98	TP	NA	NA	NA
YGL205W	POX1	Fatty-acyl coenzyme A oxidase	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	-0.01	TP	1.08	1.01	TP	1.1	1	TP	1.11	0.97	TP	1.12	1	TP	1.11	0.99	TP	NA	NA	NA
YHR026W	PPA1	Proteolipid|vacuolar ATPase V0 domain subunit c"	NA	NA	1	5.6	FP	1	1	0.03	TP	1	1	0.01	TP	1.08	0.8	FP	1.1	0.65	FP	1.11	0.61	FP	1.12	0.6	FP	1.11	0.68	FP	Oth	See other vacuolar ATPase components.	NA
YMR267W	PPA2	Inorganic pyrophosphatase	NA	NA	1	3.4	FP	1	1	-0.04	TP	1	1	-0.02	TP	1.08	0.74	FP	1.1	0.67	FP	1.11	0.54	FP	1.12	0.49	FP	1.11	0.54	FP	Mod	PPA2 deletion strain has lost mitochondrial DNA apparently because pyrophosphate produced during replication cannot be converted into phosphate [Lundin91]. The model does not run any of the reactions producing ppi[m] in the ppa2 and utilizes the cytoplasmic forms of the reactions instead.	NA
YPL148C	PPT2	Phosphopantetheine:protein transferase (PPTase)	NA	NA	1	7	FP	1	1	0.04	TP	1	1	-0.03	TP	1.08	0.64	FP	1.1	0.65	FP	1.11	0.52	FP	1.12	0.53	FP	1.11	0.51	FP	Oth	CoA biosynthesis not required in the model.	FN
YDR300C	PRO1	Gamma-glutamyl kinase	NA	NA	1	12.6	FP	1	1	-0.01	TP	1	1	0	TP	1.08	0.64	FP	1.1	0.69	FP	1.11	0.95	TP	1.12	0.97	TP	1.11	1.06	TP	Unk	Should be a proline auxotroph, but should grow fine on rich media. Model synthesizes proline from glutamate using ornithine as an intermediate.	NA
YOR323C	PRO2	Gamma-glutamyl phosphate reductase	NA	NA	NA	NA	NA	1	0	5.16	FP	1	1	-0.03	TP	1.08	1	TP	1.1	1	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.01	TP	Unk	Should be a proline auxotroph. Model synthesizes proline from glutamate using ornithine as an intermediate.	NA
YER023W	PRO3	Delta 1-pyrroline-5-carboxylate reductase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1.08	1.06	TP	1.1	1.05	TP	1.01	1.04	TP	1.11	1.11	TP	1.05	1.06	TP	Dis	Only deemed to be essential in one study [Giaever02]. The other study [Steinmetz02] shows normal growth on all substrates.	FP
YHL011C	PRS3	Ribose-phosphate pyrophosphokinase	NA	NA	1	7.6	FP	1	1	-0.02	TP	1	1	0	TP	1.08	0.66	FP	1.1	0.73	FP	1.11	1	TP	1.12	0.91	TP	1.11	0.92	TP	Oth	Prs3p has an unknown role in controlling cell growth. Its deletion causes a wide variety of phenotypes including small cell size.	NA
YBL068W	PRS4	Ribose-phosphate pyrophosphokinase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YOL061W	PRS5	Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyrophosphokinase)	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	-0.02	TP	1.08	0.99	TP	1.1	1.01	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YDL055C	PSA1	GDP-mannose pyrophosphorylase|mannose-1-phosphate guanyltransferase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YNL169C	PSD1	Phosphatidylserine decarboxylase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.02	TP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YGR170W	PSD2	Phosphatidylserine decarboxylase	NA	NA	NA	NA	NA	1	1	0.06	TP	1	1	0.05	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YKR093W	PTR2	Peptide transporter	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YPL212C	PUS1	TRNA pseudouridine synthase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.06	TP	1.08	1	TP	1.1	1.02	TP	1.11	1	TP	1.12	1.03	TP	1.11	1.04	TP	NA	NA	NA
YGL063W	PUS2	Pseudouridine synthase	NA	NA	NA	NA	NA	1	1	0.35	TP	1	1	-0.04	TP	1.08	1.02	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YNL292W	PUS4	Pseudouridine synthase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.08	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA
YLR142W	PUT1	Proline oxidase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.04	TP	1.08	1.01	TP	1.09	1	TP	0.91	1	TP	1.1	1	TP	0.99	1.01	TP	NA	NA	NA
YHR037W	PUT2	Delta-1-pyrroline-5-carboxylate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	0.97	TP	1.11	1.01	TP	NA	NA	NA
YOR348C	PUT4	Proline specific permease	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.08	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YPL147W	PXA1	ABC transporter of long-chain fatty acids	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.08	TP	1.08	1.02	TP	1.1	1.05	TP	1.11	1.05	TP	1.12	1.07	TP	1.11	1.05	TP	NA	NA	NA
YKL188C	PXA2	ABC transporter 2	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.07	TP	1.11	1.05	TP	NA	NA	NA
YGL062W	PYC1	Pyruvate carboxylase	NA	NA	NA	NA	NA	1	1	0.13	TP	1	1	-0.06	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	0.99	TP	1.11	1.04	TP	NA	NA	NA
YBR218C	PYC2	Pyruvate carboxylase	NA	NA	NA	NA	NA	1	1	0.16	TP	1	1	0.1	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YOR347C	PYK2	Pyruvate kinase, glucose-repressed isoform	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.04	TP	1.11	1.02	TP	NA	NA	NA
YHR001WA	QCR10	Ubiquinol-cytochrome c oxidoreductase complex 8.5 kDa subunit	NA	NA	NA	NA	NA	0.89	1	-0.03	TP	0.82	1	0	TP	0.98	1.01	TP	0.24	1.02	FN	0.14	1.02	FN	0.08	1.01	FN	0.17	1.03	FN	Iso	Deletion of QCR10 does not impair growth on non-fermentable carbon source [MIPS]. QCR10 is not essential to formation of cytochrome bc1 complex [Cruciat00]. Thus, the false prediction is due to way we have modeled the complex. This subunit should be made a non-essential part of the complex since it only plays structural role.	NA
YPR191W	QCR2	40 kDa ubiquinol cytochrome-c reductase core protein 2	NA	NA	0.9	4.4	TN	0.89	1	-0.01	TP	0.82	1	-0.05	TP	0.98	0.92	TP	0.24	0.87	FN	0.14	0.49	TN	0.08	0.39	TN	0.17	0.6	TN	Med	This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium.	NA
YFR033C	QCR6	Ubiquinol cytochrome C oxidoreductase subunit 6 (17 kDa)	NA	NA	NA	NA	NA	0.89	1	-0.02	TP	0.82	1	0.1	TP	0.98	1.02	TP	0.24	0.98	FN	0.14	0.87	FN	0.08	0.82	FN	0.17	0.92	FN	Iso	Deletion of QCR6 does not have significant effect on the formation or stability of cytochrome bc complex so that it should not play an essential role in complex formation as indicated by the gene-protein-reaction associations currently.	NA
YDR529C	QCR7	Ubiquinol cytochrome C oxidoreductase subunit 7 (14 kDa)	NA	NA	0.9	5.3	TN	0.89	1	-0.02	TP	0.82	1	-0.02	TP	0.98	0.67	FP	0.24	0.65	TN	0.14	0.53	TN	0.08	0.51	TN	0.17	0.59	TN	Oth	Mitochondrial maintenance not required in the model in primarily fermentative conditions.	NA
YJL166W	QCR8	Ubiquinol cytochrome C reductase subunit 8 (11 kDa)	NA	NA	0.9	6.3	TN	0.89	1	0.05	TP	0.82	1	0.15	TP	0.98	0.93	TP	0.24	0.86	FN	0.14	0.6	TN	0.08	0.52	TN	0.17	0.54	TN	Med	This is probably due to excessive respiration under the simulation conditions - glucose vs oxygen limitation, may consider increasing maximum glc uptake in YPDGE medium.	NA
YGR183C	QCR9	Ubiquinol cytochrome c oxidoreductase complex 7.3 kDa subunit 9	NA	NA	NA	NA	NA	0.89	1	0.13	TP	0.82	1	0.21	TP	0.98	0.96	TP	0.24	0.85	TN	0.14	0.6	TN	0.08	0.58	TN	0.17	0.63	TN	NA	NA	NA
YHR074W	QNS1	Glutamine-dependent NAD synthetase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	NAD biosynthesis not required in the model.	FP
YDL103C	QRI1	UDP-N-acetylglucosamine pyrophosphorylase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	UDP-N-Acetylglucosamine synthesis is not required in the model.	FP
YDL090C	RAM1	Farnesyltransferase beta subunit	NA	NA	1	7	FP	1	1	-0.02	TP	1	1	-0.02	TP	1.08	0.79	FP	1.1	0.82	FP	1.11	0.97	TP	1.12	0.79	TP	1.11	0.88	TP	Oth	Farnesyltransferases not required in the model	NA
YKL019W	RAM2	CAAX farnesyltransferase alpha subunit	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Quinone biosynthesis is not required in the model.	NA
YCR036W	RBK1	Ribokinase	NA	NA	NA	NA	NA	1	1	0.27	TP	1	1	0.24	TP	1.08	0.98	TP	1.1	0.99	TP	1.11	0.97	TP	1.12	0.94	TP	1.11	0.93	TP	NA	NA	NA
YBR002C	RER2	Cis-prenyltransferase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Quinone biosynthesis is not required in the model	FP
YIL053W	RHR2	DL-glycerol-3-phosphatase	NA	NA	NA	NA	NA	1	1	0.16	TP	1	1	-0.07	TP	1.08	0.97	TP	1.1	0.99	TP	1.11	1.06	TP	1.12	1.01	TP	1.11	1.05	TP	NA	NA	NA
YBL033C	RIB1	GTP cyclohydrolase II	NA	NA	1	10.3	FP	1	1	-0.04	TP	1	1	-0.01	TP	1.08	0.75	FP	1.1	0.73	FP	1.11	0.67	FP	1.12	0.65	FP	1.11	0.67	FP	Bio	FAD biosynthesis not required in the model	NA
YOL143C	RIB4	6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase)	NA	NA	1	4.5	FP	1	1	-0.01	TP	1	1	-0.01	TP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Riboflavin biosynthesis is not required in the model.	NA
YBR256C	RIB5	Riboflavin biosynthesis	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Riboflavin biosynthesis is not required in the model	FP
YBR153W	RIB7	Protein involved in the biosynthesis of riboflavin, second step in the riboflavin biosynthesis pathway	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Riboflavin biosynthesis is not required in the model.	NA
YEL024W	RIP1	Rieske iron-sulfur protein of the mitochondrial cytochrome bc1 complex	NA	NA	NA	NA	NA	0.89	1	0.36	TP	0.82	1	0.46	TP	0.98	0.9	TP	0.24	0.82	TN	0.14	0.54	TN	0.08	0.42	TN	0.17	0.55	TN	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YOR095C	RKI1	Ribose-5-phosphate ketol-isomerase	0.81	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	In silico slow growth.	NA
YER070W	RNR1	Ribonucleotide reductase, large (R1) subunit	NA	NA	1	22.3	FP	1	1	-0.04	TP	1	1	-0.04	TP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	DNA synthesis not required in the model.	NA
YJL026W	RNR2	Ribonucleotide reductase subunit|ribonucleotide reductase, small (R2) subunit	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	DNA synthesis not required in the model.	NA
YIL066C	RNR3	Ribonucleotide reductase, large (R1) subunit	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.05	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YGR180C	RNR4	Ribonucleotide reductase, small (R2) subunit	NA	NA	1	8.5	FP	1	1	-0.03	TP	1	1	-0.02	TP	1.08	0.81	FP	1.1	0.69	FP	1.11	0.59	FP	1.12	0.62	FP	1.11	0.6	FP	Oth	DNA synthesis not required in the model.	NA
YJL121C	RPE1	D-ribulose-5-Phosphate 3-epimerase	NA	NA	NA	NA	NA	0.97	1	0.67	TP	1	1	0.22	TP	1.08	0.92	TP	1.1	0.84	FP	1.06	0.78	FP	1.11	0.78	TP	1.08	0.92	TP	Unk	The PPP is only used at a low level on glycerol. The effect of this deletion is small in vivo anyway.	NA
YER043C	SAH1	S-adenosyl-L-homocysteine hydrolase (putative)	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YLR180W	SAM1	S-adenosylmethionine synthetase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.05	TP	1.08	0.98	TP	1.1	0.96	TP	1.11	0.98	TP	1.12	0.98	TP	1.11	0.97	TP	NA	NA	NA
YDR502C	SAM2	Methionine biosynthesis regulatior	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0.01	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YPL274W	SAM3	High affinity S-adenosylmethionine permease	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0	TP	1.08	1.02	TP	1.1	1.05	TP	1.11	1.05	TP	1.12	1.07	TP	1.11	1.06	TP	NA	NA	NA
YPL273W	SAM4	AdoMet-homocysteine methyltransferase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.05	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YMR272C	SCS7	Desaturase|hydroxylase	NA	NA	NA	NA	NA	1	1	2.17	TP	1	1	0	TP	1.08	0.99	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	0.99	TP	1.11	0.98	TP	NA	NA	NA
YKL148C	SDH1	Succinate dehydrogenase flavoprotein subunit	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	0.06	TP	1.08	1	TP	1.1	0.97	TP	1.11	0.69	FP	1.12	0.79	TP	1.11	0.61	FP	Iso	Sdh1p is not considered to be an essential part of the succinate dehydrogenase complex.	NA
YLL041C	SDH2	Succinate dehydrogenase (ubiquinone) iron-sulfur protein subunit	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0.07	TP	1.08	0.97	TP	1.01	0.97	TP	0.8	0.67	TN	0.58	0.75	TN	0.93	0.59	FP	Med	With a lower lactate uptake rate the model shows slow growth on lactate.	NA
YKL141W	SDH3	Succinate dehydrogenase cytochrome b	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Unk	The model has an isozyme that includes an alternate subunit with high imilarity to Sdh3p, but even if this is removed the mutation is non-lethal.	NA
YDR178W	SDH4	Succinate dehydrogenase membrane anchor subunit	NA	NA	NA	NA	NA	1	1	-0.07	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	0.82	TP	1.12	0.92	TP	1.11	0.74	FP	Iso	Sdh4p is not considered to be an essential part of the succinate dehydrogenase complex.	NA
YIL168W	SDL1	NA	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.03	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.04	TP	NA	NA	NA
YFL045C	SEC53	Phosphomannomutase	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YMR013C	SEC59	Membrane protein|required for core glycosylation	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Den	Substrate in this reaction is a dead-end (dolichol).	FP
YOR184W	SER1	Phosphoserine transaminase	NA	NA	NA	NA	NA	1	0	28.8	FP	0.99	1	-0.02	TP	1.07	1.03	TP	1.09	1.02	TP	1.1	1.02	TP	1.12	0.99	TP	1.11	1.04	TP	Unk	Removing AGT reaction (catalyzed by Agx1p) would fix this false positive. Agx1p is annotated as a alanine-glyoxylate aminotransferase and there is evidence that this enzymatic function is indeed found in yeast [Monschau97], but the pathway is only active on a non-fermentative carbon source.	NA
YGR208W	SER2	Phosphoserine phosphatase	NA	NA	NA	NA	NA	1	0	5.08	FP	0.99	1	0.03	TP	1.07	1.02	TP	1.09	0.99	TP	1.1	0.98	TP	1.12	0.95	TP	1.11	1	TP	Unk	Removing AGT reaction (catalyzed by Agx1p) would fix this false positive. Agx1p is annotated as a alanine-glyoxylate aminotransferase and there is evidence that this enzymatic function is indeed found in yeast [Monschau97], but the pathway is only active on a non-fermentative carbon source.	NA
YER081W	SER3	3-phosphoglycerate dehydrogenase	NA	NA	NA	NA	NA	1	1	0.33	TP	1	1	-0.08	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA
YIL074C	SER33	3-phosphoglycerate dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.05	TP	1.11	1.05	TP	NA	NA	NA
YDR023W	SES1	Serine-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YDL168W	SFA1	Glutathione-dependent formaldehyde dehydrogenase|long-chain alcohol dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YJR095W	SFC1	Succinate-fumarate transport protein	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0.01	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.08	TP	1.11	1.06	TP	NA	NA	NA
YBR263W	SHM1	Serine hydroxymethyltransferase, mitochondrial	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0.06	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.04	TP	1.11	1.02	TP	NA	NA	NA
YLR058C	SHM2	Serine hydroxymethyltransferase	NA	NA	NA	NA	NA	1	0	4.29	FP	1	1	0	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1	TP	1.11	1.01	TP	Unk	Shm2p should not be required for growth in minimal media as even a shm1/shm2 double mutant is a glycine prototroph.	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YDL052C	SLC1	1-acyl-sn-gylcerol-3-phosphate acyl transferase (putative)	NA	NA	NA	NA	NA	0	1	0.1	FN	0	1	0.02	FN	0	0.99	FN	0	1	FN	0	0.99	FN	0	1.04	FN	0	1	FN	Bio	Two distinct enzymes are necessary for PA synthesis in lipid particles: the second step, acylation of lysophosphatidic acid is catalyzed by Slc1p; a specific point mutant allows cells to grow without making sphingolipids; this deletion is lethal because PA is req'd in our biomass.	NA
YNR034W	SOL1	Multicopy Suppressor Of los1	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.05	TP	1.08	1.02	TP	1.1	1	TP	1.11	1	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YCR073WA	SOL2	Multicopy suppressor of los1-1	NA	NA	NA	NA	NA	1	1	0.12	TP	1	1	-0.01	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YHR163W	SOL3	Weak multicopy suppressor of los1-1	NA	NA	NA	NA	NA	1	1	0.31	TP	1	1	0	TP	1.08	1	TP	1.1	1.02	TP	1.11	1	TP	1.12	1	TP	1.11	1.01	TP	NA	NA	NA
YGR248W	SOL4	6-phosphogluconolactonase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.06	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.06	TP	1.11	1.05	TP	NA	NA	NA
YKL184W	SPE1	Ornithine decarboxylase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.05	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.07	TP	1.11	1.05	TP	NA	NA	NA
YOL052C	SPE2	S-adenosylmethionine decarboxylase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0	TP	1.08	1.03	TP	1.1	1.06	TP	1.11	1.05	TP	1.12	1.08	TP	1.11	1.07	TP	NA	NA	NA
YPR069C	SPE3	Putrescine aminopropyltransferase (spermidine synthase)	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.08	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YLR146C	SPE4	Spermine synthase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.04	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YOR190W	SPR1	Exo-1,3-beta-glucanase, sporulation-specific	NA	NA	NA	NA	NA	1	1	0.23	TP	1	1	-0.04	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.07	TP	1.11	1.05	TP	NA	NA	NA
YMR101C	SRT1	Cis-prenyltransferase	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.01	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YKL218C	SRY1	Pyridoxal-5'phosphate-dependent enzyme homologous to mouse glial serine racemase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.04	TP	1.08	1.04	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YDR536W	STL1	Sugar transporter-like protein	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1	TP	1.12	1.03	TP	1.11	1.01	TP	NA	NA	NA
YJR130C	STR2	Cystathionine gamma-synthase	NA	NA	NA	NA	NA	1	1	0.07	TP	1	1	0.01	TP	1.08	1.01	TP	1.1	1.04	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.03	TP	NA	NA	NA
YLR305C	STT4	Phosphatidylinositol-4-kinase|similar to VPC34	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Den	Phospholipid produced by this reaction leads to a dead-end (1D-myo-Inositol 1,4,5-trisphosphate). Also Pik1p is an isozyme.	FP
YMR054W	STV1	110 kDa subunit; not in vacuole membrane|vacuolar H-ATPase	NA	NA	NA	NA	NA	1	1	-0.06	TP	1	1	-0.05	TP	1.08	0.97	TP	1.1	0.97	TP	1.11	0.83	TP	1.12	0.86	TP	1.11	0.97	TP	NA	NA	NA
YIL162W	SUC2	Invertase (sucrose hydrolyzing enzyme)	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	1	TP	1.11	0.98	TP	1.12	0.96	TP	1.11	0.97	TP	NA	NA	NA
YBR294W	SUL1	Sulfate uptake is mediated by specific sulfate transporters SUL1 and SUL2, which control the concentration of endogenous activated sulfate intermediates.	NA	NA	NA	NA	NA	1	1	0.08	TP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YLR092W	SUL2	High affinity sulfate permease	NA	NA	NA	NA	NA	1	1	0.1	TP	1	1	0.02	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1	TP	1.11	1.01	TP	NA	NA	NA
YPL057C	SUR1	Integral membrane protein|similar to YBR161w, Hoc1p, and Och1p	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.02	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1	TP	1.12	0.97	TP	1.11	0.99	TP	NA	NA	NA
YDR297W	SUR2	Sphingosine hydroxylase	NA	NA	NA	NA	NA	1	1	0.29	TP	1	1	0	TP	1.08	1	TP	1.1	0.99	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YLR372W	SUR4	Elongase	NA	NA	1	3.4	FP	1	1	-0.01	TP	1	1	-0.02	TP	1.08	0.75	FP	1.1	0.79	FP	1.11	0.89	TP	1.12	0.91	TP	1.11	0.92	TP	Bio	Involved in sphingolipid biosynthesis. These lipids are not currently required for growth by the model.	NA
YLR354C	TAL1	Transaldolase, enzyme in the pentose phosphate pathway	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.02	TP	1.08	0.99	TP	1.1	1.02	TP	1.11	0.92	TP	1.12	1.09	TP	1.11	0.95	TP	NA	NA	NA
YBR069C	TAT1	Amino acid transport protein for valine, leucine, isoleucine, and tyrosine	NA	NA	NA	NA	NA	1	1	0.7	TP	1	1	0	TP	1.08	0.87	FP	1.1	0.98	TP	1.11	1.01	TP	1.12	1	TP	1.11	1.01	TP	Iso	There are multiple alternative isozymes for amino acid transporters.	NA
YOL020W	TAT2	Tryptophan permease, high affinity	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	-0.08	TP	1.08	1	TP	1.1	1	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YJL052W	TDH1	Glyceraldehyde-3-phosphate dehydrogenase 1	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	0	TP	1.08	0.99	TP	1.1	1.02	TP	1.11	1.05	TP	1.12	1.05	TP	1.11	1.03	TP	NA	NA	NA
YJR009C	TDH2	Glyceraldehyde 3-phosphate dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.02	TP	1.08	1	TP	1.1	1	TP	1.11	1.02	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YGR192C	TDH3	Glyceraldehyde-3-phosphate dehydrogenase 3	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.01	TP	1.08	0.97	TP	1.1	0.94	TP	1.11	0.98	TP	1.12	0.95	TP	1.11	0.98	TP	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YDL185W	TFP1	Site-specific endonuclease VDE (PI-SceI)|vacuolar ATPase V1 domain subunit A (69 kDa)|protein with three regions (ABC) that are spliced to yield the extein AC and the intein B; AC is a 69K vacuolar (H+)-ATPase, and B is a 50K site-specfic endonuclease named VDE (PI-SceI) that is homologous to HO. Cleavage is meiosis-specific and induces ge	NA	NA	1	12.2	FP	1	1	-0.03	TP	1	1	-0.02	TP	1.08	0.7	FP	1.1	0.66	FP	1.11	0.49	FP	1.12	0.57	FP	1.11	0.59	FP	Oth	The tfp1 null mutant is viable but is calcium-sensitive, lacks vacuolar (H)-ATPase activity, and is defective in vacuolar acidification and assembly of the remaining V1 subunits [SGD]. pH balancing problem.	NA
YPL234C	TFP3	Vacuolar ATPase V0 domain subunit c' (17 kDa)|vacuolar H(+) ATPase 17 kDa subunit C	NA	NA	1	7.1	FP	1	1	0.03	TP	1	1	0.04	TP	1.08	0.79	FP	1.1	0.66	FP	1.11	0.63	FP	1.12	0.62	FP	1.11	0.63	FP	Oth	See other vacuolar ATPase components.	NA
YOL055C	THI20	THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3.	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.02	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA
YPL258C	THI21	THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3.	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.1	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YPR121W	THI22	THI for thiamine metabolism. Transcribed in the presence of low level of thiamine (10-8M) and turned off in the presence of high level (10-6M) of thiamine. Under the positive control of THI2 and THI3.	NA	NA	NA	NA	NA	1	1	0.02	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	0.99	TP	1.11	1	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YPL214C	THI6	TMP pyrophosphorylase|hydroxyethylthiazole kinase	NA	NA	NA	NA	NA	1	1	0.07	TP	1	1	0	TP	1.08	0.94	TP	1.1	0.98	TP	1.11	1.02	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA
YLR237W	THI7	Thiamine transporter	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	0.01	TP	1.08	1.04	TP	1.1	1.07	TP	1.11	1.07	TP	1.12	1.1	TP	1.11	1.08	TP	NA	NA	NA
YOR143C	THI80	Thiamin pyrophosphokinase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Thiamin biosynthesis not required in the model	FP
YHR025W	THR1	Homoserine kinase	NA	NA	NA	NA	NA	1	1	6.34	TP	1	1	-0.08	TP	1.08	0.99	TP	1.1	0.92	TP	1.11	0.89	TP	1.12	0.76	FP	1.11	0.97	TP	Dis	This should only be a threonine auxotroph [SGD]. May play some other uncharacterized role.	NA
YCR053W	THR4	Threonine synthase	NA	NA	NA	NA	NA	1	0	7.67	FP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1	TP	1.12	0.99	TP	1.11	1.03	TP	Unk	Threonine can be synthesized by the model from glycine using Gly1p. If CYSTL (Cys1p) and AHCi (Sah1p) reactions are removed the false positive prediction is corrected and both of these have putative assignments, but neither can be removed from the model.	NA
YIL078W	THS1	Threonine-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	1.08	1.2	TP	1.1	1.23	TP	1.11	1.38	TP	1.12	1.24	TP	1.11	1.25	TP	Oth	Protein synthesis not required in the model	NA
YPR074C	TKL1	Transketolase 1	NA	NA	NA	NA	NA	1	1	4.11	TP	1	1	0.1	TP	1.08	0.99	TP	1.1	0.97	TP	1.11	0.9	TP	1.12	1	TP	1.11	1.02	TP	NA	NA	NA
YJR066W	TOR1	Phosphatidylinositol kinase homolog	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YKL203C	TOR2	Putative protein/phosphatidylinositol kinase involved in signaling activation of translation initiation, distribution of the actin cytoskeleton, and meiosis	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Den	Phospholipid produced by this reaction leads to a dead end (phosphatidyl-1D-myo-inositol 3,4-bisphosphate).	FP
YDR050C	TPI1	Triosephosphate isomerase	0.2	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	0.22	0.98	FN	1.04	0.93	TP	1.04	0.93	TP	0.41	0.93	FN	0.89	0.92	TP	Dis	Mutant is unable to grow on glucose as sole carbon source. If ethanol or acetate is added to media containing glucose or galactose, cells are viable. Impaired growth probably due to NADH/energy shortage on glucose [Compagno01]. In one study this gene is found to be essential [Giaever02], wheras in the other one it has no phenotype [Steinmetz02].	FP

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YBR126C	TPS1	Trehalose-6-phosphate synthase/phosphatase complex 56 kDa synthase subunit	NA	NA	1	6.8	FP	0	1	-0.06	TN	1	1	-0.02	TP	1.08	0.81	FP	1.1	0.83	FP	1.11	0.91	TP	1.12	0.86	TP	1.11	0.89	TP	Med	Essential for growth on glucose and fructose [MIPS]. Deletion of TPS1 totally abolishes trehalose-6-phosphate synthase activity and measurable trehalose production, but YP media contains trehalose so TPS1 should not be required.	NA
YDR074W	TPS2	Trehalose-6-phosphate phosphatase	NA	NA	1	18	FP	0	1	0	TN	1	1	-0.05	TP	1.08	0.96	TP	1.1	0.95	TP	1.11	1.06	TP	1.12	1.03	TP	1.11	1.02	TP	Med	See TPS1.	NA
YMR261C	TPS3	Trehalose-6-phosphate synthase/phosphatase complex 115 kDa regulatory subunit	NA	NA	NA	NA	NA	1	1	0.1	TP	1	1	0	TP	1.08	0.99	TP	1.1	0.98	TP	1.11	0.99	TP	1.12	0.96	TP	1.11	0.97	TP	NA	NA	NA
YDR007W	TRP1	N-(5'-phosphoribosyl)-anthranilate isomerase	NA	NA	NA	NA	NA	0	0	5.83	TN	1	1	0.02	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.05	TP	1.11	1.03	TP	NA	NA	NA
YER090W	TRP2	Anthranilate synthase component	NA	NA	NA	NA	NA	1	1	2.88	TP	1	1	-0.05	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.05	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YKL211C	TRP3	Anthranilate synthase component II|indole-3-phosphate	NA	NA	NA	NA	NA	0	0	7.77	TN	1	1	-0.07	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.06	TP	1.11	1.04	TP	NA	NA	NA
YDR354W	TRP4	Anthranilate phosphoribosyl transferase	NA	NA	NA	NA	NA	0	1	2.64	TN	1	1	-0.03	TP	1.08	0.99	TP	1.1	1	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	Weak false negative	NA
YGL026C	TRP5	Tryptophan synthetase	NA	NA	NA	NA	NA	0	1	1.4	TN	1	1	0.06	TP	1.08	0.97	TP	1.1	0.99	TP	1.11	0.95	TP	1.12	0.99	TP	1.11	1	TP	NA	Weak false negative	NA
YDR353W	TRR1	Thioredoxin reductase|EC 1.6.4.5	0	TN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
YHR106W	TRR2	Thioredoxin reductase	NA	NA	NA	NA	NA	1	1	-0.05	TP	1	1	-0.04	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YBR265W	TSC10	3-ketosphinganine reductase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Sphingolipid synthesis not required in the model	FP
YML100W	TSL1	Similar to TPS3 gene product|trehalose-6-phosphate synthase/phosphatase complex 123 kDa regulatory subunit	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.07	TP	1.08	1.02	TP	1.1	1.05	TP	1.11	1.04	TP	1.12	1.08	TP	1.11	1.06	TP	NA	NA	NA
YBR166C	TYR1	Prephenate dehydrogenase (NADP+)	NA	NA	1	3.5	FP	1	1	0	TP	1	1	-0.01	TP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Unk	Should be a tyrosine auxotroph, but the media contains tyrosine. Also, the model has an alternative reaction with no gene association.	NA
YGR185C	TYS1	Tyrosine-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YGR019W	UGA1	Gamma-aminobutyrate (GABA) transaminase (4-aminobutyrate aminotransferase)	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YBR006W	UGA2	Succinate semialdehyde dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0.2	TP	1.08	1	TP	1.1	1	TP	1.11	0.99	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA
YDL210W	UGA4	GABA-specific transport protein	NA	NA	NA	NA	NA	1	1	0.11	TP	1	1	-0.05	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YKL035W	UGP1	Uridinephosphoglucose pyrophosphorylase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Reaction produces UDPglc, which is not required in our model.	FP
YKL216W	URA1	Dihydroorotate dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.03	TP	1.08	1	TP	1.1	0.98	TP	1.11	0.98	TP	1.12	1.01	TP	1.11	1	TP	NA	NA	NA
YMR271C	URA10	Orotate phosphoribosyltransferase 2	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.07	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YJL130C	URA2	Aspartate transcarbamylase|carbamoyl phosphate synthetase|glutamine amidotransferase	NA	NA	NA	NA	NA	1	1	-0.06	TP	1	1	0	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.02	TP	1.11	1.03	TP	NA	NA	NA
YLR420W	URA4	Dihydrooratase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	1	TP	1.11	1.04	TP	1.12	1.06	TP	1.11	1.06	TP	NA	NA	NA
YML106W	URA5	Orotate phosphoribosyltransferase 1	NA	NA	NA	NA	NA	1	1	0.03	TP	1	1	0.01	TP	1.08	1	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.03	TP	1.11	1.01	TP	NA	NA	NA
YKL024C	URA6	Uridine-monophosphate kinase (uridylate kinase)	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	RNA and protein synthesis not required in the model.	FP
YBL039C	URA7	CTP synthase	NA	NA	1	3.2	FP	1	1	-0.03	TP	1	1	0	TP	1.08	0.82	FP	1.1	0.89	TP	1.11	0.86	TP	1.12	0.91	TP	1.11	0.85	TP	Med	Model does not require ctp to grow on complex media.	NA
YJR103W	URA8	CTP synthase	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.07	TP	1.08	1.01	TP	1.1	1	TP	1.11	1.01	TP	1.12	1	TP	1.11	1	TP	NA	NA	NA
YDR400W	URH1	Uridine nucleosidase (uridine ribohydrolase); EC 3.2.2.3	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.01	TP	1.08	1.01	TP	1.1	1	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	1	TP	NA	NA	NA
YNR012W	URK1	Uridine kinase	NA	NA	NA	NA	NA	1	1	0.06	TP	1	1	0	TP	1.08	0.97	TP	1.1	0.95	TP	1.11	0.99	TP	1.12	1.01	TP	1.11	1	TP	NA	NA	NA
YJR049C	UTR1	Associated with ferric reductase	NA	NA	NA	NA	NA	1	1	0.14	TP	1	1	-0.07	TP	1.08	0.95	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	0.95	TP	1.11	0.97	TP	NA	NA	NA
YGR094W	VAS1	Valine-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YGR065C	VHT1	H+-biotin symporter	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	Biotin not required in our model, but bakers' yeast is auxotrophic for biotin (vitamin H) and depends on the efficient uptake of this compound from the environment [Stolz99].	NA
YPR036W	VMA13	Vacuolar H(+) ATPase V1 sector 54 kDa subunit	NA	NA	1	5.9	FP	1	1	-0.04	TP	1	1	0.03	TP	1.08	0.73	FP	1.1	0.61	FP	1.11	0.59	FP	1.12	0.62	FP	1.11	0.68	FP	Oth	See other vacuolar ATPase components.	NA
YBR127C	VMA2	Vacuolar ATPase V1 domain subunit B (60 kDa)	NA	NA	1	10.6	FP	1	1	-0.03	TP	1	1	-0.02	TP	1.08	0.86	FP	1.1	0.7	FP	1.11	0.75	FP	1.12	0.7	FP	1.11	0.73	FP	Oth	See other vacuolar ATPase components.	NA
YOR332W	VMA4	E subunit of V1 sector|vacuolar H(+) ATPase 27 kDa subunit	NA	NA	1	5.2	FP	1	1	0.02	TP	1	1	-0.03	TP	1.08	0.9	TP	1.1	0.87	TP	1.11	0.65	FP	1.12	0.61	FP	1.11	0.66	FP	Oth	See other vacuolar ATPase components.	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YKL080W	VMA5	V1 sector hydrophilic subunit C|vacuolar ATPase V1 domain subunit C (42 kDa)|vacuolar H-ATPase	NA	NA	1	6.1	FP	1	1	-0.02	TP	1	1	-0.02	TP	1.08	0.66	FP	1.1	0.62	FP	1.11	0.57	FP	1.12	0.51	FP	1.11	0.57	FP	Oth	See other vacuolar ATPase components.	NA
YLR447C	VMA6	Vacuolar ATPase V0 domain subunit d (36 kDa)|vacuolar H(+) ATPase 36 kDa subunit (D subunit of VO sector)	NA	NA	1	10.9	FP	1	1	-0.03	TP	1	1	-0.02	TP	1.08	0.65	FP	1.1	0.59	FP	1.11	0.58	FP	1.12	0.57	FP	1.11	0.65	FP	Oth	The vma6 null mutant is viable but shows a growth defect at neutral pH and is sensitive to calcium. pH balancing problem.	NA
YGR020C	VMA7	Vacuolar ATPase V1 domain subunit F (14 kDa)	NA	NA	1	9.9	FP	1	1	-0.01	TP	1	1	0	TP	1.08	0.72	FP	1.1	0.62	FP	1.11	0.63	FP	1.12	0.64	FP	1.11	0.66	FP	Oth	See other vacuolar ATPase components.	NA
YEL051W	VMA8	V1 catalytic sector D subunit|vacuolar H-ATPase	NA	NA	1	14.4	FP	1	1	-0.02	TP	1	1	-0.01	TP	1.08	0.75	FP	1.1	0.65	FP	1.11	0.57	FP	1.12	0.58	FP	1.11	0.63	FP	Oth	The vma8 null mutant is viable but lacks vacuolar (H)-ATPase activity, cannot grow at neutral pH or on nonfermentable carbon sources, and fails to accumulate quinacrine in the vacuole [SGD]. The slow growth phenotype is probably because of problems with pH balancing.	NA
YOR270C	VPH1	V0 sector subunit|essential for vacuolar acidification and vacuolar H-ATPase activity|vacuolar ATPase V0 domain subunit a (100 kDa)|vacuolar H-ATPase	NA	NA	1	3.4	FP	1	1	0.01	TP	1	1	0.02	TP	1.08	0.88	TP	1.1	0.78	FP	1.11	0.8	TP	1.12	0.78	TP	1.11	0.91	TP	Oth	See other vacuolar ATPase components.	NA
YLR240W	VPS34	Phosphatidylinositol 3-kinase	NA	NA	1	18.9	FP	1	1	-0.01	TP	1	1	-0.01	TP	1.08	0.58	FP	1.1	0.56	FP	1.11	0.61	FP	1.12	0.55	FP	1.11	0.56	FP	Oth	PI3 kinase activity involved in signaling processes - in the model this leads to a dead end.	NA
YOL097C	WRS1	Tryptophan-tRNA ligase	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YGR194C	XKS1	Xylulokinase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0.14	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA
YJR133W	XPT1	Xanthine phosphoribosyl transferase	NA	NA	NA	NA	NA	1	1	0	TP	1	1	0.04	TP	1.08	1.03	TP	1.1	1.05	TP	1.11	1.04	TP	1.12	1.08	TP	1.11	1.06	TP	NA	NA	NA
YLR070C	XYL2	Xylitol Dehydrogenase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	0.01	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.07	TP	1.11	1.06	TP	NA	NA	NA
YAR035W	YAT1	Carnitine acetyltransferase	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.03	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.04	TP	0.97	1.03	TP	1.11	1.03	TP	NA	NA	NA
YBR184W	YBR18	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	0	TP	1.08	1	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	0.98	TP	1.11	0.98	TP	NA	NA	NA
YBR284W	YBR28	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	0.04	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YCR024C	YCR02	Hypothetical ORF	NA	NA	1	5.2	FP	1	1	-0.03	TP	1	1	-0.03	TP	1.08	0.73	FP	1.1	0.66	FP	1.11	0.65	FP	1.12	0.56	FP	1.11	0.6	FP	Oth	Protein synthesis not required in the model	NA
YDR111C	YDR11	Hypothetical ORF	NA	NA	NA	NA	NA	0.95	1	-0.02	TP	0.98	1	-0.01	TP	1.05	1.01	TP	1.09	1.04	TP	1.11	1.04	TP	0.9	1.06	TP	1.08	1.05	TP	NA	NA	NA
YDR341C	YDR34	Protein required for cell viability	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	FP
YDR531W	YDR53	Pantothenate kinase (ATP:D-pantothenate 4'-phosphotransferase, EC 2.7.1.33) catalyzes the first committed step in the universal biosynthetic pathway leading to CoA.	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Bio	CoA biosynthesis not required in the model.	NA
YEL041W	YEL04	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0.11	TP	1	1	-0.06	TP	1.08	1.03	TP	1.1	1.06	TP	1.11	1.06	TP	1.12	1.09	TP	1.11	1.06	TP	NA	NA	NA
YEL047C	YEL04	Fumurate ReDuctase Soluble	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.03	TP	1.08	1.02	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.04	TP	NA	NA	NA
YER053C	YER05	Sequence similarity to mitochondrial phosphate transporters	NA	NA	NA	NA	NA	1	1	0.22	TP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA
YER087W	YER08	Hypothetical ORF	NA	NA	1	7.5	FP	1	1	-0.02	TP	1	1	0	TP	1.08	0.97	TP	1.1	0.89	TP	1.11	0.78	FP	1.12	0.72	FP	1.11	0.78	FP	Oth	Protein synthesis not required in the model	NA
YFL030W	YFL03	NA	NA	NA	NA	NA	NA	1	1	0.08	TP	1	1	-0.06	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.03	TP	0.79	1.06	FN	1.08	1.04	TP	Med	Lower oxygen uptake rate would correct this false negative prediction.	NA
YFR055W	YFR05	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.07	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YGL245W	YGL24	Protein required for cell viability	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	FP
YGR012W	YGR01	Hypothetical ORF	NA	NA	NA	NA	NA	0	1	0	FN	1	1	0	TP	1.08	1.01	TP	1.1	0.99	TP	1.11	0.98	TP	1.12	0.99	TP	1.11	0.99	TP	Unk	Model can't make cysteine without the rxn catalyzed by this gene. Might be able to bypass this by making cys from pyr using CYS1 [KEGG].	NA
YGR043C	YGR04	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	-0.02	TP	1	1	-0.01	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YGR125W	YGR12	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0.1	TP	1	1	-0.01	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA
YGR287C	YGR28	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0.05	TP	1	1	-0.07	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.04	TP	1.11	1.03	TP	NA	NA	NA
YHL012W	YHL01	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.05	TP	1.08	1	TP	1.1	1	TP	1.11	0.96	TP	1.12	0.97	TP	1.11	0.99	TP	NA	NA	NA
YHR020W	YHR02	Protein required for cell viability	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YJL045W	YJL04	Similar to SDH1	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.06	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.03	TP	1.11	1.03	TP	NA	NA	NA
YJL068C	YJL06	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.05	TP	1.08	1	TP	1.1	1.02	TP	1.11	1.03	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YJL070C	YJL07	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	-0.01	TP	1	1	-0.04	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.04	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YJL200C	YJL20	Hypothetical ORF	NA	NA	NA	NA	NA	1	0	4.69	FP	1	1	-0.04	TP	1.08	1.02	TP	1.1	1	TP	1.11	0.99	TP	1.12	1	TP	1.11	0.98	TP	Unk	Aco1p acts as an isozyme for this reaction. For some reason YJL200C gene product is only required on minimal media.	NA
YJL216C	YJL21	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0.01	TP	1	1	-0.03	TP	1.08	1.01	TP	1.1	1.01	TP	1.11	1.02	TP	1.12	1.01	TP	1.11	1.02	TP	NA	NA	NA

ORF	Name	Annotation	Ess sim	Ess call	Slow sim	Slow exp	Slow call	MMD sim	MMD exp	MMD ave	MMD call	YPGal sim	YPGal exp	YPGal ave	YPGal call	YPD sim	YPD exp	YPD call	YPDGE sim	YPDGE exp	YPDGE call	YPG sim	YPG exp	YPG call	YPE sim	YPE exp	YPE call	YPL sim	YPL exp	YPL call	Class	Explanation	Forster et al
YKL132C	YKL13	Probable folyl-polyglutamate synthetase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.08	TP	1.08	1.02	TP	1.1	1.01	TP	1.11	1.01	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YLR089C	YLR08	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	1.26	TP	1	1	-0.05	TP	1.08	1	TP	1.1	1.03	TP	1.11	0.94	TP	1.12	0.99	TP	1.11	1.01	TP	NA	NA	NA
YLR164W	YLR16	YLR164Wp is homologous to TIM18p	NA	NA	NA	NA	NA	1	1	0.09	TP	1	1	-0.03	TP	1.08	1	TP	1.1	0.99	TP	1.11	0.99	TP	1.12	0.99	TP	1.11	0.99	TP	NA	NA	NA
YML082W	YML08	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.04	TP	1.08	1.02	TP	1.1	1.04	TP	1.11	1.04	TP	1.12	1.04	TP	1.11	1.02	TP	NA	NA	NA
YML096W	YML09	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.05	TP	1.08	1.03	TP	1.1	1.06	TP	1.11	1.04	TP	1.12	1.09	TP	1.11	1.07	TP	NA	NA	NA
YMR084W	YMR08	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.06	TP	1.08	1.03	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YMR085W	YMR08	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	-0.04	TP	1	1	-0.06	TP	1.08	1.03	TP	1.1	1.03	TP	1.11	1.02	TP	1.12	1.05	TP	1.11	1.04	TP	NA	NA	NA
YMR118C	YMR11	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0	TP	1	1	-0.02	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.02	TP	NA	NA	NA
YMR293C	YMR29	Protein similar to bacterial glutamyl-tRNA amidotransferases	NA	NA	1	3.1	FP	1	1	-0.04	TP	1	1	-0.01	TP	1.08	0.74	FP	1.1	0.7	FP	1.11	0.63	FP	1.12	0.59	FP	1.11	0.63	FP	Den	This reaction is a dead end.	NA
YKL067W	YNK1	Nucleoside diphosphate kinase	NA	NA	NA	NA	NA	0	1	-0.04	FN	0	1	-0.04	FN	0	0.99	FN	0	0.97	FN	0	0.95	FN	0	0.9	FN	0	0.94	FN	Iso	Null mutant retains 10% of nucleoside diphosphate kinase activity. Sources of remaining enzyme activity are unknown, but possibilities are discussed in [Fukuchi93]. Reaction w/o gene associations could be added to the model to represent these unidentified enzymes.	FN
YNL247W	YNL24	Protein required for cell viability	1	FP	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oth	Protein synthesis not required in the model	NA
YOR071C	YOR07	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0.04	TP	1	1	-0.07	TP	1.08	1.01	TP	1.1	1.02	TP	1.11	1.01	TP	1.12	1.01	TP	1.11	1.01	TP	NA	NA	NA
YOR192C	YOR19	Hypothetical ORF	NA	NA	NA	NA	NA	1	1	0.8	TP	1	1	-0.01	TP	1.08	1.01	TP	1.1	1.03	TP	1.11	1.03	TP	1.12	1.03	TP	1.11	1.02	TP	NA	NA	NA
YKR053C	YSR3	DHS-1-P phosphatase	NA	NA	NA	NA	NA	1	1	-0.03	TP	1	1	-0.07	TP	1.08	1.02	TP	1.1	1.02	TP	1.11	1.02	TP	1.12	1.02	TP	1.11	1.01	TP	NA	NA	NA
YJL139C	YUR1	Mannosyltransferase	NA	NA	NA	NA	NA	1	1	0.13	TP	1	1	0	TP	1.08	0.97	TP	1.1	0.99	TP	1.11	0.95	TP	1.12	0.98	TP	1.11	0.99	TP	NA	NA	NA