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