ORF	E.C. #	GENE	GENE DESCRIPTION	REACTION	Rxn Name
# CARBOHYDRATE METABOLISM					
# GLYCOLYSIS/GLUCONEOGENESIS					
YCL040W	2.7.1.2	*GLK1*	GLUCOKINASE	GLC + ATP -> G6P + ADP	glk1_1
YCL040W	2.7.1.2	*GLK1*	GLUCOKINASE	MAN + ATP -> MAN6P + ADP	glk1_2
YCL040W	2.7.1.2	*GLK1*	GLUCOKINASE	bDGLC + ATP -> bDG6P + ADP	glk1_3
YFR053C	2.7.1.1	*HXK1*	HEXOKINASE I (PI) (ALSO CALLED HEXOKINASE A)	bDGLC + ATP -> G6P + ADP	hxk1_1
YFR053C	2.7.1.1	*HXK1*	HEXOKINASE I (PI) (ALSO CALLED HEXOKINASE A)	GLC + ATP -> G6P + ADP	hxk1_2
YFR053C	2.7.1.1	*HXK1*	HEXOKINASE I (PI) (ALSO CALLED HEXOKINASE A)	MAN + ATP -> MAN6P + ADP	hxk1_3
YFR053C	2.7.1.1	*HXK1*	HEXOKINASE I (PI) (ALSO CALLED HEXOKINASE A)	ATP + FRU -> ADP + F6P	hxk1_4
YGL253W	2.7.1.1	*HXK2*	HEXOKINASE II (PII) (ALSO CALLED HEXOKINASE B)	bDGLC + ATP -> G6P + ADP	hxk2_1
YGL253W	2.7.1.1	*HXK2*	HEXOKINASE II (PII) (ALSO CALLED HEXOKINASE B)	GLC + ATP -> G6P + ADP	hxk2_2
YGL253W	2.7.1.1	*HXK2*	HEXOKINASE II (PII) (ALSO CALLED HEXOKINASE B)	MAN + ATP -> MAN6P + ADP	hxk2_3
YGL253W	2.7.1.1	*HXK2*	HEXOKINASE II (PII) (ALSO CALLED HEXOKINASE B)	ATP + FRU -> ADP + F6P	hxk2_4
YBR196C	5.3.1.9	*PGI1*	GLUCOSE-6-PHOSPHATE ISOMERASE	G6P <-> F6P	pgi1_1
YBR196C	5.3.1.9	*PGI1*	GLUCOSE-6-PHOSPHATE ISOMERASE	G6P <-> bDG6P	pgi1_2
YBR196C	5.3.1.9	*PGI1*	GLUCOSE-6-PHOSPHATE ISOMERASE	bDG6P <-> F6P	pgi1_3
YMR205C	2.7.1.11	*PFK2*	PHOSPHOFRUCTOKINASE BETA SUBUNIT	F6P + ATP -> FDP + ADP	pfk2
YGR240C	2.7.1.11	*PFK1*	PHOSPHOFRUCTOKINASE ALPHA SUBUNIT	F6P + ATP -> FDP + ADP	pfk1_1
YGR240C	2.7.1.11	*PFK1*	PHOSPHOFRUCTOKINASE ALPHA SUBUNIT	ATP + TAG6P -> ADP + TAG16P	pfk1_2
YGR240C	2.7.1.11	*PFK1*	PHOSPHOFRUCTOKINASE ALPHA SUBUNIT	ATP + S7P -> ADP + S17P	pfk1_3
YKL060C	4.1.2.13	*FBA1*	FRUCTOSE-BISPHOSPHATE ALDOLASE	FDP <-> T3P2 + T3P1	fba1_1
YDR050C	5.3.1.1	*TPI1*	TRIOSEPHOSPHATE ISOMERASE	T3P2 <-> T3P1	tpi1
YJL052W	1.2.1.12	*TDH1*	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE 1	T3P1 + PI + NAD <-> NADH + 13PDG	tdh1
YJR009C	1.2.1.12	*TDH2*	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE	T3P1 + PI + NAD <-> NADH + 13PDG	tdh2
YGR192C	1.2.1.12	*TDH3*	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE 3	T3P1 + PI + NAD <-> NADH + 13PDG	tdh3
YCR012W	2.7.2.3	*PGK1*	PHOSPHOGLYCERATE KINASE	13PDG + ADP <-> 3PG + ATP	pgk1
YKL152C	5.4.2.1	*GPM1*	PHOSPHOGLYCERATE MUTASE	13PDG <-> 23PDG	gpm1_1
YKL152C	5.4.2.1	*GPM1*	PHOSPHOGLYCERATE MUTASE	3PG <-> 2PG	gpm1_2
YDL021W	5.4.2.1	*GPM2*	SIMILAR TO GPM1 (PHOSPHOGLYCERATE MUTASE)	3PG <-> 2PG	gpm2
YOL056W	5.4.2.1	*GPM3*	PHOSPHOGLYCERATE MUTASE	3PG <-> 2PG	gpm3
YGR254W	4.2.1.11	*ENO1*	ENOLASE I	2PG <-> PEP	eno1
YHR174W	4.2.1.11	*ENO2*	ENOLASE	2PG <-> PEP	eno2
YMR323W	4.2.1.11	*ERR1*	PROTEIN WITH SIMILARITY TO ENOLASES	2PG <-> PEP	eno3

YPL281C	4.2.1.11	*ERR2*	ENOLASE RELATED PROTEIN	2PG <-> PEP	eno4
YOR393W	4.2.1.11	*ERR1*	ENOLASE RELATED PROTEIN	2PG <-> PEP	eno5
YAL038W	2.7.1.40	*CDC19*	PYRUVATE KINASE	PEP + ADP -> PYR + ATP	cdc19
YOR347C	2.7.1.40	*PYK2*	PYRUVATE KINASE, GLUCOSE-REPRESSED ISOFORM	PEP + ADP -> PYR + ATP	pyk2
YER178W	1.2.4.1	*PDA1*	PYRUVATE DEHYDROGENASE (LIPOAMIDE) ALPHA CHAIN PRECURSOR, E1 COMPONENT, ALPHA UNIT	PYRm + COAm + NADm -> NADHm + CO2m + ACCOAm	pda1
YBR221C	1.2.4.1	*PDB1*	PYRUVATE DEHYDROGENASE (LIPOAMIDE) BETA CHAIN PRECURSOR, E1 COMPONENT, BETA UNIT		
YNL071W	2.3.1.12	*LAT1*	DIHYDROLIPOAMIDE S-ACETYLTRANSFERASE, E2 COMPONENT		
# CITRATE CYCLE (TCA CYCLE)					
YNR001C	4.1.3.7	*CIT1*	CITRATE SYNTHASE, NUCLEAR ENCODED MITOCHONDRIAL PROTEIN.	ACCOAm + OAm -> COAm + CITm	cit1
YCR005C	4.1.3.7	*CIT2*	CITRATE SYNTHASE, NON-MITOCHONDRIAL CITRATE SYNTHASE	ACCOA + OA -> COA + CIT	cit2
YPR001W	4.1.3.7	*CIT3*	CITRATE SYNTHASE, MITOCHONDRIAL ISOFORM OF CITRATE SYNTHASE	ACCOAm + OAm -> COAm + CITm	cit3
YLR304C	4.2.1.3	*ACO1*	ACONITASE, MITOCHONDRIAL	CITm <-> ICITm	aco1
YJL200C	4.2.1.3	*YJL200C*	ACONITATE HYDRATASE HOMOLOG	CITm <-> ICITm	aco2
YNL037C	1.1.1.41	*IDH1*	ISOCITRATE DEHYDROGENASE (NAD+) MITO, SUBUINT1	ICITm + NADm -> CO2m + NADHm + AKGm	idh1
YOR136W	1.1.1.41	*IDH2*	ISOCITRATE DEHYDROGENASE (NAD+) MITO, SUBUNIT2		
YDL066W	1.1.1.42	*IDP1*	ISOCITRATE DEHYDROGENASE (NADP+)	ICITm + NADPm -> NADPHm + OSUCm	idp1_1
YLR174W	1.1.1.42	*IDP2*	ISOCITRATE DEHYDROGENASE (NADP+)	ICIT + NADP -> NADPH + OSUC	idp2_1
YNL009W	1.1.1.42	*IDP3*	ISOCITRATE DEHYDROGENASE (NADP+)	ICIT + NADP -> NADPH + OSUC	idp3_1
YDL066W	1.1.1.42	*IDP1*	ISOCITRATE DEHYDROGENASE (NADP+)	OSUCm -> CO2m + AKGm	idp1_2
YLR174W	1.1.1.42	*IDP2*	ISOCITRATE DEHYDROGENASE (NADP+)	OSUC -> CO2 + AKG	idp2_2
YNL009W	1.1.1.42	*IDP3*	ISOCITRATE DEHYDROGENASE (NADP+)	OSUC -> CO2 + AKG	idp3_2
YIL125W	1.2.4.2	*KGD1*	ALPHA-KETOGLUTARATE DEHYDROGENASE COMPLEX, E1 COMPONENT	AKGm + NADm + COAm -> CO2m + NADHm + SUCCOAm	kgd1a
YDR148C	2.3.1.61	*KGD2*	DIHYDROLIPOAMIDE S-SUCCINYLTRANSFERASE, E2 COMPONENT		
YGR244C	6.2.1.4/6.2.	*LSC2*	SUCCINATE--COA LIGASE (GDP-FORMING)	ATPm + SUCCm + COAm <-> ADPm + PIm + SUCCOAm	lsc2
YOR142W	6.2.1.4/6.2.	*LSC1*	SUCCINATE-COA LIGASE ALPHA SUBUNIT	ATPm + ITCm + COAm <-> ADPm + PIm + ITCCOAm	lsc1
# ELECTRON TRANSPORT SYSTEM, COMPLEX II					

YKL141W	1.3.5.1	*SDH3*	SUCCINATE DEHYDROGENASE CYTOCHROME B	SUCCm + FADm <-> FUMm + FADH2m	sdh3
YKL148C	1.3.5.1	*SDH1*	SUCCINATE DEHYDROGENASE CYTOCHROME B		
YLL041C	1.3.5.1	*SDH2*	SUCCINATE DEHYDROGENASE (UBIQUINONE) IRON-SULFUR PROTEIN SUBUNIT		
YDR178W	1.3.5.1	*SDH4*	SUCCINATE DEHYDROGENASE MEMBRANE ANCHOR SUBUNIT		
YLR164W	1.3.5.1	*YLR164W*	STRONG SIMILARITY TO SDH4P		
YMR118C	1.3.5.1	*YMR118C*	STRONG SIMILARITY TO SUCCINATE DEHYDROGENASE		
YJL045W	1.3.5.1	*YJL045W*	STRONG SIMILARITY TO SUCCINATE DEHYDROGENASE FLAVOPROTEIN		
YEL047C	1.3.99.1	*YEL047C*	SOLUBLE FUMARATE REDUCTASE, CYTOPLASMIC	FADH2m + FUM -> SUCC + FADm	frds1
YJR051W	1.3.99.1	*OSM1*	MITOCHONDRIAL SOLUBLE FUMARATE REDUCTASE INVOLVED IN OSMOTIC REGULATION	FADH2m + FUMm -> SUCCm + FADm	osm1
YPL262W	4.2.1.2	*FUM1*	FUMARATASE	FUMm <-> MALm	fum1_1
YPL262W	4.2.1.2	*FUM1*	FUMARATASE	FUM <-> MAL	fum1_2
YKL085W	1.1.1.37	*MDH1*	MITOCHONDRIAL MALATE DEHYDROGENASE	MALm + NADm <-> NADHm + OAm	mdh1
YDL078C	1.1.1.37	*MDH3*	MALATE DEHYDROGENASE, PEROXISOMAL	MAL + NAD <-> NADH + OA	mdh3
YOL126C	1.1.1.37	*MDH2*	MALATE DEHYDROGENASE, CYTOPLASMIC	MAL + NAD <-> NADH + OA	mdh2
# ANAPLEROTIC REACTIONS					
YER065C	4.1.3.1	*ICL1*	ISOCITRATE LYASE	ICIT -> GLX + SUCC	icl1
YPR006C	4.1.3.1	*ICL2*	ISOCITRATE LYASE, MAY BE NONFUNCTIONAL	ICIT -> GLX + SUCC	icl2
YIR031C	4.1.3.2	*DAL7*	MALATE SYNTHASE	ACCOA + GLX -> COA + MAL	dal7
YNL117W	4.1.3.2	*MLS1*	MALATE SYNTHASE	ACCOA + GLX -> COA + MAL	mls1
YKR097W	4.1.1.49	*PCK1*	PHOSPHOENOLPYRUVATE CARBOXYLKINASE	OA + ATP -> PEP + CO2 + ADP	pck1
YLR377C	3.1.3.11	*FBP1*	FRUCTOSE-1,6-BISPHOSPHATASE	FDP -> F6P + PI	fbp1
YGL062W	6.4.1.1	*PYC1*	PYRUVATE CARBOXYLASE	PYR + ATP + CO2 -> ADP + OA + PI	pyc1
YBR218C	6.4.1.1	*PYC2*	PYRUVATE CARBOXYLASE	PYR + ATP + CO2 -> ADP + OA + PI	pyc2
YKL029C	1.1.1.38	*MAE1*	MITOCHONDRIAL MALIC ENZYME	MALm + NADPm -> CO2m + NADPHm + PYRm	mae1
# PENTOSE PHOSPHATE CYCLE					
YNL241C	1.1.1.49	*ZWF1*	GLUCOSE-6-PHOSPHATE-1-DEHYDROGENASE	G6P + NADP <-> D6PGL + NADPH	zwf1
YNR034W	3.1.1.31	*SOL1*	POSSIBLE 6-PHOSPHOGLUCONOLACTONASE	D6PGL -> D6PGC	sol1
YCR073W	3.1.1.31	*SOL2*	POSSIBLE 6-PHOSPHOGLUCONOLACTONASE	D6PGL -> D6PGC	sol2
YHR163W	3.1.1.31	*SOL3*	POSSIBLE 6-PHOSPHOGLUCONOLACTONASE	D6PGL -> D6PGC	sol3
YGR248W	3.1.1.31	*SOL4*	POSSIBLE 6-PHOSPHOGLUCONOLACTONASE	D6PGL -> D6PGC	sol4
YGR256W	1.1.1.44	*GND2*	6-PHOPHOGLUCONATE DEHYDROGENASE	D6PGC + NADP -> NADPH + CO2 + RL5P	gnd2

YHR183W	1.1.1.44	*GND1*	6-PHOPHOGLUCONATE DEHYDROGENASE	D6PGC + NADP -> NADPH + CO2 + RL5P	gnd1
YJL121C	5.1.3.1	*RPE1*	RIBULOSE-5-P 3-EPIMERASE	RL5P <-> X5P	rpe1
YOR095C	5.3.1.6	*RKI1*	RIBOSE-5-P ISOMERASE	RL5P <-> R5P	rki1
YBR117C	2.2.1.1	*TKL2*	TRANSKETOLASE	R5P + X5P <-> T3P1 + S7P	tkl2_1
YBR117C	2.2.1.1	*TKL2*	TRANSKETOLASE	X5P + E4P <-> F6P + T3P1	tkl2_2
YPR074C	2.2.1.1	*TKL1*	TRANSKETOLASE	R5P + X5P <-> T3P1 + S7P	tkl1_1
YPR074C	2.2.1.1	*TKL1*	TRANSKETOLASE	X5P + E4P <-> F6P + T3P1	tkl1_2
YLR354C	2.2.1.2	*TAL1*	TRANSALDOLASE	T3P1 + S7P <-> E4P + F6P	tal1_1
YGR043C	2.2.1.2	*YGR043C*	TRANSALDOLASE	T3P1 + S7P <-> E4P + F6P	tal1_2
YCR036W	2.7.1.15	*RBK1*	RIBOKINASE	RIB + ATP -> R5P + ADP	rbk1_1
YCR036W	2.7.1.15	*RBK1*	RIBOKINASE	DRIB + ATP -> DR5P + ADP	rbk1_2
YKL127W	5.4.2.2	*PGM1*	PHOSPHOGLUCOMUTASE	R1P <-> R5P	pgm1_1
YKL127W	5.4.2.2	*PGM1*	PHOSPHOGLUCOMUTASE 1	G1P <-> G6P	pgm1_2
YMR105C	5.4.2.2	*PGM2*	PHOSPHOGLUCOMUTASE	R1P <-> R5P	pgm2_1
YMR105C	5.4.2.2	*PGM2*	PHOSPHOGLUCOMUTASE	G1P <-> G6P	pgm2_2
# MANNOSE					
YER003C	5.3.1.8	*PMI40*	MANNOSE-6-PHOSPHATE ISOMERASE	MAN6P <-> F6P	pmi40
YFL045C	5.4.2.8	*SEC53*	PHOSPHOMANNOMUTASE	MAN6P <-> MAN1P	sec53
YDL055C	2.7.7.13	*PSA1*	MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE, GDP-MANNOSE PYROPHOSPHORYLASE	GTP + MAN1P -> PPI + GDPMAN	psa1
# FRUCTOSE					
YIL107C	2.7.1.105	*PFK26*	6-PHOSPHOFRUCTOSE-2-KINASE	ATP + F6P -> ADP + F26P	pfk26
YOL136C	2.7.1.105	*PFK27*	6-PHOSPHOFRUCTO-2-KINASE	ATP + F6P -> ADP + F26P	pfk27
YJL155C	3.1.3.46	*FBP26*	FRUCTOSE-2,6-BIPHOSPHATASE	F26P -> F6P + PI	fbp26
*U1_*	2.7.1.56	*U1_*	1-PHOSPHOFRUCTOKINASE (FRUCTOSE 1-PHOSPHATE KINASE)	F1P + ATP -> FDP + ADP	frc3
# SORBOS	S.c. does not metabolize sorbitol, erythritol, mannitol, xylitol, ribitol, arabinitol, galactinol				
YJR159W	1.1.1.14	*SOR1*	SORBITOL DEHYDROGENASE (L-IDITOL 2-DEHYDROGENASE)	SOT + NAD -> FRU + NADH	sor1
# GALACTOSE METABOLISM					
YBR020W	2.7.1.6	*GAL1*	GALACTOKINASE	GLAC + ATP -> GAL1P + ADP	gal1
YBR018C	2.7.7.10	*GAL7*	GALACTOSE-1-PHOSPHATE URIDYL TRANSFERASE	UTP + GAL1P <-> PPI + UDPGAL	gal7
YBR019C	5.1.3.2	*GAL10*	UDP-GLUCOSE 4-EPIMERASE	UDPGAL <-> UDPG	gal10
YHL012W	2.7.7.9	*YHL012W*	UTP--GLUCOSE 1-PHOSPHATE URIDYLYLTRANSFERASE	G1P + UTP <-> UDPG + PPI	ugp1_2
YKL035W	2.7.7.9	*UGP1*	URIDINEPHOSPHOGLUCOSE PYROPHOSPHORYLASE	G1P + UTP <-> UDPG + PPI	ugp1_1

YBR184W	3.2.1.22	*YBR184W*	ALPHA-GALACTOSIDASE (MELIBIASE)	MELI -> GLC + GLAC	mel1_1
YBR184W	3.2.1.22	*YBR184W*	ALPHA-GALACTOSIDASE (MELIBIASE)	DFUC -> GLC + GLAC	mel1_2
YBR184W	3.2.1.22	*YBR184W*	ALPHA-GALACTOSIDASE (MELIBIASE)	RAF -> GLAC + SUC	mel1_3
YBR184W	3.2.1.22	*YBR184W*	ALPHA-GALACTOSIDASE (MELIBIASE)	GLACL <-> MYOI + GLAC	mel1_4
YBR184W	3.2.1.22	*YBR184W*	ALPHA-GALACTOSIDASE (MELIBIASE)	EPM <-> MAN + GLAC	mel1_5
YBR184W	3.2.1.22	*YBR184W*	ALPHA-GALACTOSIDASE (MELIBIASE)	GGL <-> GL + GLAC	mel1_6
YBR184W	3.2.1.22	*YBR184W*	ALPHA-GALACTOSIDASE (MELIBIASE)	MELT <-> SOT + GLAC	mel1_7
YBR299W	3.2.1.20	*MAL32*	MALTASE	MLT -> 2 GLC	mal32a
YGR287C	3.2.1.20	*YGR287C*	PUTATIVE ALPHA GLUCOSIDASE	MLT -> 2 GLC	mal32b
YGR292W	3.2.1.20	*MAL12*	MALTASE	MLT -> 2 GLC	mal12a
YIL172C	3.2.1.20	*YIL172C*	PUTATIVE ALPHA GLUCOSIDASE	MLT -> 2 GLC	mal12b
YJL216C	3.2.1.20	*YJL216C*	PROBABLE ALPHA-GLUCOSIDASE (MALTASE)	MLT -> 2 GLC	mal12c
YJL221C	3.2.1.20	*FSP2*	HOMOLOGY TO MALTASE(ALPHA-D-GLUCOSIDASE)	MLT -> 2 GLC	fsp2a
YJL221C	3.2.1.20	*FSP2*	HOMOLOGY TO MALTASE(ALPHA-D-GLUCOSIDASE)	6DGLC -> GLAC + GLC	fsp2b
YBR018C	2.7.7.12	*GAL7*	UDPGLUCOSE--HEXOSE-1-PHOSPHATE URIDYLYLTRANSFERASE	UDPG + GAL1P <-> G1P + UDPGAL	unkrx10
# TREHALOSE					
YBR126C	2.4.1.15	*TPS1*	TREHALOSE-6-P SYNTHETASE, 56 KD SYNTHASE SUBUNIT OF TREHALOSE-6-PHOSPHATE SYNTHASE\/PHOSPHATASE COMPLEX	UDPG + G6P -> UDP + TRE6P	tps1
YML100W	2.4.1.15	*TSL1*	TREHALOSE-6-P SYNTHETASE, 123 KD REGULATORY SUBUNIT OF TREHALOSE-6-PHOSPHATE SYNTHASE\/PHOSPHATASE COMPLEX\; HOMOLOGOUS TO TPS3 GENE PRODUCT	UDPG + G6P -> UDP + TRE6P	tsl1
YMR261C	2.4.1.15	*TPS3*	TREHALOSE-6-P SYNTHETASE, 115 KD REGULATORY SUBUNIT OF TREHALOSE-6-PHOSPHATE SYNTHASE\/PHOSPHATASE COMPLEX	UDPG + G6P -> UDP + TRE6P	tps3
YDR074W	3.1.3.12	*TPS2*	TREHALOSE-6-PHOSPHATE PHOSPHATASE	TRE6P -> TRE + PI	tps2
YPR026W	3.2.1.28	*ATH1*	ACID TREHALASE	TRE -> 2 GLC	ath1
YBR001C	3.2.1.28	*NTH2*	NEUTRAL TREHALASE, HIGHLY HOMOLOGOUS TO NTH1P	TRE -> 2 GLC	nth2
YDR001C	3.2.1.28	*NTH1*	NEUTRAL TREHALASE	TRE -> 2 GLC	nth1
# GLYCOGEN METABOLISM (SUCOROSE AND SUGAR METABOLISM)					
YEL011W	2.4.1.18	*GLC3*	BRANCHING ENZYME, 1,4-GLUCAN-6-(1,4-GLUCANO)-TRANSFERASE	GLYCOGEN + PI -> G1P	glc3
YPR160W	2.4.1.1	*GPH1*	GLYCOGEN PHOSPHORYLASE	GLYCOGEN + PI -> G1P	gph1

YFR015C	2.4.1.11	*GSY1*	GLYCOGEN SYNTHASE (UDP-GLUOCSE--STARCH GLUCOSYLTRANSFERASE)	UDPG -> UDP + GLYCOGEN	gsy1
YLR258W	2.4.1.11	*GSY2*	GLYCOGEN SYNTHASE (UDP-GLUOCSE--STARCH GLUCOSYLTRANSFERASE)	UDPG -> UDP + GLYCOGEN	gsy2
# PYRUVATE METABOLISM					
YAL054C	6.2.1.1	*ACS1*	ACETYL-COENZYME A SYNTHETASE	ATPm + ACm + COAm -> AMPm + PPIm + ACCOAm	acs1
YLR153C	6.2.1.1	*ACS2*	ACETYL-COENZYME A SYNTHETASE	ATP + AC + COA -> AMP + PPI + ACCOA	acs2
YDL168W	1.2.1.1	*SFA1*	FORMALDEHYDE DEHYDROGENASE/LONG-CHAIN ALCOHOL DEHYDROGENASE	FALD + RGT + NAD <-> FGT + NADH	sfa1_1
YJL068C	3.1.2.12	*YJL068C*	S-FORMYLGLUTATHIONE HYDROLASE	FGT <-> RGT + FOR	unkrx11
YGR087C	4.1.1.1	*PDC6*	PYRUVATE DECARBOXYLASE	PYR -> CO2 + ACAL	pdc6
YLR134W	4.1.1.1	*PDC5*	PYRUVATE DECARBOXYLASE	PYR -> CO2 + ACAL	pdc5
YLR044C	4.1.1.1	*PDC1*	PYRUVATE DECARBOXYLASE	PYR -> CO2 + ACAL	pdc1
YBL015W	3.1.2.1	*ACH1*	ACETYL COA HYDROLASE	ACCOA -> COA + AC	ach1_1
YBL015W	3.1.2.1	*ACH1*	ACETYL COA HYDROLASE	ACCOAm -> COAm + Acm	ach1_2
YDL131W	4.1.3.21	*LYS21*	PROBABLE HOMOCITRATE SYNTHASE, MITOCHONDRIAL ISOZYME PRECURSOR	ACCOA + AKG -> HCIT + COA	lys21
YDL182W	4.1.3.21	*LYS20*	HOMOCITRATE SYNTHASE, CYTOSOLIC ISOZYME	ACCOA + AKG -> HCIT + COA	lys20
YDL182W	4.1.3.21	*LYS20*	HOMOCITRATE SYNTHASE	ACCOAm + AKGm -> HCITm + COAm	lys20a
YGL256W	1.1.1.1	*ADH4*	ALCOHOL DEHYDROGENASE ISOENZYME IV	ETH + NAD <-> ACAL + NADH	adh4
YMR083W	1.1.1.1	*ADH3*	ALCOHOL DEHYDROGENASE ISOENZYME III	ETHm + NADm <-> ACALm + NADHm	adh3
YMR303C	1.1.1.1	*ADH2*	ALCOHOL DEHYDROGENASE II	ETH + NAD <-> ACAL + NADH	adh2
YBR145W	1.1.1.1	*ADH5*	ALCOHOL DEHYDROGENASE ISOENZYME V	ETH + NAD <-> ACAL + NADH	adh5
YOL086C	1.1.1.1	*ADH1*	ALCOHOL DEHYDROGENASE I	ETH + NAD <-> ACAL + NADH	adh1
YDL168W	1.1.1.1	*SFA1*	ALCOHOL DEHYDROGENASE I	ETH + NAD <-> ACAL + NADH	sfa1_2
# GLYOXYLATE AND DICARBOXYLATE METABOLISM					
GLYOXAL PATHWAY					
YML004C	4.4.1.5	*GLO1*	LACTOYLGLUTATHIONE LYASE, GLYOXALASE I	RGT + MTHGXL <-> LGT	glo1
YDR272W	3.1.2.6	*GLO2*	HYDROXYACYLGLUTATHIONE HYDROLASE	LGT -> RGT + LAC	glo2
YOR040W	3.1.2.6	*GLO4*	GLYOXALASE II (HYDROXYACYLGLUTATHIONE HYDROLASE)	LGTm -> RGTm + LACm	glo4
# ENERGY METABOLISM					
# OXIDATIVE PHOSPHORYLATION					
YBR011C	3.6.1.1	*IPP1*	INORGANIC PYROPHOSPHATASE	PPI -> 2 PI	ipp1
YMR267W	3.6.1.1	*PPA2*	MITOCHONDRIAL INORGANIC PYROPHOSPHATASE	PPIm -> 2 PIm	ppa2

*U2_*	1.2.2.1	*U2_*	FORMATE DEHYDROGENASE	FOR + Qm -> QH2m + CO2 +2 HEXT	fdng
YML120C	1.6.5.3	*NDI1*	NADH DEHYDROGENASE (UBIQUINONE)	NADHm + Qm -> QH2m + NADm	ndi1
YDL085W	1.6.5.3	*NDH2*	MITOCHONDRIAL NADH DEHYDROGENASE THAT CATALYZES THE OXIDATION OF CYTOSOLIC NADH	NADH + Qm -> QH2m + NAD	ndh2
YMR145C	1.6.5.3	*NDH1*	MITOCHONDRIAL NADH DEHYDROGENASE THAT CATALYZES THE OXIDATION OF CYTOSOLIC NADH	NADH + Qm -> QH2m + NAD	ndh1
YHR042W	1.6.2.4	*NCP1*	NADPH--FERRIHEMOPROTEIN REDUCTASE	NADPH + 2 FERIm -> NADP + 2 FEROm	ncp1
YKL141W	1.3.5.1	*SDH3*	SUCCINATE DEHYDROGENASE CYTOCHROME B	FADH2m + Qm <-> FADm + QH2m	fad
YKL148C	1.3.5.1	*SDH1*	SUCCINATE DEHYDROGENASE CYTOCHROME B		
YLL041C	1.3.5.1	*SDH2*	SUCCINATE DEHYDROGENASE CYTOCHROME B		
YDR178W	1.3.5.1	*SDH4*	SUCCINATE DEHYDROGENASE CYTOCHROME B		
# ELECTRON TRANSPORT SYSTEM, COMPLEX III					
YEL024W	1.10.2.2	*RIP1*	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT	O2m + 4 FEROm + 6 Hm -> 4 FERIm	cyto
Q0105	1.10.2.2	*CYTB*	UBIQUINOL-CYTOCHROME C REDUCTASE CYTOCHROME B SUBUNIT		
YOR065W	1.10.2.2	*CYT1*	UBIQUINOL-CYTOCHROME C REDUCTASE CYTOCHROME C1 SUBUNIT		
YBL045C	1.10.2.2	*COR1*	UBIQUINOL-CYTOCHROME C REDUCTASE CORE SUBUNIT 1		
YPR191W	1.10.2.2	*QCR1*	UBIQUINOL-CYTOCHROME C REDUCTASE CORE SUBUNIT 2		
YPR191W	1.10.2.2	*QCR2*	UBIQUINOL-CYTOCHROME C REDUCTASE		
YFR033C	1.10.2.2	*QCR6*	UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT 6		
YDR529C	1.10.2.2	*QCR7*	UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT 7		
YJL166W	1.10.2.2	*QCR8*	UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT 8		
YGR183C	1.10.2.2	*QCR9*	UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT 9		
YHR001W	1.10.2.2	*QCR10*	UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT 10		
# ELECTRON TRANSPORT SYSTEM, COMPLEX IV					
Q0045	1.9.3.1	*COX1*	CYTOCHROME C OXIDASE SUBUNIT I	QH2m + 2 FERIm + 1.5 Hm -> Qm + 2 FEROm	cytr
Q0250	1.9.3.1	*COX2*	CYTOCHROME C OXIDASE SUBUNIT I		
Q0275	1.9.3.1	*COX3*	CYTOCHROME C OXIDASE SUBUNIT I		
YDL067C	1.9.3.1	*COX9*	CYTOCHROME C OXIDASE SUBUNIT I		
YGL187C	1.9.3.1	*COX4*	CYTOCHROME C OXIDASE SUBUNIT I		
YGL191W	1.9.3.1	*COX13*	CYTOCHROME C OXIDASE SUBUNIT I		
YHR051W	1.9.3.1	*COX6*	CYTOCHROME C OXIDASE SUBUNIT I		

YIL111W	1.9.3.1	*COX5B*	CYTOCHROME C OXIDASE SUBUNIT I		
YLR038C	1.9.3.1	*COX12*	CYTOCHROME C OXIDASE SUBUNIT I		
YLR395C	1.9.3.1	*COX8*	CYTOCHROME C OXIDASE SUBUNIT I		
YMR256C	1.9.3.1	*COX7*	CYTOCHROME C OXIDASE SUBUNIT I		
YNL052W	1.9.3.1	*COX5A*	CYTOCHROME C OXIDASE SUBUNIT I		
# ATP SYNTHASE					
YBL099W	3.6.1.34	*ATP1*	F1F0-ATPASE COMPLEX, F1 ALPHA SUBUNIT	ADPm + PIm -> ATPm + 3 Hm	atp1
YPL271W	3.6.1.34	*ATP15*	F1F0-ATPASE COMPLEX, F1 EPSILON SUBUNIT		
YDL004W	3.6.1.34	*ATP16*	F-TYPE H+-TRANSPORTING ATPASE DELTA CHAIN		
Q0085	3.6.1.34	*ATP6*	F1F0-ATPASE COMPLEX, FO A SUBUNIT		
YBR039W	3.6.1.34	*ATP3*	F1F0-ATPASE COMPLEX, F1 GAMMA SUBUNIT		
YBR127C	3.6.1.34	*VMA2*	H+-ATPASE V1 DOMAIN 60 KD SUBUNIT, VACUOLAR		
YPL078C	3.6.1.34	*ATP4*	F1F0-ATPASE COMPLEX, F1 DELTA SUBUNIT		
YDR298C	3.6.1.34	*ATP5*	F1F0-ATPASE COMPLEX, OSCP SUBUNIT		
YDR377W	3.6.1.34	*ATP17*	ATP SYNTHASE COMPLEX, SUBUNIT F		
YJR121W	3.6.1.34	*ATP2*	F1F0-ATPASE COMPLEX, F1 BETA SUBUNIT		
YKL016C	3.6.1.34	*ATP7*	F1F0-ATPASE COMPLEX, FO D SUBUNIT		
YLR295C	3.6.1.34	*ATP14*	ATP SYNTHASE SUBUNIT H		
Q0080	3.6.1.34	*ATP8*	F-TYPE H+-TRANSPORTING ATPASE SUBUNIT 8		
Q0130	3.6.1.34	*ATP9*	F-TYPE H+-TRANSPORTING ATPASE SUBUNIT C		
YOL077W-	3.6.1.34	*ATP19*	ATP SYNTHASE K CHAIN, MITOCHONDRIAL		
YPR020W	3.6.1.34	*ATP20*	SUBUNIT G OF THE DIMERIC FORM OF MITOCHONDRIAL F1F0-ATP SYNTHASE		
YLR447C	3.6.1.34	*VMA6*	V-TYPE H+-TRANSPORTING ATPASE SUBUNIT AC39		
YGR020C	3.6.1.34	*VMA7*	V-TYPE H+-TRANSPORTING ATPASE SUBUNIT F		
YKL080W	3.6.1.34	*VMA5*	V-TYPE H+-TRANSPORTING ATPASE SUBUNIT C		
YDL185W	3.6.1.34	*TFP1*	V-TYPE H+-TRANSPORTING ATPASE SUBUNIT A		
YBR127C	3.6.1.34	*VMA2*	V-TYPE H+-TRANSPORTING ATPASE SUBUNIT B		
YOR332W	3.6.1.34	*VMA4*	V-TYPE H+-TRANSPORTING ATPASE SUBUNIT E		
YEL027W	3.6.1.34	*CUP5*	V-TYPE H+-TRANSPORTING ATPASE PROTEOLIPID SUBUNIT		
YHR026W	3.6.1.34	*PPA1*	V-TYPE H+-TRANSPORTING ATPASE PROTEOLIPID SUBUNIT		
YPL234C	3.6.1.34	*TFP3*	V-TYPE H+-TRANSPORTING ATPASE PROTEOLIPID SUBUNIT		
YMR054W	3.6.1.34	*STV1*	V-TYPE H+-TRANSPORTING ATPASE SUBUNIT I		

YOR270C	3.6.1.34	*VPH1*	V-TYPE H+-TRANSPORTING ATPASE SUBUNIT I		
YEL051W	3.6.1.34	*VMA8*	V-TYPE H+-TRANSPORTING ATPASE SUBUNIT D		
YHR039C-	3.6.1.34	*VMA10*	VACUOLAR ATP SYNTHASE SUBUNIT G		
YPR036W	3.6.1.34	*VMA13*	V-TYPE H+-TRANSPORTING ATPASE 54 KD SUBUNIT		
# ELECTRON TRANSPORT SYSTEM, COMPLEX IV					
Q0045	1.9.3.1	*COX1*	CYTOCHROME-C OXIDASE SUBUNIT I	4 FEROm + O2m + 6 Hm -> 4 FERIm	cox1
Q0275	1.9.3.1	*COX3*	CYTOCHROME-C OXIDASE SUBUNIT III, MITOCHONDRIALLY-CODED		
Q0250	1.9.3.1	*COX2*	CYTOCHROME-C OXIDASE SUBUNIT II		
YDL067C	1.9.3.1	*COX9*	CYTOCHROME-C OXIDASE		
YGL187C	1.9.3.1	*COX4*	CYTOCHROME-C OXIDASE CHAIN IV		
YGL191W	1.9.3.1	*COX13*	CYTOCHROME-C OXIDASE CHAIN VIA		
YHR051W	1.9.3.1	*COX6*	CYTOCHROME-C OXIDASE SUBUNIT VI		
YIL111W	1.9.3.1	*COX5B*	CYTOCHROME-C OXIDASE CHAIN VB		
YLR038C	1.9.3.1	*COX12*	CYTOCHROME-C OXIDASE, SUBUNIT VIB		
YLR395C	1.9.3.1	*COX8*	CYTOCHROME-C OXIDASE CHAIN VIII		
YMR256C	1.9.3.1	*COX7*	CYTOCHROME-C OXIDASE, SUBUNIT VII		
YNL052W	1.9.3.1	*COX5A*	CYTOCHROME-C OXIDASE CHAIN V.A PRECURSOR		
YML054C	1.1.2.3	*CYB2*	LACTIC ACID DEHYDROGENASE	2 FERIm + LLACm -> PYRm + 2 FEROm	cyb2
YDL174C	1.1.2.4	*DLD1*	MITOCHONDRIAL ENZYME D-LACTATE FERRICYTOCHROME C OXIDOREDUCTASE	2 FERIm + LACm -> PYRm + 2 FEROm	dld1
# METHANE METABOLISM					
YPL275W	1.2.1.2	*YPL275W*	PUTATIVE FORMATE DEHYDROGENASE/PUTATIVE PSEUDOGENE	FOR + NAD -> CO2 + NADH	tfo1a
YPL276W	1.2.1.2	*YPL276W*	PUTATIVE FORMATE DEHYDROGENASE/PUTATIVE PSEUDOGENE	FOR + NAD -> CO2 + NADH	tfo1b
YOR388C	1.2.1.2	*FDH1*	PROTEIN WITH SIMILARITY TO FORMATE DEHYDROGENASES	FOR + NAD -> CO2 + NADH	fdh1
# NITROGEN METABOLISM					
YBR208C	6.3.4.6	*DUR1*	UREA AMIDOLYASE CONTAINING UREA CARBOXYLASE / ALLOPHANATE HYDROLASE	ATP + UREA + CO2 <-> ADP + PI + UREAC	dur1
YBR208C	3.5.1.54	*DUR1*	ALLOPHANATE HYDROLASE	UREAC -> 2 NH3 + 2 CO2	dur2
YJL126W	3.5.5.1	*NIT2*	NITRILASE	ACNL -> INAC + NH3	nit2
# SULFUR METABOLISM					
YJR137C	1.8.7.1	*ECM17*	SULFITE REDUCTASE	H2SO3 + 3 NADPH <-> H2S + 3 NADP	ecm17
# LIPID METABOLISM					

# FATTY ACID BIOSYNTHESIS					
YER015W	6.2.1.3	*FAA2*	LONG-CHAIN-FATTY-ACID--COA LIGASE, ACYL-COA SYNTHETASE	ATP + LCCA + COA <-> AMP + PPI + ACOA	faa2
YIL009W	6.2.1.3	*FAA3*	LONG-CHAIN-FATTY-ACID--COA LIGASE, ACYL-COA SYNTHETASE	ATP + LCCA + COA <-> AMP + PPI + ACOA	faa3
YOR317W	6.2.1.3	*FAA1*	LONG-CHAIN-FATTY-ACID--COA LIGASE, ACYL-COA SYNTHETASE	ATP + LCCA + COA <-> AMP + PPI + ACOA	faa1
YMR246W	6.2.1.3	*FAA4*	ACYL-COA SYNTHASE (LONG-CHAIN FATTY ACID COA LIGASE); CONTRIBUTES TO ACTIVATION OF IMPORTED MYRISTATE	ATP + LCCA + COA <-> AMP + PPI + ACOA	faa4
YKR009C	1.1.1.-	*FOX2*	3-HYDROXYACYL-COA DEHYDROGENASE	HACOA + NAD <-> OACOA + NADH	fox2b
YIL160C	2.3.1.16	*POT1*	3-KETOACYL-COA THIOLASE	OACOA + COA -> ACOA + ACCOA	pot1_1
YPL028W	2.3.1.9	*ERG10*	ACETYL-COA C-ACETYLTRANSFERASE, ACETOACETYL-COA THIOLASE	2 ACCOA <-> COA + AACCOA	erg10_1
YPL028W	2.3.1.9	*ERG10*	ACETYL-COA C-ACETYLTRANSFERASE, ACETOACETYL-COA THIOLASE (MITOCH)	2 ACCOAm <-> COAm + AACCOAm	erg10_2
# FATTY ACIDS METABOLISM					
# MITOCHONDRIAL TYPE II FATTY ACID SYNTHASE					
YKL192C	1.6.5.3	*ACP1*	ACYL CARRIER PROTEIN, COMPONENT OF MITOCHONDRIAL TYPE II FATTY ACID SYNTHASE	NADHm + Qm -> NADm + QH2m	ACP1
YER061C	-	*CEM1*	BETA-KETOACYL-ACP SYNTHASE, MITOCHONDRIAL (3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE)		
YOR221C	-	*MCT1*	MALONYL COA:ACYL CARRIER PROTEIN TRANSFERASE		
YKL055C	-	*OAR1*	3-OXOACYL-[ACYL-CARRIER-PROTEIN] REDUCTASE		
YKL192C/	1.6.5.3/-/-/-	*ACP1/CEM*	TYPE II FATTY ACID SYNTHASE	ACACPm + 4 MALACPm + 8 NADPHm -> 8 NADPm + C100ACPm + 4 CO2m + 4 ACPm	TypeII_1
YKL192C/	1.6.5.3/-/-/-	*ACP1/CEM*	TYPE II FATTY ACID SYNTHASE	ACACPm + 5 MALACPm + 10 NADPHm -> 10 NADPm + C120ACPm + 5 CO2m + 5 ACPm	TypeII_2
YKL192C/	1.6.5.3/-/-/-	*ACP1/CEM*	TYPE II FATTY ACID SYNTHASE	ACACPm + 6 MALACPm + 12 NADPHm -> 12 NADPm + C140ACPm + 6 CO2m + 6 ACPm	TypeII_3
YKL192C/	1.6.5.3/-/-/-	*ACP1/CEM*	TYPE II FATTY ACID SYNTHASE	ACACPm + 6 MALACPm + 11 NADPHm -> 11 NADPm + C141ACPm+ 6 CO2m + 6 ACPm	TypeII_4
YKL192C/	1.6.5.3/-/-/-	*ACP1/CEM*	TYPE II FATTY ACID SYNTHASE	ACACPm + 7 MALACPm + 14 NADPHm -> 14 NADPm + C160ACPm + 7 CO2m + 7 ACPm	TypeII_5

YKL192C/	1.6.5.3/-/-/-	*ACP1/CEM*	TYPE II FATTY ACID SYNTHASE	ACACPm + 7 MALACPm + 13 NADPHm -> 13 NADPm + C161ACPm + 7 CO2m + 7 ACPm	TypeII_6
YKL192C/	1.6.5.3/-/-/-	*ACP1/CEM*	TYPE II FATTY ACID SYNTHASE	ACACPm + 8 MALACPm + 16 NADPHm -> 16 NADPm + C180ACPm + 8 CO2m + 8 ACPm	TypeII_7
YKL192C/	1.6.5.3/-/-/-	*ACP1/CEM*	TYPE II FATTY ACID SYNTHASE	ACACPm + 8 MALACPm + 15 NADPHm -> 15 NADPm + C181ACPm + 8 CO2m + 8 ACPm	TypeII_8
YKL192C/	1.6.5.3/-/-/-	*ACP1/CEM*	TYPE II FATTY ACID SYNTHASE	ACACPm + 8 MALACPm + 14 NADPHm -> 14 NADPm + C182ACPm + 8 CO2m + 8 ACPm	TypeII_9
# CYTOSOLIC FATTY ACID SYNTHESIS					
YNR016C	6.4.1.2 6.3.	*ACC1*	ACETYL-COA CARBOXYLASE (ACC) / BIOTIN CARBOXYLASE	ACCOA + ATP + CO2 <-> MALCOA + ADP + PI	acc1
YKL182W	4.2.1.61;1.	*FAS1*	FATTY-ACYL-COA SYNTHASE, BETA CHAIN	MALCOA + ACP <-> MALACP + COA	fas1_1
YPL231W	2.3.1.85;1.	*FAS2*	FATTY-ACYL-COA SYNTHASE, ALPHA CHAIN		
YKL182W	4.2.1.61;1.	*FAS1*	FATTY-ACYL-COA SYNTHASE, BETA CHAIN	ACCOA + ACP <-> ACACP + COA	fas1_2
YER061C	2.3.1.41	*CEM1*	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE	MALACPm + ACACPm -> ACPm + CO2m + 3OACPm	cem1
YGR037C/	6.4.1.2; 6.3	*ACB1/ACC*	B-KETOACYL-ACP SYNTHASE (C10,0), FATTY ACYL COA SYNTHASE	ACACP + 4 MALACP + 8 NADPH -> 8 NADP + C100ACP + 4 CO2 + 4 ACP	c100sn
YGR037C/	6.4.1.2; 6.3	*ACB1/ACC*	B-KETOACYL-ACP SYNTHASE (C12,0), FATTY ACYL COA SYNTHASE	ACACP + 5 MALACP + 10 NADPH -> 10 NADP + C120ACP + 5 CO2 + 5 ACP	c120sn
YGR037C/	6.4.1.2; 6.3	*ACB1/ACC*	B-KETOACYL-ACP SYNTHASE (C14,0)	ACACP + 6 MALACP + 12 NADPH -> 12 NADP + C140ACP + 6 CO2 + 6 ACP	c140sn
YGR037C/	6.4.1.2; 6.3	*ACB1/ACC*	B-KETOACYL-ACP SYNTHASE I (C14,1)	ACACP + 6 MALACP + 11 NADPH -> 11 NADP + C141ACP + 6 CO2 + 6 ACP	c141sy
YGR037C/	6.4.1.2; 6.3	*ACB1/ACC*	B-KETOACYL-ACP SYNTHASE I (C16,0)	ACACP + 7 MALACP + 14 NADPH -> 14 NADP + C160ACP + 7 CO2 + 7 ACP	c160sn
YGR037C/	6.4.1.2; 6.3	*ACB1/ACC*	B-KETOACYL-ACP SYNTHASE I (C16,1)	ACACP + 7 MALACP + 13 NADPH -> 13 NADP + C161ACP + 7 CO2 + 7 ACP	c161sy
YGR037C/	6.4.1.2; 6.3	*ACB1/ACC*	B-KETOACYL-ACP SYNTHASE I (C18,0)	ACACP + 8 MALACP + 16 NADPH -> 16 NADP + C180ACP + 8 CO2 + 8 ACP	c180sy
YGR037C/	6.4.1.2; 6.3	*ACB1/ACC*	B-KETOACYL-ACP SYNTHASE I (C18,1)	ACACP + 8 MALACP + 15 NADPH -> 15 NADP + C181ACP + 8 CO2 + 8 ACP	c181sy
YGR037C/	6.4.1.2; 6.3	*ACB1/ACC*	B-KETOACYL-ACP SYNTHASE I (C18,2)	ACACP + 8 MALACP + 14 NADPH -> 14 NADP + C182ACP + 8 CO2 + 8 ACP	c182sy
YKL182W	4.2.1.61	*FAS1*	3-HYDROXYPALMITOYL-[ACYL-CARRIER PROTEIN] DEHYDRATASE	3HPACP <-> 2HDACP	fas1_3

YKL182W	1.3.1.9	*FAS1*	ENOYL-ACP REDUCTASE	AACP + NAD <-> 23DAACP + NADH	fas1_4
# FATTY ACID DEGRADATION					
YGL205W/	1.3.3.6/2.3.	*POX1/FOX*	FATTY ACID DEGRADATION	C140 + ATP + 7 COA + 7 FADm + 7 NAD -> AMP + PPI + 7 FADH2m + 7 NADH + 7 ACCOA	c140dg
YGL205W/	1.3.3.6/2.3.	*POX1/FOX*	FATTY ACID DEGRADATION	C160 + ATP + 8 COA + 8 FADm + 8 NAD -> AMP + PPI + 8 FADH2m + 8 NADH + 8 ACCOA	c160dg
YGL205W/	1.3.3.6/2.3.	*POX1/FOX*	FATTY ACID DEGRADATION	C180 + ATP + 9 COA + 9 FADm + 9 NAD -> AMP + PPI + 9 FADH2m + 9 NADH + 9 ACCOA	c180dg
# PHOSPHOLIPID BIOSYNTHESIS					
*U3_*		*U3_*	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE	GL3P + 0.017 C100ACP + 0.062 C120ACP + 0.1 C140ACP + 0.27 C160ACP + 0.169 C161ACP + 0.055 C180ACP + 0.235 C181ACP + 0.093 C182ACP -> AGL3P + ACP	Gat1_1
*U4_*		*U4_*	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE	GL3P + 0.017 C100ACP + 0.062 C120ACP + 0.1 C140ACP + 0.27 C160ACP + 0.169 C161ACP + 0.055 C180ACP + 0.235 C181ACP + 0.093 C182ACP -> AGL3P + ACP	Gat2_1
*U5_*		*U5_*	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE	T3P2 + 0.017 C100ACP + 0.062 C120ACP + 0.1 C140ACP + 0.27 C160ACP + 0.169 C161ACP + 0.055 C180ACP + 0.235 C181ACP + 0.093 C182ACP -> AT3P2 + ACP	Gat1_2
*U6_*		*U6_*	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE	T3P2 + 0.017 C100ACP + 0.062 C120ACP + 0.1 C140ACP + 0.27 C160ACP + 0.169 C161ACP + 0.055 C180ACP + 0.235 C181ACP + 0.093 C182ACP -> AT3P2 + ACP	Gat2_2
*U7_*		*U7_*	ACYLDIHYDROXYACETONEPHOSPHATE REDUCTASE	AT3P2 + NADPH -> AGL3P + NADP	ADHAPR
YDL052C	2.3.1.51	*SLC1*	1-ACYLGLYCEROL-3-PHOSPHATE ACYLTRANSFERASE	AGL3P + 0.017 C100ACP + 0.062 C120ACP + 0.100 C140ACP + 0.270 C160ACP + 0.169 C161ACP + 0.055 C180ACP + 0.235 C181ACP + 0.093 C182ACP -> PA + ACP	slc1

*U8_*	2.3.1.51	*U8_*	1-ACYLGLYCEROL-3-PHOSPHATE ACYLTRANSFERASE	AGL3P + 0.017 C100ACP + 0.062 C120ACP + 0.100 C140ACP + 0.270 C160ACP + 0.169 C161ACP + 0.055 C180ACP + 0.235 C181ACP + 0.093 C182ACP -> PA + ACP	AGAT
YBR029C	2.7.7.41	*CDS1*	CDP-DIACYLGLYCEROL SYNTHETASE	PAm + CTPm <-> CDPDGm + PPIm	cds1a
YBR029C	2.7.7.41	*CDS1*	CDP-DIACYLGLYCEROL SYNTHETASE	PA + CTP <-> CDPDG + PPI	cds1b
YER026C	2.7.8.8	*CHO1*	PHOSPHATIDYLSERINE SYNTHASE	CDPDG + SER <-> CMP + PS	cho1a
YER026C	2.7.8.8	*CHO1*	PHOSPHATIDYLSERINE SYNTHASE	CDPDGm + SERm <-> CMPm + PSm	cho1b
YGR170W	4.1.1.65	*PSD2*	PHOSPHATIDYLSERINE DECARBOXYLASE LOCATED IN VACUOLE OR GOLGI	PS -> PE + CO2	psd2
YNL169C	4.1.1.65	*PSD1*	PHOSPHATIDYLSERINE DECARBOXYLASE 1	PSm -> PEm + CO2m	psd1
YGR157W	2.1.1.17	*CHO2*	PHOSPHATIDYLETHANOLAMINE N-METHYLTRANSFERASE	SAM + PE -> SAH + PMME	cho2
YJR073C	2.1.1.16	*OPI3*	METHYLENE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE.	SAM + PMME -> SAH + PDME	opi3_1
YJR073C	2.1.1.16	*OPI3*	PHOSPHATIDYL-N-METHYLETHANOLAMINE N-METHYLTRANSFERASE	PDME + SAM -> PC + SAH	opi3_2
YLR133W	2.7.1.32	*CKI1*	CHOLINE KINASE	ATP + CHO -> ADP + PCHO	cki1
YGR202C	2.7.7.15	*PCT1*	CHOLINEPHOSPHATE CYTIDYLYLTRANSFERASE	PCHO + CTP -> CDPCHO + PPI	pct1
YNL130C	2.7.8.2	*CPT1*	DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE	CDPCHO + DAGLY -> PC + CMP	cpt1
YDR147W	2.7.1.82	*EKI1*	ETHANOLAMINE KINASE	ATP + ETHM -> ADP + PETHM	eki1
YGR007W	2.7.7.14	*MUQ1*	PHOSPHOETHANOLAMINE CYTIDYLYLTRANSFERASE	PETHM + CTP -> CDPETN + PPI	ect1
YHR123W	2.7.8.1	*EPT1*	ETHANOLAMINEPHOSPHOTRANSFERASE.	CDPETN + DAGLY <-> CMP + PE	ept1
YJL153C	5.5.1.4	*INO1*	MYO-INOSITOL-1-PHOSPHATE SYNTHASE	G6P -> MI1P	ino1
YHR046C	3.1.3.25	*INM1*	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE	MI1P -> MYOI + PI	impa1
YPR113W	2.7.8.11	*PIS1*	PHOSPHATIDYLINOSITOL SYNTHASE	CDPDG + MYOI -> CMP + PINS	pis1
YJR066W	2.7.1.137	*TOR1*	1-PHOSPHATIDYLINOSITOL 3-KINASE	ATP + PINS -> ADP + PINSP	tor1
YKL203C	2.7.1.137	*TOR2*	1-PHOSPHATIDYLINOSITOL 3-KINASE	ATP + PINS -> ADP + PINSP	tor2
YLR240W	2.7.1.137	*VPS34*	1-PHOSPHATIDYLINOSITOL 3-KINASE	ATP + PINS -> ADP + PINSP	vps34
YNL267W	2.7.1.67	*PIK1*	PHOSPHATIDYLINOSITOL 4-KINASE (PI 4-KINASE), GENERATES PTDINS 4-P	ATP + PINS -> ADP + PINS4P	pik1
YLR305C	2.7.1.67	*STT4*	PHOSPHATIDYLINOSITOL 4-KINASE	ATP + PINS -> ADP + PINS4P	sst4
YFR019W	2.7.1.68	*FAB1*	PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE, 1-PHOSPHATIDYLINOSITOL-4-PHOSPHATE KINASE	PINS4P + ATP -> D45PI + ADP	fab1

YDR208W	2.7.1.68	*MSS4*	PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE; REQUIRED FOR PROPER ORGANIZATION OF THE ACTIN CYTOSKELETON	PINS4P + ATP -> D45PI + ADP	mss4
YPL268W	3.1.4.11	*PLC1*	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE	D45PI -> TPI + DAGLY	plc1
YCL004W	2.7.8.8	*PGS1*	CDP-DIACYLGLYCEROL--SERINE O-PHOSPHATIDYLTRANSFERASE	CDPDGm + GL3Pm <-> CMPm + PGPm	pgs1
*U9_*	3.1.3.27	*U9_*	PHOSPHATIDYLGLYCEROL PHOSPHATE PHOSPHATASE A	PGPm -> PIm + PGm	pgpa
YDL142C	2.7.8.5	*CRD1*	CARDIOLIPIN SYNTHASE	CDPDGm + PGm -> CMPm + CLm	crd1
YDR284C		*DPP1*	DIACYLGLYCEROL PYROPHOSPHATE PHOSPHATASE	PA -> DAGLY + PI	dpp1
YDR503C		*LPP1*	LIPID PHOSPHATE PHOSPHATASE	DGPP -> PA + PI	lpp1
# SPHINGOGLYCOLIPID METABOLISM					
YDR062W	2.3.1.50	*LCB2*	SERINE C-PALMITOYLTRANSFERASE	PALCOA + SER -> COA + DHSPH + CO2	lcb2
YMR296C	2.3.1.50	*LCB1*	SERINE C-PALMITOYLTRANSFERASE	PALCOA + SER -> COA + DHSPH + CO2	lcb1
YBR265W	1.1.1.102	*TSC10*	3-DEHYDROSPHINGANINE REDUCTASE	DHSPH + NADPH -> SPH + NADP	tsc10
YDR297W		*SUR2*	SYRINGOMYCIN RESPONSE PROTEIN 2	SPH + O2 + NADPH -> PSPH + NADP	sur2
*U10_*		*U10_*	CERAMIDE SYNTHASE	PSPH + C260COA -> CER2 + COA	csyna
*U11_*		*U11_*	CERAMIDE SYNTHASE	PSPH + C240COA -> CER2 + COA	csynb
YMR272C		*SCS7*	CERAMIDE HYDROXYLASE THAT HYDROXYLATES THE C-26 FATTY-ACYL MOIETY OF INOSITOL-PHOSPHORYLCERAMIDE	CER2 + NADPH + O2 -> CER3 + NADP	scs7
YKL004W		*AUR1*	IPS SYNTHASE, AUREOBASIDIN A RESISTANCE PROTEIN	CER3 + PINS -> IPC	aur1
YBR036C		*CSG2*	PROTEIN REQUIRED FOR SYNTHESIS OF THE MANNOSYLATED SPHINGOLIPIDS	IPC + GDPMAN -> MIPC	csg2
YPL057C		*SUR1*	PROTEIN REQUIRED FOR SYNTHESIS OF THE MANNOSYLATED SPHINGOLIPIDS	IPC + GDPMAN -> MIPC	sur1
YDR072C	2.-.-.-	*IPT1*	MIP2C SYNTHASE, MANNOSYL DIPHOSPHORYLINOSITOL CERAMIDE SYNTHASE	MIPC + PINS -> MIP2C	ipt1
YOR171C		*LCB4*	LONG CHAIN BASE KINASE, INVOLVED IN SPHINGOLIPID METABOLISM	SPH + ATP -> DHSP + ADP	lcb4_1
YLR260W		*LCB5*	LONG CHAIN BASE KINASE, INVOLVED IN SPHINGOLIPID METABOLISM	SPH + ATP -> DHSP + ADP	lcb5_1
YOR171C		*LCB4*	LONG CHAIN BASE KINASE, INVOLVED IN SPHINGOLIPID METABOLISM	PSPH + ATP -> PHSP + ADP	lcb4_2

YLR260W		*LCB5*	LONG CHAIN BASE KINASE, INVOLVED IN SPHINGOLIPID METABOLISM	PSPH + ATP -> PHSP + ADP	lcb5_2
YJL134W		*LCB3*	SPHINGOID BASE-PHOSPHATE PHOSPHATASE, PUTATIVE REGULATOR OF SPHINGOLIPID METABOLISM AND STRESS RESPONSE	DHSP -> SPH + PI	lcb3
YKR053C		*YSR3*	SPHINGOID BASE-PHOSPHATE PHOSPHATASE, PUTATIVE REGULATOR OF SPHINGOLIPID METABOLISM AND STRESS RESPONSE	DHSP -> SPH + PI	ysr3
YDR294C		*DPL1*	DIHYDROSPHINGOSINE-1-PHOSPHATE LYASE	DHSP -> PETHM + C16A	dpl1
# STEROL BIOSYNTHESIS					
YML126C	4.1.3.5	*HMGS*	3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE	H3MCOA + COA <-> ACCOA + AACCOA	hmgs
YLR450W	1.1.1.34	*HMG2*	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A (HMG-COA) REDUCTASE ISOZYME	MVL + COA + 2 NADP <-> H3MCOA + 2 NADPH	hmg2
YML075C	1.1.1.34	*HMG1*	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A (HMG-COA) REDUCTASE ISOZYME	MVL + COA + 2 NADP <-> H3MCOA + 2 NADPH	hmg1
YMR208W	2.7.1.36	*ERG12*	MEVALONATE KINASE	ATP + MVL -> ADP + PMVL	erg12_1
YMR208W	2.7.1.36	*ERG12*	MEVALONATE KINASE	CTP + MVL -> CDP + PMVL	erg12_2
YMR208W	2.7.1.36	*ERG12*	MEVALONATE KINASE	GTP + MVL -> GDP + PMVL	erg12_3
YMR208W	2.7.1.36	*ERG12*	MEVALONATE KINASE	UTP + MVL -> UDP + PMVL	erg12_4
YMR220W	2.7.4.2	*ERG8*	48 KDA PHOSPHOMEVALONATE KINASE	ATP + PMVL -> ADP + PPMVL	erg8
YNR043W	4.1.1.33	*MVD1*	DIPHOSPHOMEVALONATE DECARBOXYLASE	ATP + PPMVL -> ADP + PI + IPPP + CO2	mvd1
YPL117C	5.3.3.2	*IDI1*	ISOPENTENYL DIPHOSPHATE:DIMETHYLALLYL DIPHOSPHATE ISOMERASE (IPP ISOMERASE)	IPPP <-> DMPP	idi1
YJL167W	2.5.1.1	*ERG20*	PRENYLTRANSFERASE	DMPP + IPPP -> GPP + PPI	erg20_1
YJL167W	2.5.1.10	*ERG20*	FARNESYL DIPHOSPHATE SYNTHETASE (FPP SYNTHETASE)	GPP + IPPP -> FPP + PPI	erg20_2
YHR190W	2.5.1.21	*ERG9*	SQUALENE SYNTHASE.	2 FPP + NADPH -> NADP + SQL	erg9
YGR175C	1.14.99.7	*ERG1*	SQUALENE MONOOXYGENASE	SQL + O2 + NADP -> S23E + NADPH	erg1
YHR072W	5.4.99.7	*ERG7*	2,3-OXIDOSQUALENE-LANOSTEROL CYCLASE	S23E -> LNST	erg7
YHR007C	1.14.14.1	*ERG11*	CYTOCHROME P450 LANOSTEROL 14A-DEMETHYLASE	LNST + RFP + O2 -> IGST + OFP	erg11_1
YNL280C	1.-.-.-	*ERG24*	C-14 STEROL REDUCTASE	IGST + NADPH -> DMZYMST + NADP	erg24
YGR060W	1.-.-.-	*ERG25*	C-4 STEROL METHYL OXIDASE	3 O2 + DMZYMST -> IMZYMST	erg25_1
YGL001C	5.3.3.1	*ERG26*	C-3 STEROL DEHYDROGENASE (C-4 DECARBOXYLASE)	IMZYMST -> IIMZYMST + CO2	erg26_1
YLR100C		*YLR100C*	C-3 STEROL KETO REDUCTASE	IIMZYMST + NADPH -> MZYMST + NADP	erg11_2
YGR060W	1.-.-.-	*ERG25*	C-4 STEROL METHYL OXIDASE	3 O2 + MZYMST -> IZYMST	erg25_2

YGL001C	5.3.3.1	*ERG26*	C-3 STEROL DEHYDROGENASE (C-4 DECARBOXYLASE)	IZYMST -> IIZYMST + CO2	erg26_2
YLR100C		*YLR100C*	C-3 STEROL KETO REDUCTASE	IIZYMST + NADPH -> ZYMST + NADP	erg11_3
YML008C	2.1.1.41	*ERG6*	S-ADENOSYL-METHIONINE DELTA-24-STEROL-C-METHYLTRANSFERASE	ZYMST + SAM -> FEST + SAH	erg6
YMR202W		*ERG2*	C-8 STEROL ISOMERASE	FEST -> EPST	erg2
YLR056W	1.-.-.-	*ERG3*	C-5 STEROL DESATURASE	EPST + O2 + NADPH -> NADP + ERTROL	erg3
YMR015C	1.14.14.-	*ERG5*	C-22 STEROL DESATURASE	ERTROL + O2 + NADPH -> NADP + ERTEOL	erg5
YGL012W	1.-.-.-	*ERG4*	STEROL C-24 REDUCTASE	ERTEOL + NADPH -> ERGOST + NADP	erg4
*U12_*		*U12_*		LNST + 3 O2 + 4 NADPH + NAD -> MZYMST + CO2 + 4 NADP + NADH	unkrxn3
*U13_*		*U13_*		MZYMST + 3 O2 + 4 NADPH + NAD -> ZYMST + CO2 + 4 NADP + NADH	unkrxn4
*U14_*	5.3.3.5	*U14_*	CHOLESTENOL DELTA-ISOMERASE	ZYMST + SAM -> ERGOST + SAH	cdisoa
# NUCLEOTIDE METABOLISM					
# HISTIDINE BIOSYNTHESIS					
YOL061W	2.7.6.1	*PRS5*	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE	R5P + ATP <-> PRPP + AMP	prs5
YBL068W	2.7.6.1	*PRS4*	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 4	R5P + ATP <-> PRPP + AMP	prs4
YER099C	2.7.6.1	*PRS2*	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2	R5P + ATP <-> PRPP + AMP	prs2
YHL011C	2.7.6.1	*PRS3*	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 3	R5P + ATP <-> PRPP + AMP	prs3
YKL181W	2.7.6.1	*PRS1*	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE	R5P + ATP <-> PRPP + AMP	prs1
YIR027C	3.5.2.5	*DAL1*	ALLANTOINASE	ATN <-> ATT	dal1
YIR029W	3.5.3.4	*DAL2*	ALLANTOICASE	ATT <-> UGC + UREA	dal2
YIR032C	3.5.3.19	*DAL3*	UREIDOGLYCOLATE HYDROLASE	UGC <-> GLX + 2 NH3 + CO2	dal3
# PURINE METABOLISM					
YJL005W	4.6.1.1	*CYR1*	ADENYLATE CYCLASE	ATP -> cAMP + PPI	cyr1
YDR454C	2.7.4.8	*GUK1*	GUANYLATE KINASE	GMP + ATP <-> GDP + ADP	guk1_1
YDR454C	2.7.4.8	*GUK1*	GUANYLATE KINASE	DGMP + ATP <-> DGDP + ADP	guk1_2
YDR454C	2.7.4.8	*GUK1*	GUANYLATE KINASE	GMP + DATP <-> GDP + DADP	guk1_3
YMR300C	2.4.2.14	*ADE4*	PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE	PRPP + GLN -> PPI + GLU + PRAM	ade4
YGL234W	6.3.4.13	*ADE5,7*	GLYCINAMIDE RIBOTIDE SYNTHETASE AND AMINOIMIDAZOLE RIBOTIDE SYNTHETASE	PRAM + ATP + GLY <-> ADP + PI + GAR	ade5
YDR408C	2.1.2.2	*ADE8*	GLYCINAMIDE RIBOTIDE TRANSFORMYLASE	GAR + FTHF -> THF + FGAR	ade8
YGR061C	6.3.5.3	*ADE6*	5'-PHOSPHORIBOSYLFORMYL GLYCINAMIDINE SYNTHETASE	FGAR + ATP + GLN -> GLU + ADP + PI + FGAM	ade6

YGL234W	6.3.3.1	*ADE5,7*	PHOSPHORIBOSYLFORMYLGLYCINAMIDE CYCLO-LIGASE	FGAM + ATP -> ADP + PI + AIR	ade7
YOR128C	4.1.1.21	*ADE2*	PHOSPHORIBOSYLAMINO-IMIDAZOLE-CARBOXYLASE	CAIR <-> AIR + CO2	ade2
YAR015W	6.3.2.6	*ADE1*	PHOSPHORIBOSYL AMINO IMIDAZOLESUCCINOCARBOZAMIDE SYNTHETASE	CAIR + ATP + ASP <-> ADP + PI + SAICAR	ade1
YLR359W	4.3.2.2	*ADE13*	5'-PHOSPHORIBOSYL-4-(N-SUCCINOCARBOXAMIDE)-5-AMINOIMIDAZOLE LYASE	SAICAR <-> FUM + AICAR	ade13_1
YLR028C	2.1.2.3	*ADE16*	5-AMINOIMIDAZOLE-4-CARBOXAMIDE RIBONUCLEOTIDE (AICAR) TRANSFORMYLASE\/IMP CYCLOHYDROLASE	AICAR + FTHF <-> THF + PRFICA	ade16_1
YMR120C	2.1.2.3	*ADE17*	5-AMINOIMIDAZOLE-4-CARBOXAMIDE RIBONUCLEOTIDE (AICAR) TRANSFORMYLASE\/IMP CYCLOHYDROLASE	AICAR + FTHF <-> THF + PRFICA	ade17_1
YLR028C	3.5.4.10	*ADE16*	5-AMINOIMIDAZOLE-4-CARBOXAMIDE RIBONUCLEOTIDE (AICAR) TRANSFORMYLASE\/IMP CYCLOHYDROLASE	PRFICA <-> IMP	ade16_2
YMR120C	2.1.2.3	*ADE17*	IMP CYCLOHYDROLASE	PRFICA <-> IMP	ade17_2
YNL220W	6.3.4.4	*ADE12*	ADENYLOSUCCINATE SYNTHETASE	IMP + GTP + ASP -> GDP + PI + ASUC	ade12
YLR359W	4.3.2.2	*ADE13*	ADENYLOSUCCINATE LYASE	ASUC <-> FUM + AMP	ade13_2
YAR073W	1.1.1.205	*FUN63*	PUTATIVE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE	IMP + NAD -> NADH + XMP	fun63
YHR216W	1.1.1.205	*PUR5*	PURINE EXCRETION	IMP + NAD -> NADH + XMP	pur5
YML056C	1.1.1.205	*IMD4*	PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP	IMP + NAD -> NADH + XMP	prm5
YLR432W	1.1.1.205	*IMD3*	PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP	IMP + NAD -> NADH + XMP	prm4
YAR075W	1.1.1.205	*YAR075W*	PROTEIN WITH STRONG SIMILARITY TO INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE, FRAMESHIFTED FROM YAR073W, POSSIBLE PSEUDOGENE	IMP + NAD -> NADH + XMP	prm6
YMR217W	6.3.5.2, 6.3	*GUA1*	GMP SYNTHASE	XMP + ATP + GLN -> GLU + AMP + PPI + GMP	gua1
YML035C	3.5.4.6	*AMD1*	AMP DEAMINASE	AMP -> IMP + NH3	amd1
YGL248W	3.1.4.17	*PDE1*	3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE, LOW AFFINITY	cAMP -> AMP	pde1
YOR360C	3.1.4.17	*PDE2*	3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE, HIGH AFFINITY	cAMP -> AMP	pde2_1
YOR360C	3.1.4.17	*PDE2*		cdAMP -> DAMP	pde2_2
YOR360C	3.1.4.17	*PDE2*		cIMP -> IMP	pde2_3

YOR360C	3.1.4.17	*PDE2*		cGMP -> GMP	pde2_4
YOR360C	3.1.4.17	*PDE2*		cCMP -> CMP	pde2_5
YDR530C	2.7.7.53	*APA2*	5',5'''-P-1,P-4-TETRAPHOSPHATE PHOSPHORYLASE II	ADP + ATP -> PI + ATRP	apa2
YCL050C	2.7.7.53	*APA1*	5',5'''-P-1,P-4-TETRAPHOSPHATE PHOSPHORYLASE II	ADP + GTP -> PI + ATRP	apa1_1
YCL050C	2.7.7.53	*APA1*	5',5'''-P-1,P-4-TETRAPHOSPHATE PHOSPHORYLASE II	GDP + GTP -> PI + GTRP	apa1_3
# PYRIMIDINE METABOLISM					
YJL130C	2.1.3.2	*URA2*	ASPARTATE-CARBAMOYLTRANSFERASE	CAP + ASP -> CAASP + PI	ura2_1
YLR420W	3.5.2.3	*URA4*	DIHYDROORATASE	CAASP <-> DOROA	ura4
YKL216W	1.3.3.1	*URA1*	DIHYDROOROTATE DEHYDROGENASE	DOROA + O2 <-> H2O2 + OROA	ura1_1
YKL216W	1.3.3.1	*PYRD*	DIHYDROOROTATE DEHYDROGENASE	DOROA + Qm <-> QH2m + OROA	ura1_2
YML106W	2.4.2.10	*URA5*	OROTATE PHOSPHORIBOSYLTRANSFERASE 1	OROA + PRPP <-> PPI + OMP	ura5
YMR271C	2.4.2.10	*URA10*	OROTATE PHOSPHORIBOSYLTRANSFERASE 2	OROA + PRPP <-> PPI + OMP	ura10
YEL021W	4.1.1.23	*URA3*	OROTIDINE-5'-PHOSPHATE DECARBOXYLASE	OMP -> CO2 + UMP	ura3
YKL024C	2.7.4.14	*URA6*	NUCLEOSIDE-PHOSPHATE KINASE	ATP + UMP <-> ADP + UDP	npk
YHR128W	2.4.2.9	*FUR1*	UPRTASE, URACIL PHOSPHORIBOSYLTRANSFERASE	URA + PRPP -> UMP + PPI	fur1
YPR062W	3.5.4.1	*FCY1*	CYTOSINE DEAMINASE	CYTS -> URA + NH3	fcy1
*U15_*	2.7.1.21	*U15_*	THYMIDINE (DEOXYURIDINE) KINASE	DU + ATP -> DUMP + ADP	tdk1
*U16_*	2.7.1.21	*U16_*	THYMIDINE (DEOXYURIDINE) KINASE	DT + ATP -> ADP + DTMP	tdk2
YNR012W	2.7.1.48	*URK1*	URIDINE KINASE	URI + GTP -> UMP + GDP	urk1_1
YNR012W	2.7.1.48	*URK1*	CYTODINE KINASE	CYTD + GTP -> GDP + CMP	urk1_2
YNR012W	2.7.1.48	*URK1*	URIDINE KINASE, CONVERTS ATP AND URIDINE TO ADP AND UMP	URI + ATP -> ADP + UMP	urk1_3
YLR209C	2.4.2.4	*PNP1*	PROTEIN WITH SIMILARITY TO HUMAN PURINE NUCLEOSIDE PHOSPHORYLASE, THYMIDINE (DEOXYURIDINE) PHOSPHORYLASE, PURINE NUCLEOTIDE PHOSPHORYLASE	DU + PI <-> URA + DR1P	deoa1
YLR209C	2.4.2.4	*PNP1*	PROTEIN WITH SIMILARITY TO HUMAN PURINE NUCLEOSIDE PHOSPHORYLASE, THYMIDINE (DEOXYURIDINE) PHOSPHORYLASE	DT + PI <-> THY + DR1P	deoa2
YLR245C	3.5.4.5	*CDD1*	CYTIDINE DEAMINASE	CYTD -> URI + NH3	cdd1_1
YLR245C	3.5.4.5	*CDD1*	CYTIDINE DEAMINASE	DC -> NH3 + DU	cdd1_2
YJR057W	2.7.4.9	*CDC8*	DTMP KINASE	DTMP + ATP <-> ADP + DTDP	cdc8
YDR353W	1.6.4.5	*TRR1*	THIOREDOXIN REDUCTASE	OTHIO + NADPH -> NADP + RTHIO	trr1
YHR106W	1.6.4.5	*TRR2*	MITOCHONDRIAL THIOREDOXIN REDUCTASE	OTHIOm + NADPHm -> NADPm + RTHIOm	trr2
YBR252W	3.6.1.23	*DUT1*	DUTP PYROPHOSPHATASE (DUTPASE)	DUTP -> PPI + DUMP	dut1
YOR074C	2.1.1.45	*CDC21*	THYMIDYLATE SYNTHASE	DUMP + METTHF -> DHF + DTMP	cdc21

*U17_*	2.7.4.14	*U17_*	CYTIDYLATE KINASE	DCMP + ATP <-> ADP + DCDP	cmka1
*U18_*	2.7.4.14	*U18_*	CYTIDYLATE KINASE	CMP + ATP <-> ADP + CDP	cmka2
YHR144C	3.5.4.12	*DCD1*	DCMP DEAMINASE	DCMP <-> DUMP + NH3	dcd1
YBL039C	6.3.4.2	*URA7*	CTP SYNTHASE, HIGHLY HOMOLOGUS TO URA8 CTP SYNTHASE	UTP + GLN + ATP -> GLU + CTP + ADP + PI	ura7_1
YJR103W	6.3.4.2	*URA8*	CTP SYNTHASE	UTP + GLN + ATP -> GLU + CTP + ADP + PI	ura8_1
YBL039C	6.3.4.2	*URA7*	CTP SYNTHASE, HIGHLY HOMOLOGUS TO URA8 CTP SYNTHASE	ATP + UTP + NH3 -> ADP + PI + CTP	ura7_2
YJR103W	6.3.4.2	*URA8*	CTP SYNTHASE	ATP + UTP + NH3 -> ADP + PI + CTP	ura8_2
YNL292W	4.2.1.70	*PUS4*	PSEUDOURIDINE SYNTHASE	URA + R5P <-> PURI5P	pus4
YPL212C	4.2.1.70	*PUS1*	INTRANUCLEAR PROTEIN WHICH EXHIBITS A NUCLEOTIDE-SPECIFIC INTRON-DEPENDENT TRNA PSEUDOURIDINE SYNTHASE ACTIVITY	URA + R5P <-> PURI5P	pus1
YGL063W	4.2.1.70	*PUS2*	PSEUDOURIDINE SYNTHASE 2	URA + R5P <-> PURI5P	pus2
YFL001W	4.2.1.70	*DEG1*	SIMILAR TO RRNA METHYLTRANSFERASE (CAENORHABDITIS ELEGANS) AND HYPOTHETICAL 28K PROTEIN (ALKALINE ENDOGLUCANASE GENE 5' REGION) FROM BACILLUS SP.	URA + R5P <-> PURI5P	deg1
# SALVAGE PATHWAYS					
YML022W	2.4.2.7	*APT1*	ADENINE PHOSPHORIBOSYLTRANSFERASE	AD + PRPP -> PPI + AMP	apt1
YDR441C	2.4.2.7	*APT2*	SIMILAR TO ADENINE PHOSPHORIBOSYLTRANSFERASE	AD + PRPP -> PPI + AMP	apt2
YNL141W	3.5.4.4	*AAH1*	ADENINE AMINOHYDROLASE (ADENINE DEAMINASE)	ADN -> INS + NH3	aah1a
YNL141W	3.5.4.4	*AAH1*	ADENINE AMINOHYDROLASE (ADENINE DEAMINASE)	DA -> DIN + NH3	aah1b
YLR209C	2.4.2.1	*PNP1*	PURINE NUCLEOTIDE PHOSPHORYLASE, XANTHOSINE PHOSPHORYLASE	DIN + PI <-> HYXN + DR1P	xapa1
YLR209C	2.4.2.1	*PNP1*	XANTHOSINE PHOSPHORYLASE, PURINE NUCLEOTIDE PHOSPHORYLASE	DA + PI <-> AD + DR1P	xapa2
YLR209C	2.4.2.1	*PNP1*	XANTHOSINE PHOSPHORYLASE	DG + PI <-> GN + DR1P	xapa3
YLR209C	2.4.2.1	*PNP1*	XANTHOSINE PHOSPHORYLASE, PURINE NUCLEOTIDE PHOSPHORYLASE	HYXN + R1P <-> INS + PI	xapa4
YLR209C	2.4.2.1	*PNP1*	XANTHOSINE PHOSPHORYLASE, PURINE NUCLEOTIDE PHOSPHORYLASE	AD + R1P <-> PI + ADN	xapa5
YLR209C	2.4.2.1	*PNP1*	XANTHOSINE PHOSPHORYLASE, PURINE NUCLEOTIDE PHOSPHORYLASE	GN + R1P <-> PI + GSN	xapa6

YLR209C	2.4.2.1	*PNP1*	XANTHOSINE PHOSPHORYLASE, PURINE NUCLEOTIDE PHOSPHORYLASE	XAN + R1P <-> PI + XTSINE	xapa7
YJR133W	2.4.2.22	*XPT1*	XANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE	XAN + PRPP -> XMP + PPI	gpt1
YDR400W	3.2.2.1	*URH1*	PURINE NUCLEOSIDASE	GSN -> GN + RIB	pur21
YDR400W	3.2.2.1	*URH1*	PURINE NUCLEOSIDASE	ADN -> AD + RIB	pur11
YJR105W	2.7.1.20	*YJR105W*	ADENOSINE KINASE	ADN + ATP -> AMP + ADP	prm2
YDR226W	2.7.4.3	*ADK1*	CYTOSOLIC ADENYLATE KINASE	ATP + AMP <-> 2 ADP	adk1_1
YDR226W	2.7.4.3	*ADK1*	CYTOSOLIC ADENYLATE KINASE	GTP + AMP <-> ADP + GDP	adk1_2
YDR226W	2.7.4.3	*ADK1*	CYTOSOLIC ADENYLATE KINASE	ITP + AMP <-> ADP + IDP	adk1_3
YER170W	2.7.4.3	*ADK2*	ADENYLATE KINASE (MITOCHONDRIAL GTP:AMP PHOSPHOTRANSFERASE)	ATPm + AMPm <-> 2 ADPm	adk2_1
YER170W	2.7.4.3	*ADK2*	ADENYLATE KINASE (MITOCHONDRIAL GTP:AMP PHOSPHOTRANSFERASE)	GTPm + AMPm <-> ADPm + GDPm	adk2_2
YER170W	2.7.4.3	*ADK2*	ADENYLATE KINASE (MITOCHONDRIAL GTP:AMP PHOSPHOTRANSFERASE)	ITPm + AMPm <-> ADPm + IDPm	adk2_3
YGR180C	1.17.4.1	*RNR4*	RIBONUCLEOTIDE REDUCTASE, SMALL SUBUNIT (ALT), BETA CHAIN		
YIL066C	1.17.4.1	*RNR3*	RIBONUCLEOTIDE REDUCTASE (RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE) LARGE SUBUNIT, ALPHA CHAIN	ADP + RTHIO -> DADP + OTHIO	rnr3
YJL026W	1.17.4.1	*RNR2*	SMALL SUBUNIT OF RIBONUCLEOTIDE REDUCTASE, BETA CHAIN		
YKL067W	2.7.4.6	*YNK1*	NUCLEOSIDE-DIPHOSPHATE KINASE	UDP + ATP <-> UTP + ADP	ynk1_1
YKL067W	2.7.4.6	*YNK1*	NUCLEOSIDE-DIPHOSPHATE KINASE	CDP + ATP <-> CTP + ADP	ynk1_2
YKL067W	2.7.4.6	*YNK1*	NUCLEOSIDE-DIPHOSPHATE KINASE	DGDP + ATP <-> DGTP + ADP	ynk1_3
YKL067W	2.7.4.6	*YNK1*	NUCLEOSIDE-DIPHOSPHATE KINASE	DUDP + ATP <-> DUTP + ADP	ynk1_4
YKL067W	2.7.4.6	*YNK1*	NUCLEOSIDE-DIPHOSPHATE KINASE	DCDP + ATP <-> DCTP + ADP	ynk1_5
YKL067W	2.7.4.6	*YNK1*	NUCLEOSIDE-DIPHOSPHATE KINASE	DTDP + ATP <-> DTTP + ADP	ynk1_6
YKL067W	2.7.4.6	*YNK1*	NUCLEOSIDE-DIPHOSPHATE KINASE	DADP + ATP <-> DATP + ADP	ynk1_7
YKL067W	2.7.4.6	*YNK1*	NUCLEOSIDE DIPHOSPHATE KINASE	GDP + ATP <-> GTP + ADP	ynk1_8
YKL067W	2.7.4.6	*YNK1*	NUCLEOSIDE DIPHOSPHATE KINASE	IDP + ATP <-> ITP + IDP	ynk1_9
*U19_*	2.7.4.11	*U19_*	ADENYLATE KINASE, DAMP KINASE	DAMP + ATP <-> DADP + ADP	dampk
YNL141W	3.5.4.2	*AAH1*	ADENINE DEAMINASE	AD -> NH3 + HYXN	yicp
*U20_*	2.7.1.73	*U20_*	INOSINE KINASE	INS + ATP -> IMP + ADP	gsk1
*U21_*	2.7.1.73	*U21_*	GUANOSINE KINASE	GSN + ATP -> GMP + ADP	gsk2
YDR399W	2.4.2.8	*HPT1*	HYPOXANTHINE PHOSPHORIBOSYLTRANSFERASE	HYXN + PRPP -> PPI + IMP	hpt1_1

YDR399W	2.4.2.8	*HPT1*	HYPOXANTHINE PHOSPHORIBOSYLTRANSFERASE	GN + PRPP -> PPI + GMP	hpt1_2
*U22_*	2.4.2.3	*U22_*	URIDINE PHOSPHORYLASE	URI + PI <-> URA + R1P	udp
YKL024C	2.1.4.-	*URA6*	URIDYLATE KINASE	UMP + ATP <-> UDP + ADP	pyrh1
YKL024C	2.1.4.-	*URA6*	URIDYLATE KINASE	DUMP + ATP <-> DUDP + ADP	pyrh2
*U23_*	3.2.2.10	*U23_*	CMP GLYCOSYLASE	CMP -> CYTS + R5P	cmpg
YHR144C	3.5.4.13	*DCD1*	DCTP DEAMINASE	DCTP -> DUTP + NH3	dcd
*U24_*	3.1.3.5	*U24_*	5'-NUCLEOTIDASE	DUMP -> DU + PI	usha1
*U25_*	3.1.3.5	*U25_*	5'-NUCLEOTIDASE	DTMP -> DT + PI	usha2
*U26_*	3.1.3.5	*U26_*	5'-NUCLEOTIDASE	DAMP -> DA + PI	usha3
*U27_*	3.1.3.5	*U27_*	5'-NUCLEOTIDASE	DGMP -> DG + PI	usha4
*U28_*	3.1.3.5	*U28_*	5'-NUCLEOTIDASE	DCMP -> DC + PI	usha5
*U29_*	3.1.3.5	*U29_*	5'-NUCLEOTIDASE	CMP -> CYTD + PI	usha6
*U30_*	3.1.3.5	*U30_*	5'-NUCLEOTIDASE	AMP -> PI + ADN	usha7
*U31_*	3.1.3.5	*U31_*	5'-NUCLEOTIDASE	GMP -> PI + GSN	usha8
*U32_*	3.1.3.5	*U32_*	5'-NUCLEOTIDASE	IMP -> PI + INS	usha9
*U33_*	3.1.3.5	*U33_*	5'-NUCLEOTIDASE	XMP -> PI + XTSINE	usha12
*U34_*	3.1.3.5	*U34_*	5'-NUCLEOTIDASE	UMP -> PI + URI	usha11
YER070W	1.17.4.1	*RNR1*	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE	ADP + RTHIO -> DADP + OTHIO	rnr1_1
YER070W	1.17.4.1	*RNR1*	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE	GDP + RTHIO -> DGDP + OTHIO	rnr1_2
YER070W	1.17.4.1	*RNR1*	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE	CDP + RTHIO -> DCDP + OTHIO	rnr1_3
YER070W	1.17.4.1	*RNR1*	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE	UDP + RTHIO -> OTHIO + DUDP	rnr1_4
*U35_*	1.17.4.2	*U35_*	RIBONUCLEOSIDE-TRIPHOSPHATE REDUCTASE	ATP + RTHIO -> DATP + OTHIO	nrdd1
*U36_*	1.17.4.2	*U36_*	RIBONUCLEOSIDE-TRIPHOSPHATE REDUCTASE	GTP + RTHIO -> DGTP + OTHIO	nrdd2
*U37_*	1.17.4.2	*U37_*	RIBONUCLEOSIDE-TRIPHOSPHATE REDUCTASE	CTP + RTHIO -> DCTP + OTHIO	nrdd3
*U38_*	1.17.4.2	*U38_*	RIBONUCLEOSIDE-TRIPHOSPHATE REDUCTASE	UTP + RTHIO -> OTHIO + DUTP	nrdd4
*U39_*	3.6.1.-	*U39_*	NUCLEOSIDE TRIPHOSPHATASE	GTP -> GSN + 3 PI	mutt1
*U40_*	3.6.1.-	*U40_*	NUCLEOSIDE TRIPHOSPHATASE	DGTP -> DG + 3 PI	mutt2
YML035C	3.2.2.4	*AMD1*	AMP DEAMINASE	AMP -> AD + R5P	amn
YBR284W	3.2.2.4	*YBR284W*	PROTEIN WITH SIMILARITY TO AMP DEAMINASE	AMP -> AD + R5P	amn1
YJL070C	3.2.2.4	*YJL070C*	PROTEIN WITH SIMILARITY TO AMP DEAMINASE	AMP -> AD + R5P	amn2
# AMINO ACID METABOLISM					
# GLUTAMATE METABOLISM (AMINOSUGARS METABOLISM)					
YMR250W	4.1.1.15	*GAD1*	GLUTAMATE DECARBOXYLASE B	GLU -> GABA + CO2	btn2
YGR019W	2.6.1.19	*UGA1*	AMINOBUTYRATE AMINOTRANSAMINASE 2	GABA + AKG -> SUCCSAL + GLU	uga1
YBR006W	1.2.1.16	*YBR006W*	SUCCINATE SEMIALDEHYDE DEHYDROGENASE –NADP	SUCCSAL + NADP -> SUCC + NADPH	gabda

YKL104C	2.6.1.16	*GFA1*	GLUTAMINE_FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE (GLUCOSEAMINE-6-PHOSPHATE SYNTHASE)	F6P + GLN -> GLU + GA6P	gfa1
YFL017C	2.3.1.4	*GNA1*	GLUCOSAMINE-PHOSPHATE N-ACETYLTRANSFERASE	ACCOA + GA6P <-> COA + NAGA6P	gna1
YEL058W	5.4.2.3	*PCM1*	PHOSPHOACETYLGLUCOSAMINE MUTASE	NAGA1P <-> NAGA6P	pcm1a
YDL103C	2.7.7.23	*QRI1*	N-ACETYLGLUCOSAMINE-1-PHOSPHATE-URIDYLTRANSFERASE	UTP + NAGA1P <-> UDPNAG + PPI	qri1
YBR023C	2.4.1.16	*CHS3*	CHITIN SYNTHASE 3	UDPNAG -> CHIT + UDP	chs3
YBR038W	2.4.1.16	*CHS2*	CHITIN SYNTHASE 2	UDPNAG -> CHIT + UDP	chs2
YNL192W	2.4.1.16	*CHS1*	CHITIN SYNTHASE 2	UDPNAG -> CHIT + UDP	chs1
YHR037W	1.5.1.12	*PUT2*	DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE	GLUGSALm + NADPm -> NADPHm + GLUm	put2_1
*U41_*		*U41_*		P5Cm + NADm -> NADHm + GLUm	put2
YDL171C	1.4.1.14	*GLT1*	GLUTAMATE SYNTHASE (NADH)	AKG + GLN + NADH -> NAD + 2 GLU	glt1
YDL215C	1.4.1.4	*GDH2*	GLUTAMATE DEHYDROGENASE	GLU + NAD -> AKG + NH3 + NADH	gdh2
YAL062W	1.4.1.4	*GDH3*	NADP-LINKED GLUTAMATE DEHYDROGENASE	AKG + NH3 + NADPH -> GLU + NADP	gdh3
YOR375C	1.4.1.4	*GDH1*	NADP-SPECIFIC GLUTAMATE DEHYDROGENASE	AKG + NH3 + NADPH -> GLU + NADP	gdh1
YPR035W	6.3.1.2	*GLN1*	GLUTAMINE SYNTHETASE	GLU + NH3 + ATP -> GLN + ADP + PI	gln1
YEL058W	5.4.2.3	*PCM1*	PHOSPHOGLUCOSAMINE MUTASE	GA6P <-> GA1P	pcm1b
*U42_*	3.5.1.2	*U42_*	GLUTAMINASE A	GLN -> GLU + NH3	glnasea
*U43_*	3.5.1.2	*U43_*	GLUTAMINASE B	GLN -> GLU + NH3	glnaseb
# GLUCOSAMINE					
U44_	5.3.1.10	*U44_*	GLUCOSAMINE-6-PHOSPHATE DEAMINASE	GA6P -> F6P + NH3	nagb
# ARABINOSE					
YBR149W	1.1.1.117	*ARA1*	D-ARABINOSE 1-DEHYDROGENASE (NAD(P)+).	ARAB + NAD -> ARABLAC + NADH	ara1_1
YBR149W	1.1.1.117	*ARA1*	D-ARABINOSE 1-DEHYDROGENASE (NAD(P)+).	ARAB + NADP -> ARABLAC + NADPH	ara1_2
# XYLOSE					
YGR194C	2.7.1.17	*XKS1*	XYLULOKINASE	XUL + ATP -> X5P + ADP	xks1
# MANNITOL					
*U45_*	1.1.1.17	*U45_*	MANNITOL-1-PHOSPHATE 5-DEHYDROGENASE	MNT6P + NAD <-> F6P + NADH	mtld
# ALANINE AND ASPARTATE METABOLISM					
YKL106W	2.6.1.1	*AAT1*	ASPARATE TRANSAMINASE	OAm + GLUm <-> ASPm + AKGm	aat1_1
YLR027C	2.6.1.1	*AAT2*	ASPARATE TRANSAMINASE	OA + GLU <-> ASP + AKG	aat2_1
YAR035W	2.3.1.7	*YAT1*	CARNITINE O-ACETYLTRANSFERASE	COAm + ACARm -> ACCOAm + CARm	yat1
YML042W	2.3.1.7	*CAT2*	CARNITINE O-ACETYLTRANSFERASE	ACCOA + CAR -> COA + ACAR	cat2
YDR111C	2.6.1.2	*YDR111C*	PUTATIVE ALANINE TRANSAMINASE	PYR + GLU <-> AKG + ALA	alab

YLR089C	2.6.1.2	*YLR089C*	ALANINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (GLUTAMIC--	PYRm + GLUm <-> AKGm + ALAm	cfx2
YPR145W	6.3.5.4	*ASN1*	ASPARAGINE SYNTHETASE	ASP + ATP + GLN -> GLU + ASN + AMP + PPI	asn1
YGR124W	6.3.5.4	*ASN2*	ASPARAGINE SYNTHETASE	ASP + ATP + GLN -> GLU + ASN + AMP + PPI	asn2
YLL062C	2.1.1.10	*MHT1*	PUTATIVE COBALAMIN-DEPENDENT HOMOCYSTEINE S-METHYLTRANSFERASE, HOMOCYSTEINE S-METHYLTRANSFERASE	SAM + HCYS -> SAH + MET	mht1
YPL273W	2.1.1.10	*SAM4*	PUTATIVE COBALAMIN-DEPENDENT HOMOCYSTEINE S-METHYLTRANSFERASE	SAM + HCYS -> SAH + MET	sam4
# ASPARAGINE					
YCR024C	6.1.1.22	*YCR024C*	ASN-TRNA SYNTHETASE, MITOCHONDRIAL	ATPm + ASPm + TRNAm -> AMPm + PPIm + ASPTRNAm	rnas
YHR019C	6.1.1.23	*DED81*	ASN-TRNA SYNTHETASE	ATP + ASP + TRNA -> AMP + PPI + ASPTRNA	ded81
YLR155C	3.5.1.1	*ASP3-1*	ASPARAGINASE, EXTRACELLULAR	ASN -> ASP + NH3	asp3_1
YLR157C	3.5.1.1	*ASP3-2*	ASPARAGINASE, EXTRACELLULAR	ASN -> ASP + NH3	asp3_2
YLR158C	3.5.1.1	*ASP3-3*	ASPARAGINASE, EXTRACELLULAR	ASN -> ASP + NH3	asp3_3
YLR160C	3.5.1.1	*ASP3-4*	ASPARAGINASE, EXTRACELLULAR	ASN -> ASP + NH3	asp3_4
YDR321W	3.5.1.1	*ASP1*	ASPARAGINASE	ASN -> ASP + NH3	asp1
# GLYCINE, SERINE AND THREONINE METABOLISM					
YER081W	1.1.1.95	*SER3*	PHOSPHOGLYCERATE DEHYDROGENASE	3PG + NAD -> NADH + PHP	ser3
YIL074C	1.1.1.95	*SER33*	PHOSPHOGLYCERATE DEHYDROGENASE	3PG + NAD -> NADH + PHP	ser33
YOR184W	2.6.1.52	*SER1*	PHOSPHOSERINE TRANSAMINASE	PHP + GLU -> AKG + 3PSER	ser1_1
YGR208W	3.1.3.3	*SER2*	PHOSPHOSERINE PHOSPHATASE	3PSER -> PI + SER	ser2
YBR263W	2.1.2.1	*SHM1*	GLYCINE HYDROXYMETHYLTRANSFERASE	THFm + SERm <-> GLYm + METTHFm	shm1
YLR058C	2.1.2.1	*SHM2*	GLYCINE HYDROXYMETHYLTRANSFERASE	THF + SER <-> GLY + METTHF	shm2
YFL030W	2.6.1.44	*YFL030W*	PUTATIVE ALANINE GLYOXYLATE AMINOTRANSFERASE (SERINE PYRUVATE AMINOTRANSFERASE)	ALA + GLX <-> PYR + GLY	agt
YDR019C	2.1.2.10	*GCV1*	GLYCINE CLEAVAGE T PROTEIN (T SUBUNIT OF GLYCINE DECARBOXYLASE COMPLEX	GLYm + THFm + NADm -> METTHFm + NADHm + CO2 + NH3	gcv1_1
YDR019C	2.1.2.10	*GCV1*	GLYCINE CLEAVAGE T PROTEIN (T SUBUNIT OF GLYCINE DECARBOXYLASE COMPLEX	GLY + THF + NAD -> METTHF + NADH + CO2 + NH3	gcv1_2
YER052C	2.7.2.4	*HOM3*	ASPARTATE KINASE, ASPARTATE KINASE I, II, III	ASP + ATP -> ADP + BASP	hom3

YDR158W	1.2.1.11	*HOM2*	ASPARTIC BETA SEMI-ALDEHYDE DEHYDROGENASE, ASPARTATE SEMIALDEHYDE DEHYDROGENASE	BASP + NADPH -> NADP + PI + ASPSA	hom2
YJR139C	1.1.1.3	*HOM6*	HOMOSERINE DEHYDROGENASE I	ASPSA + NADH -> NAD + HSER	hom6_1
YJR139C	1.1.1.3	*HOM6*	HOMOSERINE DEHYDROGENASE I	ASPSA + NADPH -> NADP + HSER	hom6_2
YHR025W	2.7.1.39	*THR1*	HOMOSERINE KINASE	HSER + ATP -> ADP + PHSER	thr1
YCR053W	4.2.99.2	*THR4*	THREONINE SYNTHASE	PHSER -> PI + THR	thr4_1
YGR155W	4.2.1.22	*CYS4*	CYSTATHIONINE BETA-SYNTHASE	SER + HCYS -> LLCT	cys4
YEL046C	4.1.2.5	*GLY1*	THREONINE ALDOLASE	GLY + ACAL -> THR	gly1
YMR189W	1.4.4.2	*GCV2*	GLYCINE DECARBOXYLASE COMPLEX (P-SUBUNIT), GLYCINE SYNTHASE (P-SUBUNIT), GLYCINE CLEAVAGE SYSTEM (P-SUBUNIT)	GLYm + LIPOm <-> SAPm + CO2m	gcv2
YCL064C	4.2.1.16	*CHA1*	THREONINE DEAMINASE	THR -> NH3 + OBUT	cha1_1
YER086W	4.2.1.16	*ILV1*	L-SERINE DEHYDRATASE	THRm -> NH3m + OBUTm	ilv1
YCL064C	4.2.1.13	*CHA1*	CATABOLIC SERINE (THREONINE) DEHYDRATASE	SER -> PYR + NH3	cha1_2
YIL167W	4.2.1.13	*YIL167W*	CATABOLIC SERINE (THREONINE) DEHYDRATASE	SER -> PYR + NH3	sdl1
*U46_*	1.1.1.103	*U46_*	THREONINE DEHYDROGENASE	THR + NAD -> GLY + AC + NADH	tdh1c
# METHIONINE METABOLISM					
YFR055W	4.4.1.8	*YFR055W*	CYSTATHIONINE-B-LYASE	LLCT -> HCYS + PYR + NH3	metc
YER043C	3.3.1.1	*SAH1*	PUTATIVE S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE	SAH -> HCYS + ADN	sah1
YER091C	2.1.1.14	*MET6*	VITAMIN B12-(COBALAMIN)-INDEPENDENT ISOZYME OF METHIONINE SYNTHASE (ALSO CALLED N5-METHYLTETRAHYDROFOLATE HOMOCYSTEINE METHYLTRANSFERASE OR 5-METHYLTETRAHYDROPTEROYL TRIGLUTAMATE HOMOCYSTEINE METHYLTRANSFERASE)	HCYS + MTHPTGLU -> THPTGLU + MET	met6
*U47_*	2.1.1.13	*U47_*	METHIONINE SYNTHASE	HCYS + MTHF -> THF + MET	met6_2
YAL012W	4.4.1.1	*CYS3*	CYSTATHIONINE GAMMA-LYASE	LLCT -> CYS + NH3 + OBUT	cys3
YNL277W	2.3.1.31	*MET2*	HOMOSERINE O-TRANS-ACETYLASE	ACCOA + HSER <-> COA + OAHSER	met2
YLR303W	4.2.99.10	*MET17*	O-ACETYLHOMOSERINE (THIOL)-LYASE	OAHSER + METH -> MET + AC	met17_1
YLR303W	4.2.99.8	*MET17*	O-ACETYLHOMOSERINE (THIOL)-LYASE	OAHSER + H2S -> AC + HCYS	met17_2
YLR303W	4.2.99.8, 4	*MET17*	O-ACETYLHOMOSERINE SULFHYDRYLASE (OAH SHLASE); CONVERTS O-ACETYLHOMOSERINE INTO HOMOCYSTEINE	OAHSER + H2S -> AC + HCYS	met17_3
YML082W	4.2.99.9	*YML082W*	PUTATIVE CYSTATHIONINE GAMMA-SYNTHASE	OSLHSER <-> SUCC + OBUT + NH3	met17h
YDR502C	2.5.1.6	*SAM2*	S-ADENOSYLMETHIONINE SYNTHETASE	MET + ATP -> PPI + PI + SAM	sam2

YLR180W	2.5.1.6	*SAM1*	S-ADENOSYLMETHIONINE SYNTHETASE	MET + ATP -> PPI + PI + SAM	sam1
YLR172C	2.1.1.98	*DPH5*	DIPHTHINE SYNTHASE	SAM + CALH -> SAH + DPTH	dph5
# CYSTEINE BIOSYNTHESIS					
YJR010W	2.7.7.4	*MET3*	ATP SULFURYLASE	SLF + ATP -> PPI + APS	met3
YKL001C	2.7.1.25	*MET14*	ADENYLYLSULFATE KINASE	APS + ATP -> ADP + PAPS	met14
YFR030W	1.8.1.2	*MET10*	SULFITE REDUCTASE	H2SO3 + 3 NADPH <-> H2S + 3 NADP	met10
*U48_*	2.3.1.30	*U48_*	SERINE TRANSACETYLASE	SER + ACCOA -> COA + ASER	cys1
YGR012W	4.2.99.8	*YGR012W*	PUTATIVE CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE) (O-	ASER + H2S -> AC + CYS	sul11
YOL064C	3.1.3.7	*MET22*	3' - 5' BISPHOSPHATE NUCLEOTIDASE	PAP -> AMP + PI	met22
YPR167C	1.8.99.4	*MET16*	PAPS REDUCTASE	PAPS + RTHIO -> OTHIO + H2SO3 + PAP	met16
YCL050C	2.7.7.5	*APA1*	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE PHOSPHORYLASE I	ADP + SLF <-> PI + APS	apa1_2
# BRANCHED CHAIN AMINO ACID METABOLISM (VALINE, LEUCINE AND ISOLEUCINE)					
YHR208W	2.6.1.42	*BAT1*	BRANCHED CHAIN AMINO ACID AMINOTRANSFERASE	OICAPm + GLUm <-> AKGm + LEUm	bat1_1
YHR208W	2.6.1.42	*BAT1*	BRANCHED CHAIN AMINO ACID AMINOTRANSFERASE	OMVALm + GLUm <-> AKGm + ILEm	bat1_2
YJR148W	2.6.1.42	*BAT2*	BRANCHED-CHAIN AMINO ACID TRANSAMINASE, HIGHLY SIMILAR TO MAMMALIAN ECA39, WHICH IS REGULATED BY THE ONCOGENE MYC	OMVAL + GLU <-> AKG + ILE	bat2_1
YJR148W	2.6.1.42	*BAT2*	BRANCHED CHAIN AMINO ACID AMINOTRANSFERASE	OIVAL + GLU <-> AKG + VAL	bat2_2
YJR148W	2.6.1.42	*BAT2*	BRANCHED-CHAIN AMINO ACID TRANSAMINASE, HIGHLY SIMILAR TO MAMMALIAN ECA39, WHICH IS REGULATED BY THE ONCOGENE MYC	OICAP + GLU <-> AKG + LEU	bat2_3
YMR108W	4.1.3.18	*ILV2*	ACETOLACTATE SYNTHASE, LARGE SUBUNIT	OBUTm + PYRm -> ABUTm + CO2m	ilv2_1
YCL009C	4.1.3.18	*ILV6*	ACETOLACTATE SYNTHASE, SMALL SUBUNIT		
YMR108W	4.1.3.18	*ILV2*	ACETOLACTATE SYNTHASE, LARGE SUBUNIT	2 PYRm -> CO2m + ACLACm	ilv2_2
YCL009C	4.1.3.18	*ILV6*	ACETOLACTATE SYNTHASE, SMALL SUBUNIT		
YLR355C	1.1.1.86	*ILV5*	KETO-ACID REDUCTOISOMERASE	ACLACm + NADPHm -> NADPm + DHVALm	ilv5_1
YLR355C	1.1.1.86	*ILV5*	KETO-ACID REDUCTOISOMERASE	ABUTm + NADPHm -> NADPm + DHMVAm	ilv5_2
YJR016C	4.2.1.9	*ILV3*	DIHYDROXY ACID DEHYDRATASE	DHVALm -> OIVALm	ilv3_1
YJR016C	4.2.1.9	*ILV3*	DIHYDROXY ACID DEHYDRATASE	DHMVAm -> OMVALm	ilv3_2
YNL104C	4.1.3.12	*LEU4*	ALPHA-ISOPROPYLMALATE SYNTHASE (2-ISOPROPYLMALATE SYNTHASE)	ACCOAm + OIVALm -> COAm + IPPMALm	leu4
YGL009C	4.2.1.33	*LEU1*	ISOPROPYLMALATE ISOMERASE	CBHCAP <-> IPPMAL	leu1_1
YGL009C	4.2.1.33	*LEU1*	ISOPROPYLMALATE ISOMERASE	PPMAL <-> IPPMAL	leu1_2
YCL018W	1.1.1.85	*LEU2*	BETA-IPM (ISOPROPYLMALATE) DEHYDROGENASE	IPPMAL + NAD -> NADH + OICAP + CO2	leu2

# LYSINE BIOSYNTHESIS/DEGRADATION					
*U49_*	4.2.1.79	*U49_*	2-METHYLCITRATE DEHYDRATASE	HCITm <-> HACNm	lys3
YDR234W	4.2.1.36	*LYS4*	HOMOACONITATE HYDRATASE	HICITm <-> HACNm	lys4
YIL094C	1.1.1.155	*LYS12*	HOMOISOCITRATE DEHYDROGENASE (STRATHERN:1.1.1.87)	HICITm + NADm <-> OXAm + CO2m + NADHm	lys12
*U50_*		*U50_*	NON-ENZYMATIC	OXAm <-> CO2m + AKAm	lys12b
*U51_*	2.6.1.39	*U51_*	2-AMINOADIPATE TRANSAMINASE	AKA + GLU <-> AMA + AKG	amit
YBR115C	1.2.1.31	*LYS2*	L-AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE, LARGE SUBUNIT	AMA + NADPH + ATP -> AMASA + NADP + AMP + PPI	lys2_1
YGL154C	1.2.1.31	*LYS5*	L-AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE, SMALL SUBUNIT		
YBR115C	1.2.1.31	*LYS2*	L-AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE, LARGE SUBUNIT	AMA + NADH + ATP -> AMASA + NAD + AMP + PPI	lys2_2
YGL154C	1.2.1.31	*LYS5*	L-AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE, SMALL SUBUNIT		
YNR050C	1.5.1.10	*LYS9*	SACCHAROPINE DEHYDROGENASE (NADP+, L-GLUTAMATE FORMING)	GLU + AMASA + NADPH <-> SACP + NADP	lys9
YIR034C	1.5.1.7	*LYS1*	SACCHAROPINE DEHYDROGENASE (NAD+, L-LYSINE FORMING)	SACP + NAD <-> LYS + AKG + NADH	lys1a
YDR037W	6.1.1.6	*KRS1*	LYSYL-TRNA SYNTHETASE, CYTOSOLIC	ATP + LYS + LTRNA -> AMP + PPI + LLTRNA	krs1
YNL073W	6.1.1.6	*MSK1*	LYSYL-TRNA SYNTHETASE, MITOCHONDRIAL	ATPm + LYSm + LTRNAm -> AMPm + PPIm + LLTRNAm	msk1
YDR368W	1.1.1.-	*YPR1*	SIMILAR TO ALDO-KETO REDUCTASE		
# ARGININE METABOLISM					
YMR062C	2.3.1.1	*ECM40*	AMINO-ACID N-ACETYLTRANSFERASE	GLUm + ACCOAm -> COAm + NAGLUm	ecm40_1
YER069W	2.7.2.8	*ARG5*	ACETYLGLUTAMATE KINASE	NAGLUm + ATPm -> ADPm + NAGLUPm	arg6
YER069W	1.2.1.38	*ARG5*	N-ACETYL-GAMMA-GLUTAMYL-PHOSPHATE REDUCTASE AND ACETYLGLUTAMATE KINASE	NAGLUPm + NADPHm -> NADPm + PIm + NAGLUSm	arg5
YOL140W	2.6.1.11	*ARG8*	ACETYLORNITHINE AMINOTRANSFERASE	NAGLUSm + GLUm -> AKGm + NAORNm	arg8
YMR062C	2.3.1.35	*ECM40*	GLUTAMATE N-ACETYLTRANSFERASE	NAORNm + GLUm -> ORNm + NAGLUm	ecm40_2
YJL130C	6.3.5.5	*URA2*	CARBAMOYL-PHOPHATE SYNTHETASE, ASPARTATE TRANSCARBAMYLASE, AND GLUTAMINE AMIDOTRANSFERASE	GLN + 2 ATP + CO2 -> GLU + CAP + 2 ADP + PI	ura2_2
YJR109C	6.3.5.5	*CPA2*	CARBAMYL PHOSPHATE SYNTHETASE, LARGE CHAIN	GLN + 2 ATP + CO2 -> GLU + CAP + 2 ADP + PI	cpa2

YOR303W	6.3.5.5	*CPA1*	CARBAMOYL PHOSPHATE SYNTHETASE, SAMLL CHAIN, ARGININE SPECIFIC		
YJL088W	2.1.3.3	*ARG3*	ORNITHINE CARBAMOYLTRANSFERASE	ORN + CAP -> CITR + PI	arg3
YLR438W	2.6.1.13	*CAR2*	ORNITHINE TRANSAMINASE	ORN + AKG -> GLUGSAL + GLU	car2
YOL058W	6.3.4.5	*ARG1*	ARGINOSUCCINATE SYNTHETASE	CITR + ASP + ATP <-> AMP + PPI + ARGSUCC	arg1
YHR018C	4.3.2.1	*ARG4*	ARGININOSUCCINATE LYASE	ARGSUCC <-> FUM + ARG	arg4
YKL184W	4.1.1.17	*SPE1*	ORNITHINE DECARBOXYLASE	ORN -> PTRSC + CO2	spe1
YOL052C	4.1.1.50	*SPE2*	S-ADENOSYLMETHIONINE DECARBOXYLASE	SAM <-> DSAM + CO2	spe2
YPR069C	2.5.1.16	*SPE3*	PUTRESCINE AMINOPROPYLTRANSFERASE (SPERMIDINE SYNTHASE)	PTRSC + SAM -> SPRMD + 5MTA	spe3
YLR146C	2.5.1.22	*SPE4*	SPERMINE SYNTHASE	DSAM + SPRMD -> 5MTA + SPRM	spe4
YDR242W	3.5.1.4	*AMD2*	AMIDASE	GBAD -> GBAT + NH3	amd2_1
YMR293C	3.5.1.4	*YMR293C*	PROBABLE AMIDASE	GBAD -> GBAT + NH3	amd
YPL111W	3.5.3.1	*CAR1*	ARGINASE	ARG -> ORN + UREA	car1
YDR341C	6.1.1.19	*YDR341C*	ARGINYL-TRNA SYNTHETASE	ATP + ARG + ATRNA -> AMP + PPI + ALTRNA	atrna
YHR091C	6.1.1.19	*MSR1*	ARGINYL-TRNA SYNTHETASE	ATP + ARG + ATRNA -> AMP + PPI + ALTRNA	msr1
YHR068W	1.5.99.6	*DYS1*	DEOXYHYPUSINE SYNTHASE	SPRMD + Qm -> DAPRP + QH2m	dys1
# HISTIDINE METABOLISM					
YER055C	2.4.2.17	*HIS1*	ATP PHOSPHORIBOSYLTRANSFERASE	PRPP + ATP -> PPI + PRBATP	his1
YCL030C	3.6.1.31	*HIS4*	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE / PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE / HISTIDINOL DEHYDROGENASE	PRBATP -> PPI + PRBAMP	his4_1
YCL030C	3.5.4.19	*HIS4*	HISTIDINOL DEHYDROGENASE	PRBAMP -> PRFP	his4_2
YIL020C	5.3.1.16	*HIS6*	PHOSPHORIBOSYL-5-AMINO-1-PHOSPHORIBOSYL-4-IMIDAZOLECARBOXIAMIDE ISOMERASE	PRFP -> PRLP	his6
YOR202W	4.2.1.19	*HIS3*	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE	DIMGP -> IMACP	his3
YIL116W	2.6.1.9	*HIS5*	HISTIDINOL-PHOSPHATE AMINOTRANSFERASE	IMACP + GLU -> AKG + HISOLP	his5
YFR025C	3.1.3.15	*HIS2*	HISTIDINOLPHOSPHATASE	HISOLP -> PI + HISOL	his2
YCL030C	1.1.1.23	*HIS4*	PHOSPHORIBOSYL-AMP CYCLOHYDROLASE / PHOSPHORIBOSYL-ATP PYROPHOSPHOHYDROLASE / HISTIDINOL DEHYDROGENASE	HISOL + 2 NAD -> HIS + 2 NADH	his4_3
YBR248C	2.4.2.-	*HIS7*	GLUTAMINE AMIDOTRANSFERASE:CYCLASE	PRLP + GLN -> GLU + AICAR + DIMGP	his7
YPR033C	6.1.1.21	*HTS1*	HISTIDYL-TRNA SYNTHETASE	ATP + HIS + HTRNA -> AMP + PPI + HHTRNA	hts1
YBR034C	2.1.1.-	*HMT1*	HNRNP ARGININE N-METHYLTRANSFERASE	SAM + HIS -> SAH + MHIS	hmt1
YCL054W	2.1.1.-	*SPB1*	PUTATIVE RNA METHYLTRANSFERASE		

YML110C	2.1.1.-	*COQ5*	UBIQUINONE BIOSYNTHESIS METHLYTRANSFERASE COQ5		
YOR201C	2.1.1.-	*PET56*	RRNA (GUANOSINE-2'-O-)-METHYLTRANSFERASE		
YPL266W	2.1.1.-	*DIM1*	DIMETHYLADENOSINE TRANSFERASE		

PHENYLALANINE, TYROSINE AND TRYPTOPHAN BIOSYNTHESIS (AROMATIC AMINO ACIDS)

YBR249C	4.1.2.15	*ARO4*	3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE (DAHP) SYNTHASE ISOENZYME	E4P + PEP -> PI + 3DDAH7P	aro4
YDR035W	4.1.2.15	*ARO3*	DAHP SYNTHASE\; A.K.A. PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE, PHENYLALANINE-INHIBITED\; PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE\; 2-DEHYDRO-3-DEOXYPHOSPHOHEPTONATE ALDOLASE\; 3-DEOXY-D-ARABINE-HEPTULOSONATE-7-PHOSPHATE SYNTHASE	E4P + PEP -> PI + 3DDAH7P	aro3
YDR127W	4.6.1.3	*ARO1*	PENTAFUNCTIONAL AROM POLYPEPTIDE (CONTAINS: 3-DEHYDROQUINATE SYNTHASE, 3-DEHYDROQUINATE DEHYDRATASE (3-DEHYDROQUINASE), SHIKIMATE 5-DEHYDROGENASE, SHIKIMATE KINASE, AND EPSP SYNTHASE)	3DDAH7P -> DQT + PI	aro1_1
YDR127W	4.2.1.10	*ARO1*	3-DEHYDROQUINATE DEHYDRATASE	DQT -> DHSK	aro1_2
YDR127W	1.1.1.25	*ARO1*	SHIKIMATE DEHYDROGENASE	DHSK + NADPH -> SME + NADP	aro1_3
YDR127W	2.7.1.71	*ARO1*	SHIKIMATE KINASE I, II	SME + ATP -> ADP + SME5P	aro1_4
YDR127W	2.5.1.19	*ARO1*	3-PHOSPHOSHIKIMATE-1-CARBOXYVINYLTRANSFERASE	SME5P + PEP -> 3PSME + PI	aro1_5
YGL148W	4.6.1.4	*ARO2*	CHORISMATE SYNTHASE	3PSME -> PI + CHOR	aro2
YPR060C	5.4.99.5	*ARO7*	CHORISMATE MUTASE	CHOR -> PHEN	aro7
YNL316C	4.2.1.51	*PHA2*	PREPHENATE DEHYDRATASE	PHEN -> CO2 + PHPYR	pha2
YHR137W	2.6.1.-	*ARO9*	PUTATIVE AROMATIC AMINO ACID AMINOTRANSFERASE II	PHPYR + GLU <-> AKG + PHE	aro9_1
YBR166C	1.3.1.13	*TYR1*	PREPHENATE DEHYDROGENASE (NADP+)	PHEN + NADP -> 4HPP + CO2 + NADPH	tyr1
YGL202W	2.6.1.-	*ARO8*	AROMATIC AMINO ACID AMINOTRANSFERASE I	4HPP + GLU -> AKG + TYR	aro8
YHR137W	2.6.1.-	*ARO9*	AROMATIC AMINO ACID AMINOTRANSFERASE II	4HPP + GLU -> AKG + TYR	aro9_2
*U52_*	1.3.1.12	*U52_*	PREPHANATE DEHYDROGENASE	PHEN + NAD -> 4HPP + CO2 + NADH	tyra2
YER090W	4.1.3.27	*TRP2*	ANTHRANILATE SYNTHASE	CHOR + GLN -> GLU + PYR + AN	trp2_1
YKL211C	4.1.3.27	*TRP3*	ANTHRANILATE SYNTHASE	CHOR + GLN -> GLU + PYR + AN	trp3_1
YDR354W	2.4.2.18	*TRP4*	ANTHRANILATE PHOSPHORIBOSYL TRANSFERASE	AN + PRPP -> PPI + NPRAN	trp4
YDR007W	5.3.1.24	*TRP1*	N-(5'-PHOSPHORIBOSYL)-ANTHRANILATE ISOMERASE	NPRAN -> CPAD5P	trp1

YKL211C	4.1.1.48	*TRP3*	INDOLEGLYCEROL PHOSPHATE SYNTHASE	CPAD5P -> CO2 + IGP	trp3_2
YGL026C	4.2.1.20	*TRP5*	TRYPTOPHAN SYNTHETASE	IGP + SER -> T3P1 + TRP	trp5
YDR256C	1.11.1.6	*CTA1*	CATALASE A	2 H2O2 -> O2	cta1
YGR088W	1.11.1.6	*CTT1*	CYTOPLASMIC CATALASE T	2 H2O2 -> O2	ctt1
YKL106W	2.6.1.1	*AAT1*	ASPARATE AMINOTRANSFERASE	4HPP + GLU <-> AKG + TYR	aat1_2
YLR027C	2.6.1.1	*AAT2*	ASPARATE AMINOTRANSFERASE	4HPP + GLU <-> AKG + TYR	aat2_2
YMR170C	1.2.1.5	*ALD2*	CYTOSOLIC ALDEYHDE DEHYDROGENASE	ACAL + NAD -> NADH + AC	ald2
YMR169C	1.2.1.5	*ALD3*	STRONG SIMILARITY TO ALDEHYDE DEHYDROGENASE	ACAL + NAD -> NADH + AC	ald3
YOR374W	1.2.1.3	*ALD4*	MITOCHONDRIAL ALDEHYDE DEHYDROGENASE	ACALm + NADm -> NADHm + ACm	ald4_1
YOR374W	1.2.1.3	*ALD4*	MITOCHONDRIAL ALDEHYDE DEHYDROGENASE	ACALm + NADPm -> NADPHm + ACm	ald4_2
YER073W	1.2.1.3	*ALD5*	MITOCHONDRIAL ALDEHYDE DEHYDROGENASE	ACALm + NADPm -> NADPHm + ACm	ald5_1
YPL061W	1.2.1.3	*ALD6*	CYTOSOLIC ALDEHYDE DEHYDROGENASE	ACAL + NADP -> NADPH + AC	ald6
YJR078W	1.13.11.11	*YJR078W*	PROTEIN WITH SIMILARITY TO INDOLEAMINE 2,3-DIOXYGENASES, WHICH CATALYZE CONVERSION OF TRYPTOPHAN AND OTHER INDOLE DERIVATIVES INTO KYNURENINES, TRYPTOPHAN 2,3-DIOXYGENASE	TRP + O2 -> FKYN	tdo2
*U53_*	3.5.1.9	*U53_*	KYNURENINE FORMAMIDASE	FKYN -> FOR + KYN	kfor
YLR231C	3.7.1.3	*YLR231C*	PROBABLE KYNURENINASE (L-KYNURENINE HYDROLASE)	KYN -> ALA + AN	kynu_1
YBL098W	1.14.13.9	*YBL098W*	KYNURENINE 3-HYDROXYLASE, NADPH-DEPENDENT FLAVIN MONOOXYGENASE THAT CATALYZES THE HYDROXYLATION OF KYNURENINE TO 3-HYDROXYKYNURENINE IN TRYPTOPHAN DEGRADATION AND NICOTINIC ACID SYNTHESIS, KYNURENINE 3-MONOOXYGENASE	KYN + NADPH + O2 -> HKYN + NADP	kmo
YLR231C	3.7.1.3	*YLR231C*	PROBABLE KYNURENINASE (L-KYNURENINE HYDROLASE)	HKYN -> HAN + ALA	kynu_2
YJR025C	1.13.11.6	*BNA1*	3-HYDROXYANTHRANILATE 3,4-DIOXYGENASE (3-HAO) (3-HYDROXYANTHRANILIC ACID DIOXYGENASE) (3-HYDROXYANTHRANILATEHYDROXYANTHRANILIC ACID DIOXYGENASE) (3-HYDROXYANTHRANILATE OXYGENASE)	HAN + O2 -> CMUSA	bna1
*U54_*	4.1.1.45	*U54_*	PICOLINIC ACID DECARBOXYLASE	CMUSA -> CO2 + AM6SA	aaaa
*U55_*	1.2.1.32	*U55_*		AM6SA + NAD -> AMUCO + NADH	aaab
*U56_*	1.5.1.-	*U56_*		AMUCO + NADPH -> AKA + NADP + NH3	aaac
*U57_*	1.3.11.27	*U57_*	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE	4HPP + O2 -> HOMOGEN + CO2	tyrdega

*U58_*	1.13.11.5	*U58_*	HOMOGENTISATE 1,2-DIOXYGENASE	HOMOGEN + O2 -> MACAC	tyrdegb
*U59_*	5.2.1.2	*U59_*	MALEYL-ACETOACETATE ISOMERASE	MACAC -> FUACAC	tyrdegc
*U60_*	3.7.1.2	*U60_*	FUMARYLACETOACETASE	FUACAC -> FUM + ACTAC	trydegd
YDR268W	6.1.1.2	*MSW1*	TRYPTOPHANYL-TRNA SYNTHETASE, MITOCHONDRIAL	ATPm + TRPm + TRNAm -> AMPm + PPIm + TRPTRNAm	msw1
YDR242W	3.5.1.4	*AMD2*	PUTATIVE AMIDASE	PAD -> PAC + NH3	amd2_2
YDR242W	3.5.1.4	*AMD2*	PUTATIVE AMIDASE	IAD -> IAC + NH3	amd2_3
*U61_*	2.6.1.29	*U61_*	DIAMINE TRANSAMINASE	SPRMD + ACCOA -> ASPERMD + COA	spra
*U62_*	1.5.3.11	*U62_*	POLYAMINE OXIDASE	ASPERMD + O2 -> APRUT + APROA + H2O2	sprb
*U63_*	1.5.3.11	*U63_*	POLYAMINE OXIDASE	APRUT + O2 -> GABAL + APROA + H2O2	sprc
*U64_*	2.6.1.29	*U64_*	DIAMINE TRANSAMINASE	SPRM + ACCOA -> ASPRM + COA	sprd
*U65_*	1.5.3.11	*U65_*	POLYAMINE OXIDASE	ASPRM + O2 -> ASPERMD + APROA + H2O2	spre
# PROLINE BIOSYNTHESIS					
YDR300C	2.7.2.11	*PRO1*	GAMMA-GLUTAMYL KINASE, GLUTAMATE KINASE	GLU + ATP -> ADP + GLUP	pro1
YOR323C	1.2.1.41	*PRO2*	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE	GLUP + NADH -> NAD + PI + GLUGSAL	pro2_1
YOR323C	1.2.1.41	*PRO2*	GAMMA-GLUTAMYL PHOSPHATE REDUCTASE	GLUP + NADPH -> NADP + PI + GLUGSAL	pro2_2
*U66_*		*U66_*	SPONTANEOUS CONVERSION (STRATHERN)	GLUGSAL <-> P5C	gps1
*U67_*		*U67_*	SPONTANEOUS CONVERSION (STRATHERN)	GLUGSALm <-> P5Cm	gps2
YER023W	1.5.1.2	*PRO3*	PYRROLINE-5-CARBOXYLATE REDUCTASE	P5C + NADPH -> PRO + NADP	pro3_1
YER023W	1.5.1.2	*PRO3*	PYRROLINE-5-CARBOXYLATE REDUCTASE	PHC + NADPH -> HPRO + NADP	pro3_3
YER023W	1.5.1.2	*PRO3*	PYRROLINE-5-CARBOXYLATE REDUCTASE	PHC + NADH -> HPRO + NAD	pro3_4
YLR142W	1.5.3.-	*PUT1*	PROLINE OXIDASE	PROm + NADm -> P5Cm + NADHm	pro3_5
# METABOLISM OF OTHER AMINO ACID					
# BETA-ALANINE METABOLISM					
*U68_*	1.2.1.3	*U68_*	ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL 1	GABALm + NADm -> GABAm + NADHm	ald1
YER073W	1.2.1.3	*ALD5*	MITOCHONDRIAL ALDEHYDE DEHYDROGENASE	LACALm + NADm <-> LLACm + NADHm	ald5_2
# CYANOAMINO ACID METABOLISM					
YJL126W	3.5.5.1	*NIT2*	NITRILASE	APROP -> ALA + NH3	nit2_1
YJL126W	3.5.5.1	*NIT2*	NITRILASE	ACYBUT -> GLU + NH3	nit2_2
# PROTEINS, PEPTIDES AND AMINO ACIDS METABOLISM					
YLR195C	2.3.1.97	*NMT1*	GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE	TCOA + GLP -> COA + TGLP	nmt1
YDL040C	2.3.1.88	*NAT1*	PEPTIDE ALPHA-N-ACETYLTRANSFERASE	ACCOA + PEPD -> COA + APEP	nat1
YGR147C	2.3.1.88	*NAT2*	PEPTIDE ALPHA-N-ACETYLTRANSFERASE	ACCOA + PEPD -> COA + APEP	nat2
# GLUTATHIONE BIOSYNTHESIS					
YJL101C	6.3.2.2	*GSH1*	GAMMA-GLUTAMYLCYSTEINE SYNTHETASE	CYS + GLU + ATP -> GC + PI + ADP	gsh1
YOL049W	6.3.2.3	*GSH2*	GLUTATHIONE SYNTHETASE	GLY + GC + ATP -> RGT + PI + ADP	gsh2

YBR244W	1.11.1.9	*GPX2*	GLUTATHIONE PEROXIDASE	2 RGT + H2O2 <-> OGT	gpx2
YIR037W	1.11.1.9	*HYR1*	GLUTATHIONE PEROXIDASE	2 RGT + H2O2 <-> OGT	hyr1
YKL026C	1.11.1.9	*GPX1*	GLUTATHIONE PEROXIDASE	2 RGT + H2O2 <-> OGT	gpx1
YPL091W	1.6.4.2	*GLR1*	GLUTATHIONE OXIDOREDUCTASE	NADPH + OGT -> NADP + RGT	glr1
YLR299W	2.3.2.2	*ECM38*	GAMMA-GLUTAMYLTRANSPEPTIDASE	RGT + ALA -> CGLY + ALAGLY	ecm38
# METABOLISM OF COMPLEX CARBOHYDRATES					
# STARCH AND SUCROSE METABOLISM					
YGR032W	2.4.1.34	*GSC2*	1,3-BETA-GLUCAN SYNTHASE	UDPG -> 13GLUCAN + UDP	gsc2
YLR342W	2.4.1.34	*FKS1*	1,3-BETA-GLUCAN SYNTHASE	UDPG -> 13GLUCAN + UDP	fks1
YMR306W	2.4.1.34	*FKS3*	PROTEIN WITH SIMILARITY TO FKS1P AND GSC2P	UDPG -> 13GLUCAN + UDP	fks3
YDR261C	3.2.1.58	*EXG2*	EXO-1,3-B-GLUCANASE	13GLUCAN -> GLC	exg2
YGR282C	3.2.1.58	*BGL2*	CELL WALL ENDO-BETA-1,3-GLUCANASE	13GLUCAN -> GLC	bgl2
YLR300W	3.2.1.58	*EXG1*	EXO-1,3-BETA-GLUCANASE	13GLUCAN -> GLC	exg1
YOR190W	3.2.1.58	*SPR1*	SPORULATION-SPECIFIC EXO-1,3-BETA-GLUCANASE	13GLUCAN -> GLC	spr1
# GLYCOPROTEIN BIOSYNTHESIS / DEGRADATION					
YMR013C	2.7.1.108	*SEC59*	DOLICHOL KINASE	CTP + DOL -> CDP + DOLP	sec59
YPR183W	2.4.1.83	*DPM1*	DOLICHYL-PHOSPHATE BETA-D-MANNOSYLTRANSFERASE	GDPMAN + DOLP -> GDP + DOLMANP	dpm1
YAL023C	2.4.1.109	*PMT2*	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE	DOLMANP -> DOLP + MANNAN	pmt2
YDL093W	2.4.1.109	*PMT5*	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE	DOLMANP -> DOLP + MANNAN	pmt5
YDL095W	2.4.1.109	*PMT1*	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE	DOLMANP -> DOLP + MANNAN	pmt1
YGR199W	2.4.1.109	*PMT6*	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE	DOLMANP -> DOLP + MANNAN	pmt6
YJR143C	2.4.1.109	*PMT4*	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE	DOLMANP -> DOLP + MANNAN	pmt4
YOR321W	2.4.1.109	*PMT3*	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE	DOLMANP -> DOLP + MANNAN	pmt3
YBR199W	2.4.1.131	*KTR4*	GLYCOLIPID 2-ALPHA-MANNOSYLTRANSFERASE	MAN2PD + 2 GDPMAN -> 2 GDP + 2MANPD	ktr4
YBR205W	2.4.1.131	*KTR3*	GLYCOLIPID 2-ALPHA-MANNOSYLTRANSFERASE	MAN2PD + 2 GDPMAN -> 2 GDP + 2MANPD	ktr3
YDR483W	2.4.1.131	*KRE2*	GLYCOLIPID 2-ALPHA-MANNOSYLTRANSFERASE	MAN2PD + 2 GDPMAN -> 2 GDP + 2MANPD	kre2
YJL139C	2.4.1.131	*YUR1*	GLYCOLIPID 2-ALPHA-MANNOSYLTRANSFERASE	MAN2PD + 2 GDPMAN -> 2 GDP + 2MANPD	yur1
YKR061W	2.4.1.131	*KTR2*	GLYCOLIPID 2-ALPHA-MANNOSYLTRANSFERASE	MAN2PD + 2 GDPMAN -> 2 GDP + 2MANPD	ktr2
YOR099W	2.4.1.131	*KTR1*	GLYCOLIPID 2-ALPHA-MANNOSYLTRANSFERASE	MAN2PD + 2 GDPMAN -> 2 GDP + 2MANPD	ktr1

YPL053C	2.4.1.131	*KTR6*	GLYCOLIPID 2-ALPHA-MANNOSYLTRANSFERASE	MAN2PD + 2 GDPMAN -> 2 GDP + 2MANPD	ktr6
# AMINOSUGARS METABOLISM					
YER062C	3.1.3.21	*HOR2*	DL-GLYCEROL-3-PHOSPHATASE	GL3P -> GL + PI	hor2
YIL053W	3.1.3.21	*RHR2*	DL-GLYCEROL-3-PHOSPHATASE	GL3P -> GL + PI	rhr2
YLR307W	3.5.1.41	*CDA1*	CHITIN DEACETYLASE	CHIT -> CHITO + AC	cda1
YLR308W	3.5.1.41	*CDA2*	CHITIN DEACETYLASE	CHIT -> CHITO + AC	cda2
# METABOLSIM OF COMPLEX LIPIDS					
# GLYCEROL (GLYCEROLIPID METABOLISM)					
YFL053W	2.7.1.29	*DAK2*	DIHYDROXYACETONE KINASE	GLYN + ATP -> T3P2 + ADP	dak2
YML070W	2.7.1.29	*DAK1*	PUTATIVE DIHYDROXYACETONE KINASE	GLYN + ATP -> T3P2 + ADP	dak1
YDL022W	1.1.1.8	*GPD1*	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD)	T3P2 + NADH -> GL3P + NAD	gpd1
YOL059W	1.1.1.8	*GPD2*	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD)	T3P2 + NADH -> GL3P + NAD	gpd2
YHL032C	2.7.1.30	*GUT1*	GLYCEROL KINASE	GL + ATP -> GL3P + ADP	gut1
YIL155C	1.1.99.5	*GUT2*	GLYCEROL-3-PHOSPHATE DEHYDROGENASE	GL3P + FADm -> T3P2 + FADH2m	gut2
*U69_*		*U69_*		DAGLY + 0.017 C100ACP + 0.062 C120ACP + 0.100 C140ACP + 0.270 C160ACP + 0.169 C161ACP + 0.055 C180ACP + 0.235 C181ACP + 0.093 C182ACP -> TAGLY + ACP	daga
# METABOLISM OF COFACTORS, VITAMINS, AND OTHER SUBSTANCES					
# THIAMINE (VITAMIN B1) METABOLISM					
YOR143C	2.7.6.2	*THI80*	THIAMIN PYROPHOSPHOKINASE	ATP + THIAMIN -> AMP + TPP	thi80_1
YOR143C	2.7.6.2	*THI80*	THIAMIN PYROPHOSPHOKINASE	ATP + TPP -> AMP + TPPP	thi80_2
*U70_*		*U70_*	THIC PROTEIN	AIR -> AHM	thic
YOL055C	2.7.1.49	*THI20*	BIPARTITE PROTEIN CONSISTING OF N-TERMINAL HYDROXYMETHYLPYRIMIDINE PHOSPHATE (HMP-P) KINASE DOMAIN, NEEDED FOR THIAMINE BIOSYNTHESIS, FUSED TO C-TERMINAL PET18P-LIKE DOMAIN OF INDETERMINANT FUNCTION	AHM + ATP -> AHMP + ADP	thi20
YPL258C	2.7.1.49	*THI21*	BIPARTITE PROTEIN CONSISTING OF N-TERMINAL HYDROXYMETHYLPYRIMIDINE PHOSPHATE (HMP-P) KINASE DOMAIN, NEEDED FOR THIAMINE BIOSYNTHESIS, FUSED TO C-TERMINAL PET18P-LIKE DOMAIN OF INDETERMINANT FUNCTION	AHM + ATP -> AHMP + ADP	thi21

YPR121W	2.7.1.49	*THI22*	BIPARTITE PROTEIN CONSISTING OF N-TERMINAL HYDROXYMETHYLPYRIMIDINE PHOSPHATE (HMP-P) KINASE DOMAIN, NEEDED FOR THIAMINE BIOSYNTHESIS, FUSED TO C-TERMINAL PET18P-LIKE DOMAIN OF INDETERMINANT FUNCTION	AHM + ATP -> AHMP + ADP	thi22
YOL055C	2.7.4.7	*THI20*	HMP-PHOSPHATE KINASE	AHMP + ATP -> AHMPP + ADP	thid
*U71_*		*U71_*	HYPOTHETICAL	T3P1 + PYR -> DTP	unkrxn1
*U72_*		*U72_*	THIG PROTEIN	DTP + TYR + CYS -> THZ + HBA + CO2	thig
*U73_*		*U73_*	THIE PROTEIN	DTP + TYR + CYS -> THZ + HBA + CO2	thie
*U74_*		*U74_*	THIF PROTEIN	DTP + TYR + CYS -> THZ + HBA + CO2	thif
*U75_*		*U75_*	THIH PROTEIN	DTP + TYR + CYS -> THZ + HBA + CO2	thih
YPL214C	2.7.1.50	*THI6*	HYDROXYETHYLTHIAZOLE KINASE	THZ + ATP -> THZP + ADP	thim
YPL214C	2.5.1.3	*THI6*	TMP PYROPHOSPHORYLASE, HYDROXYETHYLTHIAZOLE KINASE	THZP + AHMPP -> THMP + PPI	thi6
*U76_*	2.7.4.16	*U76_*	THIAMIN PHOSPHATE KINASE	THMP + ATP <-> TPP + ADP	thil
*U77_*	3.1.3.-	*U77_*	(DL)-GLYCEROL-3-PHOSPHATASE 2	THMP -> THIAMIN + PI	unkrxn8
# RIBOFLAVIN METABOLISM					
YBL033C	3.5.4.25	*RIB1*	GTP CYCLOHYDROLASE II	GTP -> D6RP5P + FOR + PPI	rib1
YBR153W	3.5.4.26	*RIB7*	HTP REDUCTASE, SECOND STEP IN THE RIBOFLAVIN BIOSYNTHESIS PATHWAY	D6RP5P -> A6RP5P + NH3	ribd1
YBR153W	1.1.1.193	*RIB7*	PYRIMIDINE REDUCTASE	A6RP5P + NADPH -> A6RP5P2 + NADP	rib7
*U78_*		*U78_*	PYRIMIDINE PHOSPHATASE	A6RP5P2 -> A6RP + PI	prm
*U79_*		*U79_*	3,4 DIHYDROXY-2-BUTANONE-4-PHOSPHATE SYNTHASE	RL5P -> DB4P + FOR	ribb
YBR256C	2.5.1.9	*RIB5*	RIBOFLAVIN BIOSYNTHESIS PATHWAY ENZYME, 6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE, APHA CHAIN	DB4P + A6RP -> D8RL + PI	rib5
YOL143C	2.5.1.9	*RIB4*	RIBOFLAVIN BIOSYNTHESIS PATHWAY ENZYME, 6,7-DIMETHYL-8-RIBITYLLUMAZINE SYNTHASE, BETA CHAIN		
YAR071W	3.1.3.2	*PHO11*	ACID PHOSPHATASE	FMN -> RIBFLAV + PI	pho11
YDR236C	2.7.1.26	*FMN1*	RIBOFLAVIN KINASE	RIBFLAV + ATP -> FMN + ADP	fmn1_1
YDR236C	2.7.1.26	*FMN1*	RIBOFLAVIN KINASE	RIBFLAVm + ATPm -> FMNm + ADPm	fmn1_2
YDL045C	2.7.7.2	*FAD1*	FAD SYNTHETASE	FMN + ATP -> FAD + PPI	fad1
*U80_*	2.7.7.2	*U80_*	FAD SYNTHETASE	FMNm + ATPm -> FADm + PPIm	fad1b
# VITAMIN B6 (PYRIDOXINE) BIOSYNTHESIS METABOLISM					
*U81_*	2.7.1.35	*U81_*	PYRIDOXINE KINASE	PYRDX + ATP -> P5P + ADP	pdxka

*U82_*	2.7.1.35	*U82_*	PYRIDOXINE KINASE	PDLA + ATP -> PDLA5P + ADP	pdxkb
*U83_*	2.7.1.35	*U83_*	PYRIDOXINE KINASE	PL + ATP -> PL5P + ADP	pdxkc
YBR035C	1.4.3.5	*PDX3*	PYRIDOXINE 5'-PHOSPHATE OXIDASE	PDLA5P + O2 -> PL5P + H2O2 + NH3	pdx3_1
YBR035C	1.4.3.5	*PDX3*	PYRIDOXINE 5'-PHOSPHATE OXIDASE	P5P + O2 <-> PL5P + H2O2	pdx3_2
YBR035C	1.4.3.5	*PDX3*	PYRIDOXINE 5'-PHOSPHATE OXIDASE	PYRDX + O2 <-> PL + H2O2	pdx3_3
YBR035C	1.4.3.5	*PDX3*	PYRIDOXINE 5'-PHOSPHATE OXIDASE	PL + O2 + NH3 <-> PDLA + H2O2	pdx3_4
YBR035C	1.4.3.5	*PDX3*	PYRIDOXINE 5'-PHOSPHATE OXIDASE	PDLA5P + O2 -> PL5P + H2O2 + NH3	pdx3_5
YOR184W	2.6.1.52	*SER1*	HYPOTHETICAL TRANSAMINASE/PHOSPHOSERINE TRANSAMINASE	OHB + GLU <-> PHT + AKG	ser1_2
YCR053W	4.2.99.2	*THR4*	THREONINE SYNTHASE	PHT -> 4HLT + PI	thr4_2
*U84_*	3.1.3.-	*U84_*	HYPOTHETICAL ENZYME	PDLA5P -> PDLA + PI	hor2b
# PANTOTHENATE AND COA BIOSYNTHESIS					
*U85_*		*U85_*		3 MALCOA -> CHCOA + 2 COA + 2 CO2	bio1
*U86_*	2.3.1.47	*U86_*	8-AMINO-7-OXONONANOATE SYNTHASE	ALA + CHCOA <-> CO2 + COA + AONA	biof
YNR058W	2.6.1.62	*BIO3*	7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE (DAPA) AMINOTRANSFERASE	SAM + AONA <-> SAMOB + DANNA	bio3
YNR057C	6.3.3.3	*BIO4*	DETHIOBIOTIN SYNTHETASE	CO2 + DANNA + ATP <-> DTB + PI + ADP	bio4
YGR286C	2.8.1.6	*BIO2*	BIOTIN SYNTHASE	DTB + CYS <-> BT	bio2
# FOLATE BIOSYNTHESIS					
YGR267C	3.5.4.16	*FOL2*	GTP CYCLOHYDROLASE I	GTP -> FOR + AHTD	fol2
*U87_*	3.6.1.-	*U87_*	DIHYDRONEOPTERIN TRIPHOSPHATE PYROPHOSPHORYLASE	AHTD -> PPI + DHPP	ntpa
YDR481C	3.1.3.1	*PHO8*	GLYCEROPHOSPHATASE, ALKALINE PHOSPHATASE; NUCLEOSIDE TRIPHOSPHATASE	AHTD -> DHP + 3 PI	pho8
YDL100C	3.6.1.-	*YDL100C*	DIHYDRONEOPTERIN MONOPHOSPHATE DEPHOSPHORYLASE	DHPP -> DHP + PI	dhdnpa
YNL256W	4.1.2.25	*FOL1*	DIHYDRONEOPTERIN ALDOLASE	DHP -> AHHMP + GLAL	fol1_1
YNL256W	2.7.6.3	*FOL1*	6-HYDROXYMETHYL-7,8 DIHYDROPTERIN PYROPHOSPHOKINASE	AHHMP + ATP -> AMP + AHHMD	fol1_2
YNR033W	4.1.3.-	*ABZ1*	AMINODEOXYCHORISMATE SYNTHASE	CHOR + GLN -> ADCHOR + GLU	abz1
*U88_*	4.-.-.-	*U88_*	AMINODEOXYCHORISMATE LYASE	ADCHOR -> PYR + PABA	pabc
YNL256W	2.5.1.15	*FOL1*	DIHYDROPTEROATE SYNTHASE	PABA + AHHMD -> PPI + DHPT	fol1_3
YNL256W	2.5.1.15	*FOL1*	DIHYDROPTEROATE SYNTHASE	PABA + AHHMP -> DHPT	fol1_4
*U89_*	6.3.2.12	*U89_*	DIHYDROFOLATE SYNTHASE	DHPT + ATP + GLU -> ADP + PI + DHF	folc
YOR236W	1.5.1.3	*DFR1*	DIHYDROFOLATE REDUCTASE	DHFm + NADPHm -> NADPm + THFm	dfr1_1
YOR236W	1.5.1.3	*DFR1*	DIHYDROFOLATE REDUCTASE	DHF + NADPH -> NADP + THF	dfr1_2

*U90_*	6.3.3.2	*U90_*	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE	ATPm + FTHFm -> ADPm + PIm + MTHFm	ftfa
*U91_*	6.3.3.2	*U91_*	5-FORMYLTETRAHYDROFOLATE CYCLO-LIGASE	ATP + FTHF -> ADP + PI + MTHF	ftfb
YKL132C	6.3.2.17	*RMA1*	PROTEIN WITH SIMILARITY TO FOLYLPOLYGLUTAMATE SYNTHASE; CONVERTS TETRAHYDROFOLYL-[GLU(N)] + GLUTAMATE TO TETRAHYDROFOLYL-[GLU(N+1)]	THF + ATP + GLU <-> ADP + PI + THFG	rma1
YMR113W	6.3.2.17	*FOL3*	DIHYDROFOLATE SYNTHETASE	THF + ATP + GLU <-> ADP + PI + THFG	fol3
YOR241W	6.3.2.17	*MET7*	FOLYLPOLYGLUTAMATE SYNTHETASE, INVOLVED IN METHIONINE BIOSYNTHESIS AND MAINTENANCE OF MITOCHONDRIAL GENOME	THF + ATP + GLU <-> ADP + PI + THFG	met7
# ONE CARBON POOL BY FOLATE					
YPL023C	1.5.1.20	*MET12*	METHYLENE TETRAHYDROFOLATE REDUCTASE	METTHFm + NADPHm -> NADPm + MTHFm	met12
YGL125W	1.5.1.20	*MET13*	METHYLENE TETRAHYDROFOLATE REDUCTASE	METTHFm + NADPHm -> NADPm + MTHFm	met13
YBR084W	1.5.1.5	*MIS1*	THE MITOCHONDRIAL TRIFUNCTIONAL ENZYME C1-TETRAHYDROFLATE SYNTHASE	METTHFm + NADPm <-> METHFm + NADPHm	mis1_1
YGR204W	1.5.1.5	*ADE3*	THE CYTOPLASMIC TRIFUNCTIONAL ENZYME C1-TETRAHYDROFOLATE SYNTHASE	METTHF + NADP <-> METHF + NADPH	ade3_1
YBR084W	6.3.4.3	*MIS1*	THE MITOCHONDRIAL TRIFUNCTIONAL ENZYME C1-TETRAHYDROFLATE SYNTHASE	THFm + FORm + ATPm -> ADPm + PIm + FTHFm	mis1_2
YGR204W	6.3.4.3	*ADE3*	THE CYTOPLASMIC TRIFUNCTIONAL ENZYME C1-TETRAHYDROFOLATE SYNTHASE	THF + FOR + ATP -> ADP + PI + FTHF	ade3_2
YBR084W	3.5.4.9	*MIS1*	THE MITOCHONDRIAL TRIFUNCTIONAL ENZYME C1-TETRAHYDROFLATE SYNTHASE	METHFm <-> FTHFm	mis1_3
YGR204W	3.5.4.9	*ADE3*	THE CYTOPLASMIC TRIFUNCTIONAL ENZYME C1-TETRAHYDROFOLATE SYNTHASE	METHF <-> FTHF	ade3_3
YKR080W	1.5.1.15	*MTD1*	NAD-DEPENDENT 5,10-METHYLENETETRAHYDRAFOLATE DEHYDROGENASE	METTHF + NAD -> METHF + NADH	mtd1
YBL013W	2.1.2.9	*FMT1*	METHIONYL-TRNA TRANSFORMYLASE	FTHFm + MTRNAm -> THFm + FMRNAm	fmt1
# COENZYME A BIOSYNTHESIS					
YBR176W	2.1.2.11	*ECM31*	KETOPENTOATE HYDROXYMETHYL TRANSFERASE	OIVAL + METTHF -> AKP + THF	ecm31
YHR063C	1.1.1.169	*PAN5*	PUTATIVE KETOPANTOATE REDUCTASE (2-DEHYDROPANTOATE 2-REDUCTASE) INVOLVED IN COENZYME A SYNTHESIS, HAS SIMILARITY TO CBS2P, KETOPANTOATE REDUCTASE	AKP + NADPH -> NADP + PANT	pane
YLR355C	1.1.1.86	*ILV5*	KETOL-ACID REDUCTOISOMERASE	AKPm + NADPHm -> NADPm + PANTm	ilv5_3
YIL145C	6.3.2.1	*YIL145C*	PANTOATE-B-ALANINE LIGASE	PANT + bALA + ATP -> AMP + PPI + PNTO	panca

YDR531W	2.7.1.33	*YDR531W*	PUTATIVE PANTOTHENATE KINASE INVOLVED IN COENZYME A BIOSYNTHESIS, PANTOTHENATE KINASE	PNTO + ATP -> ADP + 4PPNTO	coaa
*U92_*	6.3.2.5	*U92_*	PHOSPHOPANTOTHENATE-CYSTEINE LIGASE	4PPNTO + CTP + CYS -> CMP + PPI + 4PPNCYS	pclig
*U93_*	4.1.1.36	*U93_*	PHOSPHOPANTOTHENATE-CYSTEINE DECARBOXYLASE	4PPNCYS -> CO2 + 4PPNTE	pcdcl
*U94_*	2.7.7.3	*U94_*	PHOSPHO-PANTETHIENE ADENYLYLTRANSFERASE	4PPNTE + ATP -> PPI + DPCOA	patrana
*U95_*	2.7.7.3	*U95_*	PHOSPHO-PANTETHIENE ADENYLYLTRANSFERASE	4PPNTEm + ATPm -> PPIm + DPCOAm	patranb
*U96_*	2.7.1.24	*U96_*	DEPHOSPHOCOA KINASE	DPCOA + ATP -> ADP + COA	dphcoaka
*U97_*	2.7.1.24	*U97_*	DEPHOSPHOCOA KINASE	DPCOAm + ATPm -> ADPm + COAm	dphcoakb
*U98_*	4.1.1.11	*U98_*	ASPARTATE ALPHA-DECARBOXYLASE	ASP -> CO2 + bALA	pancb
YPL148C	2.7.8.7	*PPT2*	ACYL CARRIER-PROTEIN SYNTHASE, PHOSPHOPANTETHEINE PROTEIN TRANSFERASE FOR ACP1P	COA -> PAP + ACP	acps
# NAD BIOSYNTHESIS					
YGL037C	3.5.1.19	*PNC1*	NICOTINAMIDASE	NAM <-> NAC + NH3	nadh
YOR209C	2.4.2.11	*NPT1*	NAPRTASE	NAC + PRPP -> NAMN + PPI	npt1
*U99_*	1.4.3.-	*U99_*	ASPARTATE OXIDASE	ASP + FADm -> FADH2m + ISUCC	nadb
*U100_*	1.4.3.16	*U100_*	QUINOLATE SYNTHASE	ISUCC + T3P2 -> PI + QA	nada
YFR047C	2.4.2.19	*QPT1*	QUINOLATE PHOSPHORIBOSYL TRANSFERASE	QA + PRPP -> NAMN + CO2 + PPI	nadc
YLR328W	2.7.7.18	*YLR328W*	NICOTINAMIDE MONONUCLEOTIDE (NMN) ADENYLYLTRANSFERASE	NAMN + ATP -> PPI + NAAD	nadd1
YHR074W	6.3.5.1	*QNS1*	DEAMIDO-NAD AMMONIA LIGASE	NAAD + ATP + NH3 -> NAD + AMP + PPI	nade
YJR049C	2.7.1.23	*UTR1*	NAD KINASE, POLYPHOSPHATE KINASE (EC 2.7.4.1) / NAD+ KINASE (EC 2.7.1.23)	NAD + ATP -> NADP + ADP	nadf_1
YEL041W	2.7.1.23	*YEL041W*	NAD KINASE, POLYPHOSPHATE KINASE (EC 2.7.4.1) / NAD+ KINASE (EC 2.7.1.23)	NAD + ATP -> NADP + ADP	nadf_2
YPL188W	2.7.1.23	*POS5*	NAD KINASE, POLYPHOSPHATE KINASE (EC 2.7.4.1) / NAD+ KINASE (EC 2.7.1.23)	NAD + ATP -> NADP + ADP	nadf_5
*U101_*	3.1.2.-	*U101_*	NADP PHOSPHATASE	NADP -> NAD + PI	nadphps
*U102_*	3.2.2.5	*U102_*		NAD -> NAM + ADPRIB	nadi
*U103_*	2.4.2.1	*U103_*	STRONG SIMILARITY TO PURINE-NUCLEOSIDE PHOSPHORYLASES	ADN + PI <-> AD + RIP	nadg1
*U104_*	2.4.2.1	*U104_*	STRONG SIMILARITY TO PURINE-NUCLEOSIDE PHOSPHORYLASES	GSN + PI <-> GN + RIP	nadg2
# NICOTINIC ACID SYNTHESIS FROM TRP					

YFR047C	2.4.2.19	*QPT1*	QUINOLATE PHOSPHORIBOSYL TRANSFERASE	QAm + PRPPm -> NAMNm + CO2m + PPIm	mnadc
YLR328W	2.7.7.18	*YLR328W*	NAMN ADENYLYL TRANSFERASE	NAMNm + ATPm -> PPIm + NAADm	mnadd1
YLR328W	2.7.7.18	*YLR328W*	NAMN ADENYLYL TRANSFERASE	NMNm + ATPm -> NADm + PPIm	mnadd2
YHR074W	6.3.5.1	*QNS1*	DEAMIDO-NAD AMMONIA LIGASE	NAADm + ATPm + NH3m -> NADm + AMPm + PPIm	mnade
YJR049C	2.7.1.23	*UTR1*	NAD KINASE, POLYPHOSPHATE KINASE (EC 2.7.4.1) / NAD+ KINASE (EC 2.7.1.23)	NADm + ATPm -> NADPm + ADPm	mnadf_1
YPL188W	2.7.1.23	*POS5*	NAD KINASE, POLYPHOSPHATE KINASE (EC 2.7.4.1) / NAD+ KINASE (EC 2.7.1.23)	NADm + ATPm -> NADPm + ADPm	mnadf_2
YEL041W	2.7.1.23	*YEL041W*	NAD KINASE, POLYPHOSPHATE KINASE (EC 2.7.4.1) / NAD+ KINASE (EC 2.7.1.23)	NADm + ATPm -> NADPm + ADPm	mnadf_5
*U105_*	3.1.2.-	*U105_*	NADP PHOSPHATASE	NADPm -> NADm + PIm	mnadphps
YLR209C	2.4.2.1	*PNP1*	STRONG SIMILARITY TO PURINE-NUCLEOSIDE PHOSPHORYLASES	ADNm + PIm <-> ADm + RIPm	mnadg1
YLR209C	2.4.2.1	*PNP1*	STRONG SIMILARITY TO PURINE-NUCLEOSIDE PHOSPHORYLASES	GSNm + PIm <-> GNm + RIPm	mnadg2
YGL037C	3.5.1.19	*PNC1*	NICOTINAMIDASE	NAMm <-> NACm + NH3m	mnadh
YOR209C	2.4.2.11	*NPT1*	NAPRTASE	NACm + PRPPm -> NAMNm + PPIm	mnpt1
*U106_*	3.2.2.5	*U106_*		NADm -> NAMm + ADPRIBm	mnadi
# UPTAKE PATHWAYS					
# PORPHYRIN AND CHLOROPHYLL METABOLISM					
YDR232W	2.3.1.37	*HEM1*	5-AMINOLEVULINATE SYNTHASE	SUCCOAm + GLYm -> ALAVm + COAm + CO2m	hem1
YGL040C	4.2.1.24	*HEM2*	AMINOLEVULINATE DEHYDRATASE	2 ALAV -> PBG	hem2
YDL205C	4.3.1.8	*HEM3*	HYDROXYMETHYLBILANE SYNTHASE	4 PBG -> HMB + 4 NH3	hem3
YOR278W	4.2.1.75	*HEM4*	UROPORPHYRINOGEN-III SYNTHASE	HMB -> UPRG	hem4
YDR047W	4.1.1.37	*HEM12*	UROPORPHYRINOGEN DECARBOXYLASE	UPRG -> 4 CO2 + CPP	hem12
YDR044W	1.3.3.3	*HEM13*	COPROPORPHYRINOGEN OXIDASE, AEROBIC	O2 + CPP -> 2 CO2 + PPHG	hem13
YER014W	1.3.3.4	*HEM14*	PROTOPORPHYRINOGEN OXIDASE	O2 + PPHGm -> PPIXm	hem14
YOR176W	4.99.1.1	*HEM15*	FERROCHELATASE	PPIXm -> PTHm	hem15
YGL245W	6.1.1.17	*YGL245W*	GLUTAMYL-TRNA SYNTHETASE, CYTOPLASMIC	GLU + ATP -> GTRNA + AMP + PPI	unrxn10
YOL033W	6.1.1.17	*MSE1*		GLUm + ATPm -> GTRNAm + AMPm + PPIm	mse1
YKR069W	2.1.1.107	*MET1*	UROPORPHYRIN-III C-METHYLTRANSFERASE	SAM + UPRG -> SAH + PC2	met1
# QUINONE BIOSYNTHESIS					
YKL211C	4.1.3.27	*TRP3*	ANTHRANILATE SYNTHASE COMPONENT II AND INDOLE-3-PHOSPHATE (MULTIFUNCTIONAL ENZYME)	CHOR -> 4HBZ + PYR	trp3_3

YER090W	4.1.3.27	*TRP2*	ANTHRANILATE SYNTHASE COMPONENT I	CHOR -> 4HBZ + PYR	trp2_2
YPR176C	2.5.1.-	*BET2*	GERANYLGERANYLTRANSFERASE TYPE II BETA SUBUNIT	4HBZ + NPP -> N4HBZ + PPI	bet2
YJL031C	2.5.1.-	*BET4*	GERANYLGERANYLTRANSFERASE TYPE II ALPHA SUBUNIT		
YGL155W	2.5.1.-	*CDC43*	GERANYLGERANYLTRANSFERASE TYPE I BETA SUBUNIT		
YBR003W	2.5.1.-	*COQ1*	HEXAPRENYL PYROPHOSPHATE SYNTHETASE, CATALYZES THE FIRST STEP IN COENZYME Q (UBIQUINONE) BIOSYNTHESIS PATHWAY	4HBZ + NPP -> N4HBZ + PPI	coq1
YNR041C	2.5.1.-	*COQ2*	PARA-HYDROXYBENZOATE--POLYPRENYLTRANSFERASE	4HBZ + NPP -> N4HBZ + PPI	coq2
YPL172C	2.5.1.-	*COX10*	PROTOHEME IX FARNESYLTRANSFERASE, MITOCHONDRIAL PRECURSOR	4HBZ + NPP -> N4HBZ + PPI	cox10
YDL090C	2.5.1.-	*RAM1*	PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT	4HBZ + NPP -> N4HBZ + PPI	ram1
YKL019W	2.5.1.-	*RAM2*	PROTEIN FARNESYLTRANSFERASE ALPHA SUBUNIT		
YBR002C	2.5.1.-	*RER2*	PUTATIVE DEHYDRODOLICHYL DIPHOSPATE SYNTHETASE	4HBZ + NPP -> N4HBZ + PPI	rer2
YMR101C	2.5.1.-	*SRT1*	PUTATIVE DEHYDRODOLICHYL DIPHOSPATE SYNTHETASE	4HBZ + NPP -> N4HBZ + PPI	srt1
YDR538W	4.1.1.-	*PAD1*	OCTAPRENYL-HYDROXYBENZOATE DECARBOXYLASE	N4HBZ -> CO2 + 2NPPP	pad1_2
*U107_*	1.13.14.-	*U107_*	2-OCTAPRENYLPHENOL HYDROXYLASE	2NPPP + O2 -> 2N6H	ubib
YPL266W	2.1.1.-	*DIM1*		2N6H + SAM -> 2NPMP + SAH	dim1
*U108_*	1.14.13.-	*U108_*	2-OCTAPRENYL-6-METHOXYPHENOL HYDROXYLASE	2NPMPm + O2m -> 2NPMBm	ubih
YML110C	2.1.1.-	*COQ5*	2-OCTAPRENYL-6-METHOXY-1,4-BENZOQUINONE METHYLASE	2NPMBm + SAMm -> 2NPMMBm + SAHm	coq5
YGR255C	1.14.13.-	*COQ6*	COQ6 MONOOXYGENASE	2NPMMBm + O2m -> 2NMHMBm	coq6b
YOL096C	2.1.1.64	*COQ3*	3-DIMETHYLUBIQUINONE 3-METHYLTRANSFERASE	2NMHMBm + SAMm -> QH2m + SAHm	ubig

MEMBRANE TRANSPORT
MITOCHONDRIAL MEMBRANE TRANSPORT
THE FOLLOWINGS DIFFUSE THROUGH THE INNER MITOCHONDRIAL MEMBRANE IN A NON-CARRIER-MEDIATED MANNER:

*U109_*		*U109_*		O2 <-> O2m	mo2
*U110_*		*U110_*		CO2 <-> CO2m	mco2
*U111_*		*U111_*		ETH <-> ETHm	meth
*U112_*		*U112_*		NH3 <-> NH3m	mnh3
*U113_*		*U113_*		MTHN <-> MTHNm	mmthn

*U114_*	*U114_*		THFm <-> THF	mthf
*U115_*	*U115_*		METTHFm <-> METTHF	mmthf
*U116_*	*U116_*		SERm <-> SER	mser
*U117_*	*U117_*		GLYm <-> GLY	mgly
*U118_*	*U118_*		CBHCAPm <-> CBHCAP	mcbh
*U119_*	*U119_*		OICAPm <-> OICAP	moicap
*U120_*	*U120_*		PROm <-> PRO	mpro
*U121_*	*U121_*		CMPm <-> CMP	mcmp
*U122_*	*U122_*		ACm <-> AC	mac
*U123_*	*U123_*		ACAR -> ACARm	macar_
*U124_*	*U124_*		CARm -> CAR	mcar_
*U125_*	*U125_*		ACLAC <-> ACLACm	maclac
*U126_*	*U126_*		ACTAC <-> ACTACm	mactc
*U127_*	*U127_*		SLF -> SLFm + Hm	mslf
*U128_*	*U128_*		THRm <-> THR	mthr
*U129_*	*U129_*		AKAm -> AKA	maka
YMR056C	*AAC1*	ADP/ATP CARRIER PROTEIN (MCF)	ADP + ATPm + PI -> Hm + ADPm + ATP + PIm	aac1
YBL030C	*PET9*	ADP/ATP CARRIER PROTEIN (MCF)	ADP + ATPm + PI -> Hm + ADPm + ATP + PIm	pet9
YBR085W	*AAC3*	ADP/ATP CARRIER PROTEIN (MCF)	ADP + ATPm + PI -> Hm + ADPm + ATP + PIm	aac3
YJR077C	*MIR1*	PHOSPHATE CARRIER	PI <-> Hm + PIm	mir1a
YER053C	*YER053C*	SIMILARITY TO C.ELEGANS MITOCHONDRIAL PHOSPHATE CARRIER	PI + OHm <-> PIm	mir1d
YLR348C	*DIC1*	DICARBOXYLATE CARRIER	MAL + SUCCm <-> MALm + SUCC	dic1_1
YLR348C	*DIC1*	DICARBOXYLATE CARRIER	MAL + PIm <-> MALm + PI	dic1_2
YLR348C	*DIC1*	DICARBOXYLATE CARRIER	SUCC + PIm -> SUCCm + PI	dic1_3
*U130_*	*U130_*		MALT + PIm <-> MALTm + PI	mmlt
YKL120W	*OAC1*	MITOCHONDRIAL OXALOACETATE CARRIER	OA <-> OAm + Hm	moab
YBR291C	*CTP1*	CITRATE TRANSPORT PROTEIN	CIT + MALm <-> CITm + MAL	ctp1_1
YBR291C	*CTP1*	CITRATE TRANSPORT PROTEIN	CIT + PEPm <-> CITm + PEP	ctp1_2
YBR291C	*CTP1*	CITRATE TRANSPORT PROTEIN	CIT + ICITm <-> CITm + ICIT	ctp1_3
*U131_*	*U131_*		IPPMAL <-> IPPMALm	mpmalR
*U132_*	*U132_*		LAC <-> LACm + Hm	mlac
*U133_*	*U133_*	PYRUVATE CARRIER	PYR <-> PYRm + Hm	pyrca

*U134_*	*U134_*	GLUTAMATE CARRIER	GLU <-> GLUm + Hm	gca
*U135_*	*U135_*		GLU + OHm -> GLUm	gcb
YOR130C	*ORT1*	ORNITHINE CARRIER	ORN + Hm <-> ORNm	ort1
YOR100C	*CRC1*	CARNITINE CARRIER	CARm + ACAR -> CAR + ACARm	crc1
*U136_*	*U136_*		OIVAL <-> OIVALm	moival
*U137_*	*U137_*		OMVAL <-> OMVALm	momval
YIL134W	*FLX1*	PROTEIN INVOLVED IN TRANSPORT OF FAD FROM CYTOSOL INTO THE MITOCHONDRIAL MATRIX	FAD + FMNm -> FADm + FMN	mfad
*U138_*	*U138_*		RIBFLAV <-> RIBFLAVm	mribo
*U139_*	*U139_*		DTB <-> DTBm	mdtb
*U140_*	*U140_*		H3MCOA <-> H3MCOAm	mmcoa
*U141_*	*U141_*		MVL <-> MVLm	mmvl
*U142_*	*U142_*		PA <-> PAm	mpa
*U143_*	*U143_*		4PPNTE <-> 4PPNTEm	mppnt
*U144_*	*U144_*		AD <-> ADm	mad
*U145_*	*U145_*		PRPP <-> PRPPm	mprpp
*U146_*	*U146_*		DHF <-> DHFm	mdhf
*U147_*	*U147_*		QA <-> QAm	mqa
*U148_*	*U148_*		OPP <-> OPPm	mopp
*U149_*	*U149_*		SAM <-> SAMm	msam
*U150_*	*U150_*		SAH <-> SAHm	msah
YJR095W	*SFC1*	MITOCHONDRIAL MEMBRANE SUCCINATE-FUMARATE TRANSPORTER, MEMBER OF THE MITOCHONDRIAL CARRIER FAMILY (MCF) OF MEMBRANE TRANSPORTERS	SUCC + FUMm -> SUCCm + FUM	sfc1
YPL134C	*ODC1*	2-OXODICARBOYLATE TRANSPORTER	AKGm + OXA <-> AKG + OXAm	odc1
YOR222W	*ODC2*	2-OXODICARBOYLATE TRANSPORTER	AKGm + OXA <-> AKG + OXAm	odc2
# MALATE ASPARTATE SHUTTLE				
# INCLUDED ELSEWHERE				
# GLYCEROL PHOSPHATE SHUTTLE				
*U151_*	*U151_*		T3P2m -> T3P2	mt3p
*U152_*	*U152_*		GL3P -> GL3Pm	mgl3p
# PLASMA MEMBRANE TRANSPORT				
# CARBOHYDRATES				
YHR092C	*HXT4*	MODERATE- TO LOW-AFFINITY GLUCOSE TRANSPORTER	GLCxt -> GLC	hxt4

YLR081W	*GAL2*	GALACTOSE (AND GLUCOSE) PERMEASE	GLCxt -> GLC	gal2_3
YOL156W	*HXT11*	LOW AFFINITY GLUCOSE TRANSPORT PROTEIN	GLCxt -> GLC	hxt11
YDR536W	*STL1*	PROTEIN MEMBER OF THE HEXOSE TRANSPORTER FAMILY	GLCxt -> GLC	stl1_1
YHR094C	*HXT1*	HIGH-AFFINITY HEXOSE (GLUCOSE) TRANSPORTER	GLCxt -> GLC	hxt1_1
YOL156W	*HXT11*	GLUCOSE PERMEASE	GLCxt -> GLC	hxt11_1
YEL069C	*HXT13*	HIGH-AFFINITY HEXOSE TRANSPORTER	GLCxt -> GLC	hxt13_1
YDL245C	*HXT15*	HEXOSE TRANSPORTER	GLCxt -> GLC	hxt15_1
YJR158W	*HXT16*	HEXOSE PERMEASE	GLCxt -> GLC	hxt16_1
YFL011W	*HXT10*	HIGH-AFFINITY HEXOSE TRANSPORTER	GLCxt -> GLC	hxt10_1
YNR072W	*HXT17*	PUTATIVE HEXOSE TRANSPORTER	GLCxt -> GLC	hxt17_1
YMR011W	*HXT2*	HIGH AFFINITY HEXOSE TRANSPORTER-2	GLCxt -> GLC	hxt2_1
YHR092C	*HXT4*	HIGH-AFFINITY GLUCOSE TRANSPORTER	GLCxt -> GLC	hxt4_1
YDR345C	*HXT3*	LOW-AFFINITY GLUCOSE TRANSPORTER	GLCxt -> GLC	hxt3_1
YHR096C	*HXT5*	HEXOSE TRANSPORTER	GLCxt -> GLC	hxt5_1
YDR343C	*HXT6*	HEXOSE TRANSPORTER	GLCxt -> GLC	hxt6_1
YDR342C	*HXT7*	HEXOSE TRANSPORTER	GLCxt -> GLC	hxt7_1
YJL214W	*HXT8*	HEXOSE PERMEASE	GLCxt -> GLC	hxt8_4
YJL219W	*HXT9*	HEXOSE PERMEASE	GLCxt -> GLC	hxt9_1
YLR081W	*GAL2*	GALACTOSE PERMEASE	GLACxt + HEXT -> GLAC	gal2_1
YFL011W	*HXT10*	HIGH-AFFINITY HEXOSE TRANSPORTER	GLACxt + HEXT -> GLAC	hxt10_4
YOL156W	*HXT11*	GLUCOSE PERMEASE	GLACxt + HEXT -> GLAC	hxt11_4
YNL318C	*HXT14*	MEMBER OF THE HEXOSE TRANSPORTER FAMILY	GLACxt + HEXT -> GLAC	hxt14
YJL219W	*HXT9*	HEXOSE PERMEASE	GLACxt + HEXT -> GLAC	hxt9_4
YDR536W	*STL1*	PROTEIN MEMBER OF THE HEXOSE TRANSPORTER FAMILY	GLACxt + HEXT -> GLAC	stl1_4
YFL055W	*AGP3*	AMINO ACID PERMEASE FOR SERINE, ASPARTATE, AND GLUTAMATE	GLUxt + HEXT <-> GLU	agp3_3
YDR536W	*STL1*	PROTEIN MEMBER OF THE HEXOSE TRANSPORTER FAMILY	GLUxt + HEXT <-> GLU	stl1_2
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	GLUxt + HEXT <-> GLU	gap8
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	GLUxt + HEXT <-> GLU	gap24
YPL265W	*DIP5*	DICARBOXYLIC AMINO ACID PERMEASE	GLUxt + HEXT <-> GLU	dip10
YDR536W	*STL1*	PROTEIN MEMBER OF THE HEXOSE TRANSPORTER FAMILY	GLUxt + HEXT <-> GLU	stl1_3

YHR094C		*HXT1*	HIGH-AFFINITY HEXOSE (GLUCOSE) TRANSPORTER	FRUxt + HEXT -> FRU	hxt1_2
YFL011W		*HXT10*	HIGH-AFFINITY HEXOSE TRANSPORTER	FRUxt + HEXT -> FRU	hxt10_2
YOL156W		*HXT11*	GLUCOSE PERMEASE	FRUxt + HEXT -> FRU	hxt11_2
YEL069C		*HXT13*	HIGH-AFFINITY HEXOSE TRANSPORTER	FRUxt + HEXT -> FRU	hxt13_2
YDL245C		*HXT15*	HEXOSE TRANSPORTER	FRUxt + HEXT -> FRU	hxt15_2
YJR158W		*HXT16*	HEXOSE PERMEASE	FRUxt + HEXT -> FRU	hxt16_2
YNR072W		*HXT17*	PUTATIVE HEXOSE TRANSPORTER	FRUxt + HEXT -> FRU	hxt17_2
YMR011W		*HXT2*	HIGH AFFINITY HEXOSE TRANSPORTER-2	FRUxt + HEXT -> FRU	hxt2_2
YDR345C		*HXT3*	LOW-AFFINITY GLUCOSE TRANSPORTER	FRUxt + HEXT -> FRU	hxt3_2
YHR092C		*HXT4*	HIGH-AFFINITY GLUCOSE TRANSPORTER	FRUxt + HEXT -> FRU	hxt4_2
YHR096C		*HXT5*	HEXOSE TRANSPORTER	FRUxt + HEXT -> FRU	hxt5_2
YDR343C		*HXT6*	HEXOSE TRANSPORTER	FRUxt + HEXT -> FRU	hxt6_2
YDR342C		*HXT7*	HEXOSE TRANSPORTER	FRUxt + HEXT -> FRU	hxt7_2
YJL214W		*HXT8*	HEXOSE PERMEASE	FRUxt + HEXT -> FRU	hxt8_5
YJL219W		*HXT9*	HEXOSE PERMEASE	FRUxt + HEXT -> FRU	hxt9_2
YHR094C		*HXT1*	HIGH-AFFINITY HEXOSE (GLUCOSE) TRANSPORTER	MANxt + HEXT -> MAN	hxt1_5
YFL011W		*HXT10*	HIGH-AFFINITY HEXOSE TRANSPORTER	MANxt + HEXT -> MAN	hxt10_3
YOL156W		*HXT11*	GLUCOSE PERMEASE	MANxt + HEXT -> MAN	hxt11_3
YEL069C		*HXT13*	HIGH-AFFINITY HEXOSE TRANSPORTER	MANxt + HEXT -> MAN	hxt13_3
YDL245C		*HXT15*	HEXOSE TRANSPORTER	MANxt + HEXT -> MAN	hxt15_3
YJR158W		*HXT16*	HEXOSE PERMEASE	MANxt + HEXT -> MAN	hxt16_3
YNR072W		*HXT17*	PUTATIVE HEXOSE TRANSPORTER	MANxt + HEXT -> MAN	hxt17_3
YMR011W		*HXT2*	HIGH AFFINITY HEXOSE TRANSPORTER-2	MANxt + HEXT -> MAN	hxt2_3
YDR345C		*HXT3*	LOW-AFFINITY GLUCOSE TRANSPORTER	MANxt + HEXT -> MAN	hxt3_3
YHR092C		*HXT4*	HIGH-AFFINITY GLUCOSE TRANSPORTER	MANxt + HEXT -> MAN	hxt4_3
YHR096C		*HXT5*	HEXOSE TRANSPORTER	MANxt + HEXT -> MAN	hxt5_3
YDR343C		*HXT6*	HEXOSE TRANSPORTER	MANxt + HEXT -> MAN	hxt6_3
YDR342C		*HXT7*	HEXOSE TRANSPORTER	MANxt + HEXT -> MAN	hxt7_3
YJL214W		*HXT8*	HEXOSE PERMEASE	MANxt + HEXT -> MAN	hxt8_6
YJL219W		*HXT9*	HEXOSE PERMEASE	MANxt + HEXT -> MAN	hxt9_3
YDR497C		*ITR1*	MYO-INOSITOL TRANSPORTER	MIxt + HEXT -> MI	itr1
YOL103W		*ITR2*	MYO-INOSITOL TRANSPORTER	MIxt + HEXT -> MI	itr2
*U153_*		*U153_*	MALTASE PERMEASE	MLTxt + HEXT -> MLT	mltup
YIL162W	3.2.1.26	*SUC2*	INVERTASE (SUCROSE HYDROLYZING ENZYME)	SUCxt -> GLCxt + FRUxt	suc2
*U154_*		*U154_*	SUCROSE	SUCxt + HEXT -> SUC	sucup
YBR298C		*MAL31*	DICARBOXYLATES	MALxt + HEXT <-> MAL	mal31

*U155_*	*U155_*	A-KETOGLUTARATE/MALATE TRANSLOCATOR	MALxt + AKG <-> MAL + AKGxt	akmup
*U156_*	*U156_*	A-METHYLGLUCOSIDE	AMGxt <-> AMG	amgup
*U157_*	*U157_*	SORBOSE	SORxt <-> SOR	sorup
*U158_*	*U158_*	ARABINOSE (LOW AFFINITY)	ARABxt <-> ARAB	arbup1
*U159_*	*U159_*	FUCOSE	FUCxt + HEXT <-> FUC	fucup
*U160_*	*U160_*		GLTLxt + HEXT -> GLTL	gltlupb
*U161_*	*U161_*	GLUCITOL	GLTxt + HEXT -> GLT	gltup
*U162_*	*U162_*	GLUCOSAMINE	GLAMxt + HEXT <-> GLAM	gaup
YLL043W	*FPS1*	GLYCEROL	GLxt <-> GL	glup
YKL217W	*JEN1*	LACTATE TRANSPORT	LACxt + HEXT <-> LAC	lacup1
*U163_*	*U163_*	MANNITOL	MNTxt + HEXT -> MNT	mntup
*U164_*	*U164_*	MELIBIOSE	MELIxt + HEXT -> MELI	melup_1
*U165_*	*U165_*	N-ACETYLGLUCOSAMINE	NAGxt + HEXT -> NAG	nagup
*U166_*	*U166_*	RHAMNOSE	RMNxt + HEXT -> RMN	rmnup
*U167_*	*U167_*	RIBOSE	RIBxt + HEXT -> RIB	ribup
*U168_*	*U168_*	TREHALOSE	TRExt + HEXT -> TRE	treup_1
*U169_*	*U169_*		TRExt -> AATRE6P	treup_2
*U170_*	*U170_*		XYLxt <-> XYL	xylup
# AMINO ACIDS				
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	ALAxt + HEXT <-> ALA	gap1_1
YPL265W	*DIP5*	DICARBOXYLIC AMINO ACID PERMEASE	ALAxt + HEXT <-> ALA	dip5
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	ALAxt + HEXT <-> ALA	gap25
YOL020W	*TAT2*	TRYPTOPHAN PERMEASE	ALAxt + HEXT <-> ALA	tat5
YOR348C	*PUT4*	PROLINE PERMEASE	ALAxt + HEXT <-> ALA	put4
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	ARGxt + HEXT <-> ARG	gap2
YEL063C	*CAN1*	PERMEASE FOR BASIC AMINO ACIDS	ARGxt + HEXT <-> ARG	can1_1
YNL270C	*ALP1*	PROTEIN WITH STRONG SIMILARITY TO PERMEASES	ARGxt + HEXT <-> ARG	alp1
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	ASNxt + HEXT <-> ASN	gap3
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	ASNxt + HEXT <-> ASN	gap21
YDR508C	*GNP1*	GLUTAMINE PERMEASE (HIGH AFFINITY)	ASNxt + HEXT <-> ASN	gnp2
YPL265W	*DIP5*	DICARBOXYLIC AMINO ACID PERMEASE	ASNxt + HEXT <-> ASN	dip6
YFL055W	*AGP3*	AMINO ACID PERMEASE FOR SERINE, ASPARTATE, AND GLUTAMATE	ASPxt + HEXT <-> ASP	agp3_2
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	ASPxt + HEXT <-> ASP	gap4

YPL265W	*DIP5*	DICARBOXYLIC AMINO ACID PERMEASE	ASPxt + HEXT <-> ASP	dip7
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	CYSxt + HEXT <-> CYS	gap5
YDR508C	*GNP1*	GLUTAMINE PERMEASE (HIGH AFFINITY)	CYSxt + HEXT <-> CYS	gnp3
YBR068C	*BAP2*	BRANCHED CHAIN AMINO ACID PERMEASE	CYSxt + HEXT <-> CYS	bap2_1
YDR046C	*BAP3*	BRANCHED CHAIN AMINO ACID PERMEASE	CYSxt + HEXT <-> CYS	bap3_1
YBR069C	*VAP1*	AMINO ACID PERMEASE	CYSxt + HEXT <-> CYS	vap7
YOL020W	*TAT2*	TRYPTOPHAN PERMEASE	CYSxt + HEXT <-> CYS	tat7
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	GLYxt + HEXT <-> GLY	gap6
YOL020W	*TAT2*	TRYPTOPHAN PERMEASE	GLYxt + HEXT <-> GLY	tat6
YPL265W	*DIP5*	DICARBOXYLIC AMINO ACID PERMEASE	GLYxt + HEXT <-> GLY	dip8
YOR348C	*PUT4*	PROLINE PERMEASE	GLYxt + HEXT <-> GLY	put5
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	GLNxt + HEXT <-> GLN	gap7
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	GLNxt + HEXT <-> GLN	gap22
YDR508C	*GNP1*	GLUTAMINE PERMEASE (HIGH AFFINITY)	GLNxt + HEXT <-> GLN	gnp1
YPL265W	*DIP5*	DICARBOXYLIC AMINO ACID PERMEASE	GLNxt + HEXT <-> GLN	dip9
YGR191W	*HIP1*	HISTIDINE PERMEASE	HISxt + HEXT <-> HIS	hip1
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	HISxt + HEXT <-> HIS	gap9
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	HISxt + HEXT <-> HIS	gap23
YBR069C	*VAP1*	AMINO ACID PERMEASE	HISxt + HEXT <-> HIS	vap6
YBR069C	*TAT1*	AMINO ACID PERMEASE THAT TRANSPORTS VALINE, LEUCINE, ISLEUCINE, TYROSINE, TRYPTOPHAN, AND THREONINE	ILExt + HEXT <-> ILE	tat1_2
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	ILExt + HEXT <-> ILE	gap10
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	ILExt + HEXT <-> ILE	gap32
YBR068C	*BAP2*	BRANCHED CHAIN AMINO ACID PERMEASE	ILExt + HEXT <-> ILE	bap2_2
YDR046C	*BAP3*	BRANCHED CHAIN AMINO ACID PERMEASE	ILExt + HEXT <-> ILE	bap3_2
YBR069C	*VAP1*	AMINO ACID PERMEASE	ILExt + HEXT <-> ILE	vap3
YBR069C	*TAT1*	AMINO ACID PERMEASE THAT TRANSPORTS VALINE, LEUCINE, ISLEUCINE, TYROSINE, TRYPTOPHAN, AND THREONINE	LEUxt + HEXT <-> LEU	tat1_3
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	LEUxt + HEXT <-> LEU	gap11
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	LEUxt + HEXT <-> LEU	gap33

YBR068C	*BAP2*	BRANCHED CHAIN AMINO ACID PERMEASE	LEUxt + HEXT <-> LEU	bap2_3
YDR046C	*BAP3*	BRANCHED CHAIN AMINO ACID PERMEASE	LEUxt + HEXT <-> LEU	bap3_3
YBR069C	*VAP1*	AMINO ACID PERMEASE	LEUxt + HEXT <-> LEU	vap4
YDR508C	*GNP1*	GLUTAMINE PERMEASE (HIGH AFFINITY)	LEUxt + HEXT <-> LEU	gnp7
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	METxt + HEXT <-> MET	gap13
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	METxt + HEXT <-> MET	gap26
YDR508C	*GNP1*	GLUTAMINE PERMEASE (HIGH AFFINITY)	METxt + HEXT <-> MET	gnp4
YBR068C	*BAP2*	BRANCHED CHAIN AMINO ACID PERMEASE	METxt + HEXT <-> MET	bap2_4
YDR046C	*BAP3*	BRANCHED CHAIN AMINO ACID PERMEASE	METxt + HEXT <-> MET	bap3_4
YGR055W	*MUP1*	HIGH-AFFINITY METHIONINE PERMEASE	METxt + HEXT <-> MET	mup1
YHL036W	*MUP3*	LOW-AFFINITY METHIONINE PERMEASE	METxt + HEXT <-> MET	mup3
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	PHExt + HEXT <-> PHEN	gap14
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	PHExt + HEXT <-> PHEN	gap29
YOL020W	*TAT2*	TRYPTOPHAN PERMEASE	PHExt + HEXT <-> PHEN	tat4
YBR068C	*BAP2*	BRANCHED CHAIN AMINO ACID PERMEASE	PHExt + HEXT <-> PHEN	bap2_5
YDR046C	*BAP3*	BRANCHED CHAIN AMINO ACID PERMEASE	PHExt + HEXT <-> PHEN	bap3_5
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	PROxt + HEXT <-> PRO	gap15
YOR348C	*PUT4*	PROLINE PERMEASE	PROxt + HEXT <-> PRO	put6
YBR069C	*TAT1*	AMINO ACID PERMEASE THAT TRANSPORTS VALINE, LEUCINE, ISLEUCINE, TYROSINE, TRYPTOPHAN, AND THREONINE	TRPxt + HEXT <-> TRP	tat1_6
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	TRPxt + HEXT <-> TRP	gap18
YBR069C	*VAP1*	AMINO ACID PERMEASE	TRPxt + HEXT <-> TRP	vap2
YOL020W	*TAT2*	TRYPTOPHAN PERMEASE	TRPxt + HEXT <-> TRP	tat3
YBR068C	*BAP2*	BRANCHED CHAIN AMINO ACID PERMEASE	TRPxt + HEXT <-> TRP	bap2_6
YDR046C	*BAP3*	BRANCHED CHAIN AMINO ACID PERMEASE	TRPxt + HEXT <-> TRP	bap3_6
YBR069C	*TAT1*	AMINO ACID PERMEASE THAT TRANSPORTS VALINE, LEUCINE, ISLEUCINE, TYROSINE, TRYPTOPHAN, AND THREONINE	TYRxt + HEXT <-> TYR	tat1_7
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	TYRxt + HEXT <-> TYR	gap19
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	TYRxt + HEXT <-> TYR	gap28
YBR068C	*BAP2*	BRANCHED CHAIN AMINO ACID PERMEASE	TYRxt + HEXT <-> TYR	bap2_7
YBR069C	*VAP1*	AMINO ACID PERMEASE	TYRxt + HEXT <-> TYR	vap1

YOL020W	*TAT2*	TRYPTOPHAN PERMEASE	TYRxt + HEXT <-> TYR	tat2
YDR046C	*BAP3*	BRANCHED CHAIN AMINO ACID PERMEASE	TYRxt + HEXT <-> TYR	bap3_7
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	VALxt + HEXT <-> VAL	gap20
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	VALxt + HEXT <-> VAL	gap31
YDR046C	*BAP3*	BRANCHED CHAIN AMINO ACID PERMEASE	VALxt + HEXT <-> VAL	bap3_8
YBR069C	*VAP1*	AMINO ACID PERMEASE	VALxt + HEXT <-> VAL	vap5
YBR068C	*BAP2*	BRANCHED CHAIN AMINO ACID PERMEASE	VALxt + HEXT <-> VAL	bap2_8
YFL055W	*AGP3*	AMINO ACID PERMEASE FOR SERINE, ASPARTATE, AND GLUTAMATE	SERxt + HEXT <-> SER	agp3_1
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	SERxt + HEXT <-> SER	gap27
YDR508C	*GNP1*	GLUTAMINE PERMEASE (HIGH AFFINITY)	SERxt + HEXT <-> SER	gnp5
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	SERxt + HEXT <-> SER	gap16
YPL265W	*DIP5*	DICARBOXYLIC AMINO ACID PERMEASE	SERxt + HEXT <-> SER	dip11
YBR069C	*TAT1*	AMINO ACID PERMEASE THAT TRANSPORTS VALINE, LEUCINE, ISLEUCINE, TYROSINE, TRYPTOPHAN, AND THREONINE	THRxt + HEXT <-> THR	tat1_1
YCL025C	*AGP1*	AMINO ACID PERMEASE FOR MOST NEUTRAL AMINO ACIDS	THRxt + HEXT <-> THR	gap30
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	THRxt + HEXT <-> THR	gap17
YDR508C	*GNP1*	GLUTAMINE PERMEASE (HIGH AFFINITY)	THRxt + HEXT <-> THR	gnp6
YNL268W	*LYP1*	LYSINE SPECIFIC PERMEASE (HIGH AFFINITY)	LYSxt + HEXT <-> LYS	lyp1
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	LYSxt + HEXT <-> LYS	gap12
YLL061W	*MMP1*	HIGH AFFINITY S-METHYLMETHIONINE PERMEASE	MMETxt + HEXT -> MMET	mmp1
YPL274W	*SAM3*	HIGH AFFINITY S-ADENOSYLMETHIONINE PERMEASE	SAMxt + HEXT -> SAM	sam3
YOR348C	*PUT4*	PROLINE PERMEASE	GABAxt + HEXT -> GABA	put7
YDL210W	*UGA4*	AMINO ACID PERMEASE WITH HIGH SPECIFICITY FOR GABA	GABAxt + HEXT -> GABA	uga4
YBR132C	*AGP2*	PLASMA MEMBRANE CARNITINE TRANSPORTER	CARxt <-> CAR	agp2
YGL077C	*HNM1*	CHOLINE PERMEASE	CHOxt + HEXT -> MET	hnm1
YNR056C	*BIO5*	TRANSMEMBRANE REGULATOR OF KAPA/DAPA TRANSPORT	BIOxt + HEXT -> BIO	bio5a
YDL210W	*UGA4*	AMINO ACID PERMEASE WITH HIGH SPECIFICITY FOR GABA	ALAVxt + HEXT -> ALAV	uga5
YKR039W	*GAP1*	GENERAL AMINO ACID PERMEASE	ORNxt + HEXT <-> ORN	gap1b

YEL063C	*CAN1*	PERMEASE FOR BASIC AMINO ACIDS	ORNxt + HEXT <-> ORN	can1b
*U171_*	*U171_*	PUTRESCINE	PTRSCxt + HEXT -> PTRSC	ptrup
*U172_*	*U172_*	SPERMIDINE & PUTRESCINE	SPRMDxt + HEXT -> SPRMD	sprup1
YKR093W	*PTR2*	DIPEPTIDE	DIPEPxt + HEXT -> DIPEP	ptr2
YKR093W	*PTR2*	OLIGOPEPTIDE	OPEPxt + HEXT -> OPEP	ptr3
YKR093W	*PTR2*	PEPTIDE	PEPTxt + HEXT -> PEPT	ptr4
YBR021W	*FUR4*	URACIL	URAxt + HEXT -> URA	uraup1
*U173_*	*U173_*	NICOTINAMIDE MONONUCLEOTIDE TRANSPORTER	NMNxt + HEXT -> NMN	nmnup
YER056C	*FCY2*	CYTOSINE PURINE PERMEASE	CYTSxt + HEXT -> CYTS	fcy2_1
YER056C	*FCY2*	ADENINE	ADxt + HEXT -> AD	fcy2_2
YER056C	*FCY2*	GUANINE	GNxt + HEXT <-> GN	fcy2_3
YER060W	*FCY21*	CYTOSINE PURINE PERMEASE	CYTSxt + HEXT -> CYTS	fcy21_1
YER060W	*FCY21*	ADENINE	ADxt + HEXT -> AD	fcy21_2
YER060W	*FCY21*	GUANINE	GNxt + HEXT <-> GN	fcy21_3
YER060W-A	*FCY22*	CYTOSINE PURINE PERMEASE	CYTSxt + HEXT -> CYTS	fcy22_1
YER060W-A	*FCY22*	ADENINE	ADxt + HEXT -> AD	fcy22_2
YER060W-A	*FCY22*	GUANINE	GNxt + HEXT <-> GN	fcy22_3
YGL186C	*YGL186C*	CYTOSINE PURINE PERMEASE	CYTSxt + HEXT -> CYTS	cytup1
YGL186C	*YGL186C*	ADENINE	ADxt + HEXT -> AD	adup1
YGL186C	*YGL186C*	GUANINE	GNxt + HEXT <-> GN	gnup
*U174_*	*U174_*	G-SYSTEM	ADNxt + HEXT -> ADN	ncgup1
*U175_*	*U175_*	G-SYSTEM	GSNxt + HEXT -> GSN	ncgup3
YBL042C	*FUI1*	URIDINE PERMEASE, G-SYSTEM	URIxt + HEXT -> URI	uriup
*U176_*	*U176_*	G-SYSTEM	CYTDxt + HEXT -> CYTD	ncgup4
*U177_*	*U177_*	G-SYSTEM (TRANSPORTS ALL NUCLEOSIDES)	INSxt + HEXT -> INS	ncgup5
*U178_*	*U178_*	G-SYSTEM	XTSINExt + HEXT -> XTSINE	ncgup6
*U179_*	*U179_*	G-SYSTEM	DTxt + HEXT -> DT	ncgup7
*U180_*	*U180_*	G-SYSTEM	DINxt + HEXT -> DIN	ncgup8
*U181_*	*U181_*	G-SYSTEM	DGxt + HEXT -> DG	ncgup9
*U182_*	*U182_*	G-SYSTEM	DAxt + HEXT -> DA	ncgup10
*U183_*	*U183_*	G-SYSTEM	DCxt + HEXT -> DC	ncgup11
*U184_*	*U184_*	G-SYSTEM	DUxt + HEXT -> DU	ncgup12
*U185_*	*U185_*	C-SYSTEM	ADNxt + HEXT -> ADN	nccup1
YBL042C	*FUI1*	URIDINE PERMEASE, C-SYSTEM	URIxt + HEXT -> URI	nccup2
*U186_*	*U186_*	C-SYSTEM	CYTDxt + HEXT -> CYTD	nccup3
*U187_*	*U187_*	C-SYSTEM	DTxt + HEXT -> DT	nccup4

*U188_*	*U188_*	C-SYSTEM	DAxt + HEXT -> DA	nccup5
*U189_*	*U189_*	C-SYSTEM	DCxt + HEXT -> DC	nccup6
*U190_*	*U190_*	C-SYSTEM	DUxt + HEXT -> DU	nccup7
*U191_*	*U191_*	NUCLEOSIDES AND DEOXYNUCLEOSIDE	ADNxt + HEXT -> ADN	ncup1
*U192_*	*U192_*	NUCLEOSIDES AND DEOXYNUCLEOSIDE	GSNxt + HEXT -> GSN	ncup2
YBL042C	*FUI1*	URIDINE PERMEASE, NUCLEOSIDES AND DEOXYNUCLEOSIDE	URIxt + HEXT -> URI	ncup3
*U193_*	*U193_*	NUCLEOSIDES AND DEOXYNUCLEOSIDE	CYTDxt + HEXT -> CYTD	ncup4
*U194_*	*U194_*	NUCLEOSIDES AND DEOXYNUCLEOSIDE	INSxt + HEXT -> INS	ncup5
*U195_*	*U195_*	NUCLEOSIDES AND DEOXYNUCLEOSIDE	DTxt + HEXT -> DT	ncup7
*U196_*	*U196_*	NUCLEOSIDES AND DEOXYNUCLEOSIDE	DINxt + HEXT -> DIN	ncup8
*U197_*	*U197_*	NUCLEOSIDES AND DEOXYNUCLEOSIDE	DGxt + HEXT -> DG	ncup9
*U198_*	*U198_*	NUCLEOSIDES AND DEOXYNUCLEOSIDE	DAxt + HEXT -> DA	ncup10
*U199_*	*U199_*	NUCLEOSIDES AND DEOXYNUCLEOSIDE	DCxt + HEXT -> DC	ncup11
*U200_*	*U200_*	NUCLEOSIDES AND DEOXYNUCLEOSIDE	DUxt + HEXT -> DU	ncup12
*U201_*	*U201_*	HYPOXANTHINE	HYXNxt + HEXT <-> HYXN	hyxnup
*U202_*	*U202_*	XANTHINE	XANxt <-> XAN	xanup
# METABOLIC BY-PRODUCTS				
YCR032W	*BPH1*	PROBABLE ACETIC ACID EXPORT PUMP, ACETATE TRANSPORT	ACxt + HEXT <-> AC	acup
*U203_*	*U203_*	FORMATE TRANSPORT	FORxt <-> FOR	forup
*U204_*	*U204_*	ETHANOL TRANSPORT	ETHxt <-> ETH	ethup
*U205_*	*U205_*	SUCCINATE TRANSPORT	SUCCxt + HEXT <-> SUCC	succup
YKL217W	*JEN1*	PYRUVATE LACTATE PROTON SYMPORT	PYRxt + HEXT -> PYR	jen1_1
# OTHER COMPOUNDS				
YHL016C	*DUR3*	UREA ACTIVE TRANSPORT	UREAxt + 2 HEXT <-> UREA	dur3
YGR121C	*MEP1*	AMMONIA TRANSPORT	NH3xt <-> NH3	mep1
YNL142W	*MEP2*	AMMONIA TRANSPORT, LOW CAPACITY HIGH AFFINITY	NH3xt <-> NH3	mep2
YPR138C	*MEP3*	AMMONIA TRANSPORT, HIGH CAPACITY LOW AFFINITY	NH3xt <-> NH3	mep3
YJL129C	*TRK1*	POTASSIUM TRANSPORTER OF THE PLASMA MEMBRANE, HIGH AFFINITY, MEMBER OF THE POTASSIUM TRANSPORTER (TRK) FAMILY OF MEMBRANE TRANSPORTERS	Kxt + HEXT <-> K	trk1
YBR294W	*SUL1*	SULFATE PERMEASE	SLFxt -> SLF	sul1

YLR092W	*SUL2*	SULFATE PERMEASE	SLFxt -> SLF	sul2
YGR125W	*YGR125W*	SULFATE PERMEASE	SLFxt -> SLF	sulup
YML123C	*PHO84*	INORGANIC PHOSPHATE TRANSPORTER, TRANSMEMBRANE PROTEIN	PIxt + HEXT <-> PI	pho84
*U206_*	*U206_*	CITRATE	CITxt + HEXT <-> CIT	citup
*U207_*	*U207_*	DICARBOXYLATES	FUMxt + HEXT <-> FUM	fumup
*U208_*	*U208_*	FATTY ACID TRANSPORT	C140xt -> C140	faup1
*U209_*	*U209_*	FATTY ACID TRANSPORT	C160xt -> C160	faup2
*U210_*	*U210_*	FATTY ACID TRANSPORT	C161xt -> C161	faup3
*U211_*	*U211_*	FATTY ACID TRANSPORT	C180xt -> C180	faup4
*U212_*	*U212_*	FATTY ACID TRANSPORT	C181xt -> C181	faup5
*U213_*	*U213_*	A-KETOGLUTARATE	AKGxt + HEXT <-> AKG	akgup
YLR138W	*NHA1*	PUTATIVE NA+/H+ ANTIPORTER	NAxt <-> NA + HEXT	nha1
YCR028C	*FEN2*	PANTOTHENATE	PNTOxt + HEXT <-> PNTO	fen2
*U214_*	*U214_*	ATP DRAIN FLUX FOR CONSTANT MAINTANENCE REQUIREMENTS	ATP -> ADP + PI	atpmt
YCR024C-A	*PMP1*	H+-ATPASE SUBUNIT, PLASMA MEMBRANE	ATP -> ADP + PI + HEXT	pmp1
YEL017C-A	*PMP2*	H+-ATPASE SUBUNIT, PLASMA MEMBRANE	ATP -> ADP + PI + HEXT	pmp2
YGL008C	*PMA1*	H+-TRANSPORTING P-TYPE ATPASE, MAJOR ISOFORM, PLASMA MEMBRANE	ATP -> ADP + PI + HEXT	pma1
YPL036W	*PMA2*	H+-TRANSPORTING P-TYPE ATPASE, MINOR ISOFORM, PLASMA MEMBRANE	ATP -> ADP + PI + HEXT	pma2
*U215_*	*U215_*	GLYCERALDEHYDE TRANSPORT	GLALxt <-> GLAL	glaltx
*U216_*	*U216_*	ACETALDEHYDE TRANSPORT	ACALxt <-> ACAL	acaltx
YLR237W	*THI7*	THIAMINE TRANSPORT PROTEIN	THMxt + HEXT -> THIAMIN	thm1
YOR071C	*YOR071C*	PROBABLE LOW AFFINITY THIAMINE TRANSPORTER	THMxt + HEXT -> THIAMIN	thm2
YOR192C	*YOR192C*	PROBABLE LOW AFFINITY THIAMINE TRANSPORTER	THMxt + HEXT -> THIAMIN	thm3
YIR028W	*DAL4*		ATNxt -> ATN	dal4
YJR152W	*DAL5*		ATTxt -> ATT	dal5
*U217_*	*U217_*		MTHNxt <-> MTHN	mthup
*U218_*	*U218_*		PAPxt <-> PAP	papx
*U219_*	*U219_*		DTTPxt <-> DTTP	dttpx
*U220_*	*U220_*		THYxt <-> THY + HEXT	thyx
*U221_*	*U221_*		GA6Pxt <-> GA6P	ga6pup

YGR065C	*VHT1*	H+/BIOTIN SYMPORTER AND MEMBER OF THE ALLANTOATE PERMEASE FAMILY OF THE MAJOR FACILITATOR SUPERFAMILY	BTxt + HEXT <-> BT	btup
*U222_*	*U222_*		AONAxt + HEXT <-> AONA	kapaup
*U223_*	*U223_*		DANNAxt + HEXT <-> DANNA	dapaup
*U224_*	*U224_*		OGTxt -> OGT	ogtup
*U225_*	*U225_*		SPRMxt -> SPRM	sprmup
*U226_*	*U226_*		PIMExt -> PIME	pimeup
*U227_*	*U227_*	OXYGEN TRANSPORT	O2xt <-> O2	o2tx
*U228_*	*U228_*	CARBON DIOXIDE TRANSPORT	CO2xt <-> CO2	co2tx
YOR011W	*AUS1*		ERGOSTxt <-> ERGOST	ergup
YOR011W	*AUS1*	PUTATIVE STEROL TRANSPORTER	ZYMSTxt <-> ZYMST	zymup
*U229_*	*U229_*		RFLAVxt + HEXT -> RIBFLAV	rflup