

Metabolic model integration of the bibliome,
genome, metabolome, and reactome of
Aspergillus niger — Supplementary
information

Mikael Rørdam Andersen, Michael Lynge Nielsen, Jens Nielsen

List of Figures

1	Map of <i>A. niger</i> metabolism in scalable vector graphics	4
2	Map of transcription on glucose/ammonium medium	5

List of Tables

I	<i>Aspergillus niger</i> reconstructed metabolic network.	6
II	List of metabolite abbreviations in model	80
III	Protein composition of <i>A. niger</i>	108
IV	RNA composition of <i>A. niger</i>	109
V	DNA composition of <i>A. niger</i>	110
VI	Small molecules in the biomass of <i>A. niger</i>	111
VII	Cell wall composition of <i>A. niger</i>	112
VIII	Lipid composition of <i>A. niger</i>	113
IX	Carbon sources available to the model	114
X	Carbon sources available to the model with no referenc	116
XI	Nitrogen sources available to the model	118
XII	Enzymatic activities found in literature, but not included in the model	119
XIII	Pathways reported in literature to be present, but not included in the reaction list of <i>A. niger</i> iMA871	127

Suppl. Figure 1: Map of *A. niger* metabolism in scalable vector graphics. EC numbers are shown for all reactions where a such is defined. A list of abbreviations for the metabolite-names is available in Suppl. Table 2.

The figure is available as a separate PDF-file due to the size of it

Suppl. Figure 2: Map of transcription on glucose/ammonium medium. Based Present/Absent calls from transcription data from Pel et al. (2007) (Pel et al., 2007). A red box denotes the transcription of at least one of the genes assigned to the reaction, green denotes a complete absence of transcription of all isoenzymes and subunits. A gray box is indicative of a process with no assigned ORF.

The figure is available as a separate PDF-file due to the size of it

Suppl. Table 1: *Aspergillus niger* reconstructed metabolic network. Abbreviations of the names of the metabolites are found in Suppl. Table 2. For each reaction the following information is noted where it is known: The EC-number and enzyme name. A list of references discussing or indicating the presence of the reaction (If a reaction is found in another *Aspergillus* sp or inferred based on observations in *A. niger*, it will be written as Hondmann (1994, *A. nidulans*) or Morozova et al. (2002, Inferred) respectively). ORF/gene numbers from the *A. niger* CBS 513.88 and ATCC 1015-genome sequences (Columns CBS and ATCC respectively). The column named "Model" shows which other *Aspergillus* models the reaction is present in, ANID; *A. nidulans* iHD666, ANIG; *A. niger* iHD20, ANEW; The reaction is only present in *A. niger* iMA871. An * indicates that an enzyme-complex catalyses this reaction.

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
Conversions							
NE1	: DGLCe \rightleftharpoons 0.33 GLCe + 0.67 bDGLCe	Non enzymatic step	Non enzymatic reaction	David et al. (2003)	ANIG, ANID		
NE2	: DGLC \rightleftharpoons 0.33 GLC + 0.67 bDGLC	Non enzymatic step	Non enzymatic reaction	Kinoshita et al. (1981)	ANIG, ANID		
r1	: GLC \rightleftharpoons bDGLC	5.1.3.3	Aldose 1-epimerase	Kinoshita et al. (1981)	ANIG, ANID	An02g09090; An11g10890	55604; 56084
r2	: GLAC \rightleftharpoons bGLAC	5.1.3.3	aldose-1-epimerase	Kinoshita et al. (1981)	ANEW	An02g09090; An11g10890	55604; 56084
r3	: LARAB \rightleftharpoons bLARAB	5.1.3.3	aldose-1-epimerase	Kinoshita et al. (1981)	ANEW	An02g09090; An11g10890	55604; 56084
r4	: bFRU \rightleftharpoons FRU	5.1.3.3	aldose-1-epimerase	Kinoshita et al. (1981)	ANEW	An02g09090; An11g10890	55604; 56084
Gluconeogenesis & Glycolysis							
Embden-Meyerhoff-Parnas Pathway							
r5	: ATP + GLC \Rightarrow ADP + G6P	2.7.1.1	Hexokinase (hxx)	Jagannathan and Singh (1953); Muller (1986); Martinelli and Kinghorn (1994); Panneman et al. (1998); Alvarez-Vasquez et al. (2000); Karaffa et al. (2001)	ANIG, ANID	An02g14380; An06g00380; An13g00510	55651; 134301; 50817
r6	: ATP + bDGLC \Rightarrow ADP + bDG6P	2.7.1.2	Glucokinase (glkA)	Panneman et al. (1996); Karaffa et al. (2001)	ANIG, ANID	An12g08610	201877
r7	: G6P \rightleftharpoons F6P	5.3.1.9	Glucose-6-phosphate isomerase	Jagannathan and Singh (1953); Martinelli and Kinghorn (1994); Ruijter and Visser (1999); Alvarez-Vasquez et al. (2000)	ANIG, ANID	An16g05420	210433
r8	: bDG6P \rightleftharpoons F6P	5.3.1.9	Glucose-6-phosphate isomerase	Jagannathan and Singh (1953); Ruijter and Visser (1999); Alvarez-Vasquez et al. (2000)	ANIG, ANID	An16g05420	210433
r9	: G6P \rightleftharpoons bDG6P	5.3.1.9	Glucose-6-phosphate isomerase	Jagannathan and Singh (1953); Ruijter and Visser (1999); Alvarez-Vasquez et al. (2000)	ANIG, ANID	An16g05420	210433
r10	: ATP + F6P \Rightarrow ADP + FDP	2.7.1.11	6-phosphofructokinase (Phosphofructokinase I, pfkA)	Jagannathan and Singh (1953); Habison et al. (1983); Martinelli and Kinghorn (1994); Alvarez-Vasquez et al. (2000); Karaffa et al. (2001)	ANIG, ANID	An18g01670	54093
r11	: FDP + H2O \Rightarrow F6P + PI	3.1.3.11	Fructose-2,6-bisphosphatase	Martinelli and Kinghorn (1994); Alvarez-Vasquez et al. (2000)	ANIG, ANID	An04g05300	214375

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r12	: FDP \rightleftharpoons T3P2 + T3P1	4.1.2.13	Fructose-bisphosphate aldolase	Jagannathan and Singh (1953); Jagannathan et al. (1956); Muller (1986); Martinelli and Kinghorn (1994)	ANIG, ANID	An02g07470; An05g02040; An14g04410; An16g00110	55586; 43928; 211172; N/A
r13	: T3P2 \rightleftharpoons T3P1	5.3.1.1	Triosephosphate isomerase (tpiA)	Inoue et al. (1988); Martinelli and Kinghorn (1994)	ANIG, ANID	An02g02920; An14g04920	206602; 56602
r14	: T3P1 + PI + NAD \rightleftharpoons 13PDG + NADH	1.2.1.12	Glyceraldehyde 3-phosphate dehydrogenase (gpdA)	Muller (1986); Martinelli and Kinghorn (1994); Alvarez-Vasquez et al. (2000)	ANIG, ANID	An16g01830	56485
r15	: ADP + 13PDG \rightleftharpoons ATP + 3PG	2.7.2.3	Phosphoglycerate kinase	David et al. (2003)	ANIG, ANID	An08g02260	208318
r16	: 3PG \rightleftharpoons 2PG	5.4.2.1	Phosphoglycerate mutase	Jagannathan and Singh (1953); Muller (1986)	ANIG, ANID	An16g02990; An16g06010	210655; 40937
r17	: 2PG \rightleftharpoons PEP + H2O	4.2.1.11	Phosphopyruvate hydratase (enolase)	Jagannathan and Singh (1953); Muller (1986); Martinelli and Kinghorn (1994)	ANIG, ANID	An18g06250	202692
r18	: ADP + PEP \rightleftharpoons ATP + PYR	2.7.1.40	Pyruvate kinase (pkiA)	Patil and Ramakrishnan (1966); Perl (1982); Meixner-Monori et al. (1984); Muller (1986); Kubicek et al. (1988); de Graaff et al. (1992); Martinelli and Kinghorn (1994); Alvarez-Vasquez et al. (2000)	ANIG, ANID	An07g08990	56137
r19	: ATP + PYR + H2O + CO2 \rightleftharpoons ADP + PI + OA	6.4.1.1	Pyruvate carboxylase (pyc)	Tachibana (1964); Bercovitz et al. (1990); Martinelli and Kinghorn (1994); Jaklitsch et al. (1991); Pel et al. (2007)	ANIG, ANID	An04g02090	213185
r20	: ATPm + PYRm + H2Om + CO2m \rightleftharpoons ADPm + P1m + OAm	6.4.1.1	Pyruvate carboxylase	Tachibana (1964); Ma et al. (1981); Bercovitz et al. (1990); Martinelli and Kinghorn (1994); Jaklitsch et al. (1991); Pel et al. (2007)	ANID	An15g02820	129399
r21	: ATP + OA \rightleftharpoons ADP + PEP + CO2	4.1.1.49	Phosphoenolpyruvate carboxykinase (ATP)	Woronick and Johnson (1960); Patil and Ramakrishnan (1966)	ANIG, ANID	An11g02550	208685
Pentose-Phosphate Shunt	r22 : G6P + NADP \rightleftharpoons D6PGL + NADPH	1.1.1.49	Glucose 6-phosphate 1-dehydrogenase (gsdA)	McDonough and Martin (1958); Muller (1985); Jaklitsch et al. (1991); Wenekes et al. (1993); van den Broek et al. (1995); Martinelli and Kinghorn (1994); Alvarez-Vasquez et al. (2000); Kirinura et al. (2000)	ANIG, ANID	An02g12140	55633
	r23 : D6PGL + H2O \rightleftharpoons D6PGC	3.1.1.31	6-Phosphogluconolactonase	Martinelli and Kinghorn (1994)	ANIG, ANID	An01g05150	206051
r24	: D6PGC + NADP \rightleftharpoons RL5P + CO2 + NADPH	1.1.1.44	Phosphogluconate dehydrogenase (decarboxylating)	McDonough and Martin (1958); Muller (1985); Martinelli and Kinghorn (1994)	ANIG, ANID	An11g06120	178461
r25	: RL5P \rightleftharpoons XUL5P	5.1.3.1	Ribulose-phosphate 3-epimerase	Martinelli and Kinghorn (1994); Muller (1985); de Groot et al. (2003)	ANIG, ANID	An09g03450	50154
r26	: R5P \rightleftharpoons RL5P	5.3.1.6	Ribose-5-phosphate isomerase	Lakshminarayana et al. (1969b); Martinelli and Kinghorn (1994); Muller (1985); de Groot et al. (2003)	ANIG, ANID	An02g02930	206607

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r27	: R5P + XUL5P \rightleftharpoons S7P + T3P1	2.2.1.1	Transketolase	Martinelli and Kinghorn (1994); de Groot et al. (2003)	ANIG, ANID	An02g06430; An08g06570	197387; 207951
r28	: E4P + XUL5P \rightleftharpoons F6P + T3P1	2.2.1.1	Transketolase	Martinelli and Kinghorn (1994); de Groot et al. (2003)	ANIG, ANID	An02g06430; An08g06570	197387; 207951
r29	: S7P + T3P1 \rightleftharpoons E4P + F6P	2.2.1.2	Transaldolase	Martinelli and Kinghorn (1994); de Groot et al. (2003)	ANIG, ANID	An07g03160; An07g03850	40065; 209713
Tricarboxylic Acid Cycle							
r31	: ACCOAm + H2Om + OAm \rightleftharpoons CITm + COAm	2.3.3.1	Citrate synthase (citA)	Muller (1975b, 1986); Bercovitz et al. (1990); Martinelli and Kinghorn (1994); Alvarez-Vasquez et al. (2000); Kubicek et al. (1988); Pel et al. (2007)	ANIG, ANID	An01g09940; An08g10920; An09g06680	35756; 176409; 202801
r32	: CITm \rightleftharpoons ACOm + H2Om	4.2.1.3	Aconitate hydratase	Muller (1975b); Neilson (1955); Muller (1986); Alvarez-Vasquez et al. (2000); Kirmura et al. (2000); Karaffa et al. (2001)	ANIG, ANID	An02g11040; An08g10530; An09g03870; An16g05760	130186; 52568; 212582; 48916
r33	: ACOm + H2Om \rightleftharpoons ICITm	4.2.1.3	Aconitate hydratase	Muller (1975b); Neilson (1955); Muller (1986); Alvarez-Vasquez et al. (2000); Karaffa et al. (2001)	ANIG, ANID	An02g11040; An08g10530; An09g03870; An16g05760	130186; 52568; 212582; 48916
r34	: ICITm + NADPm \rightleftharpoons AKGm + CO2m + NADPHm	1.1.1.42	Isocitrate dehydrogenase (icdA) (NADP+)	Patil and Ramakrishnan (1966); Muller (1975b, 1986); Meixner-Monori et al. (1986); Martinelli and Kinghorn (1994); Alvarez-Vasquez et al. (2000); Karaffa et al. (2001); Jaklitsch et al. (1991); Pel et al. (2007)	ANIG, ANID	An02g12430	47151
r30	: ICITm + NADm \rightleftharpoons AKGm + CO2m + NADHm	1.1.1.41	Isocitrate dehydrogenase (NAD+)	Muller (1975b); Jaklitsch et al. (1991); Pel et al. (2007)	ANIG, ANID	An08g05580; An18g06760	208051; 212289
r35	: ICIT + NADP \rightleftharpoons AKG + CO2 + NADPH	1.1.1.42	Isocitrate dehydrogenase (NADP+)	Patil and Ramakrishnan (1966); Muller (1975b, 1986); Meixner-Monori et al. (1986); Martinelli and Kinghorn (1994); Alvarez-Vasquez et al. (2000); Karaffa et al. (2001); Jaklitsch et al. (1991); Pel et al. (2007)	ANIG, ANID	An02g12430	47151
r36a	: AKGm + TDPE1m \rightleftharpoons AKGE1m + CO2m	1.2.4.2	alpha-ketoglutarate dehydrogenase	Muller (1975b); Meixner-Monori et al. (1985); Martinelli and Kinghorn (1994)	ANIG, ANID	An04g04750; An06g00390	212992; 47240
r36b	: AKGE1m + LPSE2m \rightleftharpoons AKGE2m + TDPE1m	2.3.1.61	Dihydrolipoamide S-succinyl transferase	Meixner-Monori et al. (1985); Martinelli and Kinghorn (1994)	ANIG, ANID	An11g11280	56101
r36c	: AKGE2m + COAm + NADm \rightleftharpoons LPSE2m + SUCCOAm + NADHm	1.8.1.4	Dihydrolipoamide dehydrogenase	Meixner-Monori et al. (1985); Martinelli and Kinghorn (1994)	ANIG, ANID	An07g06840	53232
r38	: GDPm + P1m + SUCCOAm \rightleftharpoons GTPm + SUCCm + COAm	6.2.1.4	Succinate CoA ligase (GDP forming)	David et al. (2003)	ANIG, ANID	An08g02970; An08g02980	176118; 176118
r39	: SUCCm + Qm \rightleftharpoons FUMm + QH2m	1.3.5.1	Succinate dehydrogenase (ubiquinone)	Martinelli and Kinghorn (1994); Karaffa et al. (2001)	ANIG, ANID	An14g04395; An14g04400; An02g07600; An02g12770; An07g03170	201642; 201642; 130857; 55637; 40064
r40	: FUMm + FADH2m \rightleftharpoons SUCCm + FADm	1.3.99.1	Succinate dehydrogenase	Muller (1975b); Kirmura et al. (2000); Karaffa et al. (2001)	ANIG, ANID	An01g13930; An02g05410	51710; 52233

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r41	FUM + FADH ₂ m \Rightarrow SUCC + FADm	1.3.99.1	Succinate dehydrogenase	David et al. (2003)	ANID	An16g07150	205005
r42	FUMm + H ₂ Om \rightleftharpoons MALm	4.2.1.2	Fumarate hydratase		ANIG, ANID	An12g07850	56673
r43	MAL \rightleftharpoons FUM + H ₂ O	4.2.1.2	Fumarate hydratase	Muller (1975a, 1986)	ANID	An12g07850	56673
r44	MALm + NADm \rightleftharpoons OAm + NADHm	1.1.1.37	Malate dehydrogenase	Muller (1975b); Ma et al. (1981); Bercovitz et al. (1990); Martinelli and Kinghorn (1994); Alvarez-Vasquez et al. (2000); Karaffa et al. (2001); Pel et al. (2007)	ANIG, ANID	An16g00120	N/A
r45	MAL + NAD \rightleftharpoons OA + NADH	1.1.1.37	Malate dehydrogenase	Muller (1975b); Ma et al. (1981); Muller (1986); Bercovitz et al. (1990); Jakitsch et al. (1991); Martinelli and Kinghorn (1994); Alvarez-Vasquez et al. (2000); Karaffa et al. (2001); Pel et al. (2007)	ANIG, ANID	An11g07190; An15g00070; An12g00160	48047; 183145; 212768
Anaplerotic reactions (besides Gluconeogenesis)							
Glyoxylate Shunt							
r46	ICITm \Rightarrow SUCCm + GLXm	4.1.3.1	Isocitrate lyase	Martinelli and Kinghorn (1994) Shah and Ramakrishnan (1963); Sahrabudhe et al. (1986)	ANIG, ANID	An01g09270	196237
r47	ACCOAm + H ₂ Om + GLXm \Rightarrow MALm + COAm	4.1.3.2	Malate synthase	David et al. (2003)	ANIG, ANID	An15g01860	48680
Oxidation of malate to pyruvate							
r48c	MAL + NADP \Rightarrow PYR + CO ₂ + NADPH	1.1.1.40	Malate dehydrogenase (malic enzyme)	Jernejc and Legisa (2002)	ANIG, ANID	An05g00930	211661
r48m	MALm + NADPm \Rightarrow PYRm + CO ₂ m + NADPHm	1.1.1.40	Malate dehydrogenase (malic enzyme)		ANID	An12g00160	212768
TCA intermediates metabolism							
r50	ATP + CIT + COA \Rightarrow ADP + PI + ACCOA + OA	2.3.3.8	ATP:citrate oxaloacetate-lyase ((pro-3S)-CH ₂ COO- \rightarrow -> acetyl-CoA) (ATP-dephosphorylating) mitochondrial	Pel et al. (2007); Pfitzner et al. (1987)	ANIG, ANID	An11g00530	199043
r50m	ATPm + CITm + COAm \Rightarrow ADPm + PIm + ACCOAm + OAm	2.3.3.8	ATP:citrate oxaloacetate-lyase ((pro-3S)-CH ₂ COO- \rightarrow -> acetyl-CoA) (ATP-dephosphorylating) mitochondrial	Pel et al. (2007); Pfitzner et al. (1987)	ANIG, ANID	An11g00510	208547
r37	CITm \Rightarrow OAm + ACm	4.1.3.6	Mitochondrial citrate lyase	Pel et al. (2007)	ANIG, ANID	An01g08610	51845
Oxalic acid							
r51	OA + H ₂ O \Rightarrow OXAL + AC	3.7.1.1	Oxaloacetate acetylhydrolase (oahA)	Rymowicz and Lenart (2003) Muller (1975a); Lenz et al. (1976); Muller (1986); Kubicek et al. (1988); Ruijter and Visser (1999); Pedersen et al. (2000a); Hjort and Pedersen (2000)	ANIG, ANID	An10g00820	57241
r52	OXAL \Rightarrow FOR + CO ₂	4.1.1.2	Oxalate decarboxylase	Emiliani and Riera (1968)	ANIG, ANID	An15g03980	182700
r56	OXALe \Rightarrow FORe + CO ₂ e	4.1.1.2	Oxalate decarboxylase		ANEW	An03g01140	214686
Methanol							

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r53	: METHOL + NAD \rightleftharpoons FALD + NADH	1.1.1.1	Alcohol dehydrogenase (adhA)	Lusta et al. (1991, A. terreus)	ANID	An12g09810; An17g01530; An01g12170; An01g14590; An02g02060; An02g02870; An03g01350; An04g02690; An08g09750; An09g03140; An11g04150; An11g04290; An12g09950; An13g00950; An13g03330; An14g02160; An14g07180; An16g00010; An16g00400; An16g06240	46038; 204476; 205557; 170152; 206534; 174157; 190222; 190222; 177276; 43351; 179042; 39027; 195091; 44729; 134944; N/A; 42017; 41439; 41421; 40925
r54	: FALD + NAD + H ₂ O \rightleftharpoons FOR + NADH	1.2.1.46	Formaldehyde dehydrogenase	Lusta et al. (1991, A. terreus)	ANID	An10g00230	44975
r55	: FOR + O ₂ \Rightarrow H ₂ O ₂ + CO ₂	1.2.1.2	Formate oxidase	Hauge (1957)	ANEW	An15g00410	124156
r61	: FALD + RGT + NAD \rightleftharpoons FGT + NADH	1.2.1.1	Formaldehyde dehydrogenase (glutathione)	Lusta et al. (1991, A. terreus)	ANID	An02g00080	173994
r56a	: PYRm + LIPom \Rightarrow ADHLIPom + CO ₂ m	1.2.4.1	Pyruvate dehydrogenase (lipoamide)	Alvarez-Vasquez et al. (2000); Karaffa and Kubicek (2003); Pel et al. (2007)	ANIG, ANID *	An01g00100; An07g09530; An11g04550	55510; 209315; 125186
r56b	: COAm + ADHLIPom + NADm \rightleftharpoons AC-COAm + LIPom + NADHm	2.3.1.12	Dihydrolipoamide S-acetyltransferase and lipoamide dehydrogenase	Pel et al. (2007)	ANIG, ANID *	An07g02180; An07g06840; An02g11910	53338; 53232; 197817
r58	: PYR \Rightarrow ACAL + CO ₂	4.1.1.1	Pyruvate decarboxylase	David et al. (2003)	ANIG, ANID	An02g06820; An01g01590; An09g01030; An13g03320	55573; 125264 and 170782; 189097; 192165
r59	: PYR + PI + O ₂ + H ₂ O \Rightarrow ACTP + CO ₂ + H ₂ O ₂	1.2.3.3	Pyruvate oxidase	Patil and Ramakrishnan (1966)	ANEW		
r60	: ATP + AC \Rightarrow ADP + ACTP	2.7.2.1	Acetate kinase	Pel et al. (2007)	ANIG, ANID	An02g06420	206885
r62	: T3P2 \Rightarrow MTHGXL + PI	4.2.3.3	Methylglyoxal synthase or non-enzymatic chemical reaction	Martinelli and Kinghorn (1994)	ANIG		
r63	: T3P1 \Rightarrow MTHGXL + PI	No EC	D-Lactaldehyde dehydrogenase (Methylglyoxal reductase) (MGR I)	Martinelli and Kinghorn (1994)	ANEW		
r64	: MTHGXL + NADPH \rightleftharpoons LACAL + NADP	1.1.1.78	D-Lactaldehyde dehydrogenase (Methylglyoxal reductase) (MGR I)	Inoue et al. (1988); Martinelli and Kinghorn (1994)	ANIG, ANID		
r65	: LACAL + NAD + H ₂ O \Rightarrow LAC + NADH	1.2.1.22	Lactaldehyde dehydrogenase	Inoue et al. (1988)	ANIG, ANID		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r66	LAC + NAD \rightleftharpoons PYR + NADH	1.1.1.28	D-lactate dehydrogenase	David et al. (2003)	ANIG	An01g09780	51812
r67	RGT + MTHGXL \rightleftharpoons LGT	4.4.1.5	Lactoylglutathione lyase (glyoxylase I)	Inoue et al. (1987, 1988); Martinelli and Kinghorn (1994)	ANIG, ANID	An08g09300; An11g02860; An02g05670	37996; 38904; 52241
r68	LGT + H ₂ O \Rightarrow LAC + RGT	3.1.2.6	Hydroxyacylglutathione hydrolase (glyoxylase II)	Inoue et al. (1988)	ANIG, ANID	An04g07220; An11g07320; An14g06340	214187; 48052; 184532
Methylcitrate pathway							
r69	PROPAL + NAD + H ₂ O \rightleftharpoons PROP + NADH	1.2.1.3	Aldehyde dehydrogenase (NAD+)	Sealy-Lewis and Fairhurst (1998); Kanehisa et al. (2002)	ANEW	An04g03400; An01g15170; An08g07290; An08g10820; An10g00850; An15g05890; An18g04130	57028; N/A; 55742; 37719; 57243; 40734; 187856
r70	ATPm + PROPM + COAm \rightleftharpoons AMPm	6.2.1.17	Propanoate:CoA ligase (AMP-forming)	Sealy-Lewis and Fairhurst (1998)	ANIG, ANID		
r85	ATP + PROP + COA \rightleftharpoons AMP + PPI + PROPCOA	6.2.1.17	Propanoate:CoA ligase (AMP-forming)	Sealy-Lewis and Fairhurst (1998)	ANEW		
r71	PROPCOA + H ₂ O + OAm \rightleftharpoons 2MC-ITm + COAm	2.3.3.5	2-Methylcitrate synthase	Miyakoshi et al. (1987); Sealy-Lewis and Fairhurst (1998)	ANIG, ANID	An15g01920	48684
r72	2MCITm \rightleftharpoons 2MACOm + H ₂ O	4.2.1.79	2-methylcitrate hydrolyase	Sealy-Lewis and Fairhurst (1998, Inferred)	ANIG	An15g01780	53423
r73	2MACOm + H ₂ O \rightleftharpoons 2MICITm	4.2.1.99	2-methylisocitrate dehydratase	Sealy-Lewis and Fairhurst (1998, Inferred)	ANIG		
r74	2MICITm \rightleftharpoons PYRm + SUCCm	4.1.3.30	2-methylisocitrate lyase	Miyakoshi et al. (1987)	ANIG	An12g07630	42171
4-aminobutyrate (GABA) shunt							
r75	GLUm \Rightarrow GABAm + CO ₂ m	4.1.1.15	Glutamate decarboxylase	Kumar et al. (2000)	ANID	An02g06860; An08g08840; An15g04770	173821; 52600; 210245
r76	GABAm + AKGm \Rightarrow SUCCSALm + GLUm	2.6.1.19	4-Aminobutyrate transaminase	David et al. (2003)	ANIG, ANID	An17g00910	57265
r77	SUCCSALm + NADm + H ₂ O \Rightarrow SUCCm + NADHm	1.2.1.16	Succinate-semialdehyde dehydrogenase (NAD(P)+)	Kumar and Punekar (1998)	ANIG, ANID	An15g01740; An04g02610; An14g02870	56305; 57046; 56568
ONE CARBON -METABOLISM							
Folate biosynthesis							
r78	GTP + 2 H ₂ O \Rightarrow FOR + AHTD	3.5.4.16	GTP cyclohydrolase I	Cossins and Chen (1997, Inferred)	ANID	An09g05310	212481
r79	AHTD \Rightarrow DHP + 3 PI	3.1.3.1	Glycerophosphatase, alkaline phosphatase; nucleoside triphosphatase	Rana and Shanmugasundaram (1985, A. nidulans)	ANID	An07g07520	209506
r80	DHP \Rightarrow AHHMP + GLAL	4.1.2.25	Dihydropyrimidin aldolase		ANID	An16g03880	49007
r91	GLAL + NAD + H ₂ O \rightleftharpoons GLYA + NADH	1.2.1.21	Glycolaldehyde dehydrogenase		ANEW		
r92	GLYA + O ₂ \Rightarrow GLX + H ₂ O ₂	1.1.3.15	Glycolate oxidase		ANEW	An01g14530; An12g10140	46259; 46010
r81	AHHMP + ATP \Rightarrow AMP + AHHMD	2.7.6.3	6-Hydroxymethyl-7,8-dihydropterin pyrophosphokinase		ANID	An16g05350	183733

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r82	: CHOR + GLN \Rightarrow ADCHOR + GLU	6.3.5.8	Aminodeoxychorismate synthase		ANID		
r83	: ADCHOR \Rightarrow PYR + PABA	4.1.3.38	Aminodeoxychorismate lyase		ANID		
r84	: PABA + AHHMD \Rightarrow PPI + DHPT	2.5.1.15	Dihydropteroate synthase	Cossins and Chen (1997, Inferred)	ANID	An16g03880	49007
r86	: DHPT + ATP + GLU \Rightarrow ADP + PI + DHF	6.3.2.12	Dihydrofolate synthase	Iwai et al. (1977)	ANID		
r87	: DHF + NADPH \Rightarrow NADP + THF	1.5.1.5	Dihydrofolate reductase	Balinska and Paszewski (1979, A. nidulans)	ANIG, ANID	An02g12420	47150
r88	: THF + ATP + GLU \Rightarrow ADP + PI + THFG	6.3.2.17	Tetrahydrofolylpolyglutamate synthase	Lewandowska et al. (1996, A. nidulans)	ANID	An02g02950; An04g01120; An04g02490; An04g09750	174911; 50605; 54580; 122883
Folate one-carbon pool							
r89	: ATPm + FORM + THFm \Rightarrow ADPm + PIm + FTHFm	6.3.4.3	Formate-dihydrofolate ligase Formyltetrahydrofolate synthetase, FTHFS (Trifunctional)	Cossins and Chen (1997); Kanehisa et al. (2002) Cossins and Chen (1997, Inferred)	ANID	An02g12420	47150
r90	: FTHFm \rightleftharpoons METHFm + H2Om	3.5.4.9	Methenyltetrahydrofolate cyclohydrolase (Trifunctional)	Cossins and Chen (1997, Inferred)	ANID	An02g12420	47150
r91	: METHFm + NADPHm + Hm \rightleftharpoons MET-THFm + NADPm	1.5.1.5	Methylenetetrahydrofolate dehydrogenase (NADP+)(Trifunctional)	Cossins and Chen (1997, Inferred)	ANID	An02g12420	47150
r92	: METTHFm + NADPHm + Hm \Rightarrow METHFm + NADPm	1.5.1.20	Methylenetetrahydrofolate reductase (NADPH)		ANID	An02g03270	55539
r93	: METTHF + NAD \Rightarrow METHF + NADH	1.5.1.15	Methylenetetrahydrofolate dehydrogenase (NAD+)	Lewandowska et al. (1996, A. nidulans)	ANID	An16g07400	214561
r94	: METHF + H2O \rightleftharpoons FTHF	3.5.4.9	Methenyltetrahydrofolate cyclohydrolase		ANID	An02g12420	47150
r95	: FTHF + H2O \Rightarrow FOR + THF	3.5.1.10	5-formyltetrahydrofolate deformylase		ANEW	An01g11650	196101
r96	: METTHF + NADPH \Rightarrow MTHF + NADP	1.5.1.20	Methylenetetrahydrofolate reductase (NADPH)	Balinska and Paszewski (1979, A. nidulans)	ANIG	An09g05860	50057
Coenzyme A and pantothenate biosynthesis							
r97	: OIVAlm + METTHF + THF	2.1.2.11	Ketopantoate hydroxymethyl transferase		ANID		
r98	: AKP + NADPH \Rightarrow NADP + PANT	1.1.1.169	Ketopantoate reductase (2-dehydropantoate 2-reductase)		ANID	An09g01130; An18g01140; An11g09950	56955; 42642; 178804
r99	: AKPm + NADPHm \Rightarrow NADPm + PANTm	1.1.1.169	Ketopantoate reductase (2-dehydropantoate 2-reductase)		ANID	An09g01130; An11g09950	56955; 178804
r100	: PANT + bALA + ATP \Rightarrow AMP + PPI + PNT0	6.3.2.1	Pantoate-B-alanine ligase	Shimizu et al. (1974)	ANID	An18g01970	49810
r101	: PNT0 + ATP \Rightarrow ADP + 4PPNTO	2.7.1.33	Pantothenate kinase	Shimizu et al. (1974)	ANID	An02g13550	37546
r102	: 4PPNTO + CTP + CYS \Rightarrow CMP + PPI + 4PPNCYS	6.3.2.5	Phosphopantothenate-cysteine ligase	Shimizu et al. (1974)	ANID		
r103	: 4PPNCYS \Rightarrow CO2 + 4PPNTE	4.1.1.36	Phosphopantothenate-cysteine decarboxylase	Shimizu et al. (1974)	ANID		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r104	: 4PPNTE + ATP \Rightarrow PPI + DPCOA	2.7.7.3	Phospho-pantetheine adenyltransferase (Bi- functional with 2.7.1.24)	Shimizu et al. (1974)	ANID		
r105	: DPCOA + ATP \Rightarrow ADP + COA	2.7.1.24	DephosphoCoA kinase (Bifunctional with 2.7.7.3)	Shimizu et al. (1974)	ANID		
Biotin biosynthesis							
r107	: 3 MALCOA + 4 NADPH \Rightarrow 4 NADP + CHCOA + 2 CO ₂ + 2 COA + 2 H ₂ O	6.4.1.2; 6.3.4.1; 4 2.3.1.85;1.1.1	B-ketoacyl-ACP synthase (c10.0), fatty acyl CoA synthase	Parry and Kunitani (1979); Parry and Naidu (1980) Parry and Naidu (1980, Inferred)	ANEW		
r108	: ALA + CHCOA \rightleftharpoons CO ₂ + COA + AONA	2.3.1.47	8-Amino-7-oxononanoate synthase	Parry and Naidu (1980, Inferred)	ANID	An04g01140; An11g05560; An12g00920; An15g01980 An15g01990	190614; 179151; 189889; 200589 48688
r109	: AONA + SAM \rightleftharpoons DAONA + SAMOB	2.6.1.62	adenosylmethionine-8- amino-7-oxononanoate aminotransferase	Parry and Naidu (1980, Inferred)	ANEW		
r110	: DAONA + ATP + CO ₂ \rightleftharpoons ADP + PI + DTB	6.3.3.3	dethiobiotin synthetase	Parry and Naidu (1980, Inferred)	ANEW		
r111	: DTB + S \rightleftharpoons BT	2.8.1.6	Biotin synthase	Tepper et al. (1966); Parry and Kunitani (1979); Parry and Naidu (1980)	ANID	An15g02000	51633
OTHER CARBOHYDRATES, ALCOHOLS AND ORGANIC ACIDS							
C2 METABOLISM							
Acetate/Acetaldehyde/Ethanol metabolism							
r113	: ETH + NAD \rightleftharpoons ACAL + NADH	1.1.1.1	Alcohol (adhA)	Martinelli and Kinghorn (1994) Martinelli and Kinghorn (1994)	ANIG, ANID	An12g09810; An17g01530; An01g12170; An01g14590; An02g02060; An02g02870; An03g01350; An04g02690; An08g09750; An09g03140; An11g04150; An11g04290; An12g09950; An13g00950; An13g03330; An14g02160; An14g07180; An16g00010; An16g00400; An16g06240	46038; 204476; 205557; 170152; 206534; 174157; 194416; 190222; 177276; 43351; 179042; 39027; 195091; 44729; 134944; N/A; 42017; 41439; 41421; 40925
r114	: ETH + NADP \rightleftharpoons ACAL + NADPH	1.1.1.2	Alcohol dehydrogenase (Catalysed by Glycerol de- hydrogenase II (NADP+) EC 1.1.1.72)	David et al. (2003)	ANIG	An05g02070; An10g00010; An16g02510	190030; N/A; 184073

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r115	: ACAL + NAD + H ₂ O \Rightarrow AC + NADH	1.2.1.3	Aldehyde dehydrogenase (NAD+) (aldA)	O'Connell and Kelly (1988, 1989, 1992); Martinelli and Kinghorn (1994)	ANIG, ANID	An04g03400; An01g15170; N/A; An08g07290; An08g10820; An10g00850; An15g05890; An18g04130	57028; N/A; 55742; 37719; 57243; 40734; 187856
r116	: AC + COA + ATP \Rightarrow AMP + PPI + ACCOA	6.2.1.1	Acetyl-CoA synthase (acuA)	Sealy-Lewis and Fairhurst (1998)	ANIG, ANID	An04g05620	214348
r117	: ACCOA + H ₂ O \Rightarrow COA + AC	3.1.2.1	Acetyl-CoA hydrolase	Ramakrishnan and Raina (1958); Ramakrishnan et al. (1959)	ANIG, ANID	An16g07110	214587
r118	: ETHm + NADm \rightleftharpoons ACALm + NADHm	1.1.1.1	Alcohol dehydrogenase		ANID	An12g09810; An17g01530; An01g12170; An01g14590; An02g02060; An02g02870; An03g01350; An04g02690; An08g09750; An09g03140; An11g04150; An11g04290; An12g09950; An13g00950; An13g03330; An14g02160; N/A; An14g07180; An16g00010; An16g00400; An16g06240	46038; 204476; 205557; 170152; 206534; 174157; 194416; 190222; 177276; 43351; 179042; 39027; 195091; 44729; 134944; N/A; 42017; 41439; 41421; 40925
r119	: ACALm + NADm + H ₂ Om \Rightarrow ACm + NADHm	1.2.1.3	Aldehyde dehydrogenase (NAD+) (adhA)		ANID	An04g03400; An01g15170; N/A; An08g07290; An08g10820; An10g00850; An15g05890; An18g04130	57028; N/A; 55742; 37719; 57243; 40734; 187856
r120	: ACm + COAm + ATPm \Rightarrow AMPm + PPI _m + ACCOAm	6.2.1.1	Acetyl-CoA synthase	Pel et al. (2007)	ANIG, ANID	An05g00390	185892
r121	: ACCOAm + H ₂ Om \Rightarrow COAm + ACm	3.1.2.1	Acetyl-CoA hydrolase	David et al. (2003)	ANIG, ANID	An16g07110	214587
C3 METABOLISM							
Glycerol metabolism							
r122	: GL + NAD \Rightarrow GLYN + NADH	1.1.1.6	Glycerol dehydrogenase	Martinelli and Kinghorn (1994)	ANIG, ANID	An01g06970	196413
r123	: GL + O ₂ \Rightarrow GLYL + H ₂ O ₂	1.1.3.13	Alcohol oxidase		ANID	An15g02200; An18g05480	56311; 42956
r124	: GLYL + NADPH \Rightarrow GL + NADP	1.1.1.72	Glycerol dehydrogenase	Jennings (1984); Schuurink et al. (1990); Martinelli and Kinghorn (1994)	ANIG, ANID	An01g06970	196413

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r126	: GL + O ₂ ⇒ GLYN + H ₂ O ₂	1.1.3.13	Alcohol oxidase		ANID	An15g02200; An18g05480	56311; 42956
r127	: GL + NADP ⇒ GLYN + NADPH	1.1.1.72	Glycerol dehydrogenase (NADP+)	Baliga et al. (1964); Schuurink et al. (1990)	ANEW	An01g06970	196413
r128	: GL + ATP ⇒ GL3P + ADP	2.7.1.30	Glycerol kinase	Witteveen et al. (1990); Witteveen and Visser (1995)	ANIG, ANID	An04g04890	45434
r129	: GL3P + FADm ⇒ T3P2 + FADH2m	1.1.99.5	Glycerol 3-phosphate dehydrogenase (FAD dependent) (FAD-dependent sn-glycerol-3-phosphate dehydrogenase)	Witteveen et al. (1990)	ANIG, ANID	An08g00210	55910
r130	: GLYN + ATP ⇒ T3P2 + ADP	2.7.1.29	Glycerone kinase	Witteveen et al. (1990)	ANIG, ANID	An14g06500	56628
r131	: T3P2 + NADH ⇒ GL3P + NAD	1.1.1.8	Glycerol 3-phosphate dehydrogenase (NAD+ dependent)	David et al. (2003)	ANIG, ANID	An15g07390	48886
r132	: GL3P + H ₂ O ⇒ GL + PI	3.1.3.21	Glycerol 3-phosphate phosphatase	David et al. (2003)	ANIG, ANID	An08g02530	176581
Glycerate metabolism r133	: G + NADP ⇌ 3HPYR + NADPH	1.1.1.29	glycerate dehydrogenase	Behal and Hamilton (1962); Behal (1967)	ANEW	An08g06710	207936
L-lactate r183	: LLAC + NAD ⇒ PYR + NADH	1.1.1.27	L-Lactate dehydrogenase	David et al. (2003)	ANIG, ANID	An04g08220	137087
C4 METABOLISM							
Tartrate metabolism r134	: TAR + NAD ⇌ OXGLY + NADH	1.1.1.93	Tartrate dehydrogenase	David et al. (2003)	ANIG, ANID	An01g03030	171830
D-Erythrose/Erythritol metabolism r135	: TAR ⇌ OA + H ₂ O	4.2.1.32	Tartrate dehydratase	Patil and Ramakrishnan (1966)	ANEW		
r136	: E + NADPH ⇒ EOL + NADP	1.1.1.72	Glycerol dehydrogenase	Schuurink et al. (1990)	ANIG, ANID	An01g06970	196413
r138	: E + ATP ⇒ E4P + ADP		Erythrulose kinase	David et al. (2003), Hondmann (1994, A. nidulans)	ANIG		
r139	: E4P + H ₂ O ⇒ PI + E		Erythrose 4-phosphate phosphatase	David et al. (2003), Hondmann (1994, A. nidulans)	ANIG		
r140	: EOL + NAD ⇒ E + NADH		Erythrose reductase	David et al. (2003), Hondmann (1994, A. nidulans)	ANIG		
r141	: EOL + NAD ⇒ EU + NADH		Erythrose dehydrogenase	David et al. (2003), Hondmann (1994, A. nidulans)	ANIG		
r142	: EU + ATP ⇒ EU1P + ADP		Erythrulose kinase	David et al. (2003), Hondmann (1994, A. nidulans)	ANIG		
r143	: EU1P ⇒ T3P1 + FALD	4.1.2.2	Ketotetrose-phosphate aldolase	David et al. (2003), Hondmann (1994, A. nidulans)	ANIG		
C5 METABOLISM							
L-Arabinose/Arabitol metabolism r144	: LAOL + NADP ⇌ LARAB + NADPH	1.1.1.21	L-arabinose reductase	Witteveen et al. (1989) Witteveen et al. (1989); Martinelli and Kinghorn (1994); van Kuyk et al. (2001); de Groot et al. (2003); de Groot et al. (2005)	ANIG	An01g14880; An16g01720	46249; 53686

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r145	: LAOL + NAD \rightleftharpoons LXUL + NADH	1.1.1.12	L-Arabitol dehydrogenase	Witteveen et al. (1989); Martinelli and Kinghorn (1994); vanKuyk et al. (2001); de Groot et al. (2003); de Groot et al. (2005)	ANIG, ANID	An01g10920	46405
r146	: LXUL + NADPH \rightleftharpoons XOL + NADP	1.1.1.10	L-Xylulose reductase	Martinelli and Kinghorn (1994); vanKuyk et al. (2001); de Groot et al. (2003); Witteveen et al. (1989, 1994)	ANIG, ANID	An11g03260	47908
D-Xylose/D,L-Xylulose/Xylitol metabolism							
r147	: XYL + NADPH \rightleftharpoons XOL + NADP	1.1.1.21	D-Xylose reductase (xylA) (xylitol dehydrogenase)	Witteveen et al. (1989); Martinelli and Kinghorn (1994); Witteveen et al. (1994); vanKuyk et al. (2001); Hasper et al. (2002); de Groot et al. (2003); de Groot et al. (2005)	ANIG, ANID	An01g03740	51997
r148	: XOL + NADP \Rightarrow XUL + NADPH	1.1.1.10	xylitol dehydrogenase	Witteveen et al. (1994); de Groot et al. (2003)	ANIG, ANID	An11g03260	47908
r149	: XOL + NAD \Rightarrow XUL + NADH	1.1.1.9	D-Xylulose reductase (xylitol dehydrogenase)	Witteveen et al. (1989); Martinelli and Kinghorn (1994); Witteveen et al. (1994); de Groot et al. (2003); vanKuyk et al. (2001)	ANIG, ANID	An05g02260; An07g01320; An08g09380; An12g00030; An15g04610	212968; N/A; 37988; 203198; 48775
D-arabinose metabolism							
r150	: ARABLAC + NADPH \rightleftharpoons ARAB + NADP	1.1.1.117	D-Arabinose dehydrogenase [NAD(P)+]	Witteveen et al. (1989)	ANID	An01g06970	196413
r151	: ARAB + NADPH \rightleftharpoons AOL + NADP	1.1.1.21	Aldehyde reductase	Witteveen et al. (1989, 1994)	ANIG	An01g14880; An16g01720	46249; 53686
r152	: AOL + NAD \Rightarrow XUL + NADH	1.1.1.11	D-arabitol dehydrogenase	Witteveen et al. (1989, 1994); vanKuyk et al. (2001)	ANIG, ANID	An04g09410	51398
r153	: AOL + NADP \Rightarrow XUL + NADPH	1.1.1.11	D-arabitol dehydrogenase	Witteveen et al. (1989); vanKuyk et al. (2001)	ANIG, ANID	An04g09410	51398
Xylulose							
r154	: ATP + XUL \Rightarrow ADP + XUL5P	2.7.1.17	Xylulose kinase	Witteveen et al. (1989, 1994); Martinelli and Kinghorn (1994); vanKuyk et al. (2001); de Groot et al. (2003)	ANIG, ANID	An07g03140	209771
r155	: XUL5P + FALD \rightleftharpoons T3P1 + GLYN	2.2.1.3	Dihydroxyacetone synthase	Lusta et al. (1991, A. terreus)	ANID	An14g03500	184680
Ribose							
r156	: ATP + RIB \Rightarrow ADP + R5P	2.7.1.15	Ribokinase	David et al. (2003)	ANIG, ANID	An15g07500	40855
r157	: R5P \rightleftharpoons R1P	5.4.2.2	Phosphoglucumutase	Khanna and Tewari (1963)	ANID	An02g07650	55590
r158	: RIB + NADPH \rightleftharpoons RIBOL + NADP	1.1.1.21	D-Ribose reductase	Witteveen et al. (1989)	ANIG	An01g14880; An16g01720	46249; 53686
r159	: RIBOL + NAD \Rightarrow RL + NADH	1.1.1.56	Ribitol dehydrogenase	Witteveen et al. (1989)	ANIG	An13g02310; An18g00010	192184; 42574
r160	: RIBOL + NADP \Rightarrow RL + NADPH	1.1.1.56	Ribitol dehydrogenase	Witteveen et al. (1989)	ANIG	An13g02310; An18g00010	192184; 42574
Ribulose							
r161	: ATP + RL \Rightarrow ADP + RL5P	2.7.1.47	Ribulokinase	Hondmann (1994, A. nidulans), Morozova et al. (2002, Inferred)	ANID	An14g00160	53716
r162	: RL + NADPH \Rightarrow AOL + NADP	No EC	ribulose reductase		ANEW		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
C6 METABOLISM							
Gluconic acid/Gluconate metabolism							
r163	$\text{bDGLCe} + \text{O}_2\text{e} \rightleftharpoons \text{GLCN15LACe} + \text{H}_2\text{O}_2\text{e}$	1.1.3.4	Glucose oxidase (goxC)	Muller (1977); Frederick et al. (1990); Martinelli and Kinghorn (1994); Witteveen et al. (1992); Kim et al. (2001); Leskovac et al. (2005)	ANIG, ANID	An12g03430; An12g03440; An01g14740; An07g00450	50376; 50376; 55227; 40254
r164	$\text{bDGLC} + \text{O}_2 \rightleftharpoons \text{GLCN15LAC} + \text{H}_2\text{O}_2$	1.1.3.4	Glucose oxidase (god)	Muller (1977); Frederick et al. (1990); Martinelli and Kinghorn (1994); Witteveen et al. (1992); Kim et al. (2001); Leskovac et al. (2005); Bhatti et al. (2006)	ANID	An12g03430; An12g03440; An01g14740; An07g00450	50376; 50376; 55227; 40254
r165	$\text{GLCN15LACe} + \text{H}_2\text{Oe} \Rightarrow \text{GLCNTe}$	3.1.1.17	Gluconolactonase (lactonase)	Witteveen et al. (1992, 1993); Ogawa et al. (2002)	ANIG, ANID	An12g01570	N/A
NE6	$\text{GLCN15LAC} + \text{H}_2\text{O} \Rightarrow \text{GLCNT}$	No EC	Spontaneous reaction or catalyzed by glucose oxidase	Bhatti et al. (2006)	ANIG, ANID		
r166	$\text{D6PGC} + \text{H}_2\text{O} \Rightarrow \text{GLCNT} + \text{PI}$	3.1.3.1	Alkaline phosphatase	Ramaswamy and Bheemeswar (1976); Muller (1977); Rokosu and Uadia (1980); Karaffa et al. (2001)	ANIG, ANID	An07g07520; An18g04040	209506; 42852
r167	$\text{D6PGC} + \text{H}_2\text{O} \Rightarrow \text{GLCNT} + \text{PI}$	3.1.3.2	Acid phosphatase (aphA)	Muller (1977); Wyss et al. (1998)	ANIG, ANID	An14g02650; An08g09850; An09g00310; An12g10630; An13g01750; An14g01550; An16g01730; An16g09130; An18g04140	49304; 52587; 43568; 51468; 57215; 56545; 183355; 193642; 42861
r169	$\text{GLCNT} + \text{ATP} \Rightarrow \text{D6PGC} + \text{ADP}$	2.7.1.12	Gluconokinase	Lakshminarayana et al. (1969b); Muller (1986)	ANIG	An01g07300; An01g14850	127436; 170633
r168	$\text{D6PGC} + \text{NADP} \rightleftharpoons \text{D6PDGC} + \text{NADPH}$	1.1.1.43	6-phosphogluconate dehydrogenase	Lakshminarayana et al. (1969b,c); Muller (1986)	ANEW	An11g02040	199133
r170	$\text{GLCNT} \rightleftharpoons \text{KDDGC} + \text{H}_2\text{O}$	4.2.1.39	Gluconate dehydratase	Elzainy et al. (1973); Kersters and de Ley (1975); Martinelli and Kinghorn (1994)	ANIG		
r171	$\text{KDDGC} \rightleftharpoons \text{PYR} + \text{GLXAL}$	4.1.2.14	2-keto-3-deoxygluconate aldolase	Elzainy et al. (1973); Allam et al. (1975); Martinelli and Kinghorn (1994)	ANIG		
Galactose/Galactitol metabolism							
r172	$\text{GALOL} + \text{NADP} \rightleftharpoons \text{GLAC} + \text{NADPH}$	1.1.1.21	Aldehyde reductase (Polyol dehydrogenase (NADP+))	Martinelli and Kinghorn (1994)	ANIG, ANID	An01g14880; An16g01720	46249; 53686
r173	$\text{ATP} + \text{GLAC} \Rightarrow \text{ADP} + \text{GALIP}$	2.7.1.6	Galactokinase	Martinelli and Kinghorn (1994)	ANIG, ANID	An16g04160	56431
r174	$\text{UTP} + \text{GALIP} \rightleftharpoons \text{PPI} + \text{UDPGAL}$	2.7.7.10	UTP-hexose-1-phosphate uridylyltransferase (UDP-galactose pyrophosphorylase)	Martinelli and Kinghorn (1994)	ANIG, ANID	An02g03590	174413

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r175	: UDPGAL \rightleftharpoons UDPG	5.1.3.2	UDPglucose 4-epimerase	Martinelli and Kinghorn (1994)	ANIG, ANID	An01g12220; An01g11440; An02g08750; An12g04260; An12g10410; An14g03820 An12g00820	55278; 35645; 175089; 135865; 45989; 56583 212837
r176	: UTP + G1P \Rightarrow PPI + UDPG	2.7.7.9	UTP-glucose-1-phosphate uridylyltransferase (UDP glucose pyrophosphory- lase)	Martinelli and Kinghorn (1994)	ANIG, ANID		
r177	: G6P \rightleftharpoons G1P	5.4.2.2	Phosphoglucomutase	Khanna and Tewari (1963); Mar- tinelli and Kinghorn (1994)	ANIG, ANID	An02g07650	55590
r178	: UDPG + GAL1P \rightleftharpoons G1P + UDPGAL	2.7.7.12	UDP-glucose-hexose-1- phosphate uridylyltrans- ferase		ANID	An02g03590	174413
Galactonic acid/Galactonate metabolism							
r179	: GLAC + NAD \rightleftharpoons GALN14LAC + NADH	1.1.1.48	Galactose dehydrogenase	David et al. (2003)	ANIG, ANID		
r180	: GALN14LAC + H ₂ O \rightleftharpoons GALNT	3.1.1.25	1,4-Lactonase (gamma- Lactonase)	David et al. (2003)	ANIG	An05g02030; An16g06620 N/A	212961; N/A
r181	: GALNT \rightleftharpoons 2D3DGALT + H ₂ O	4.2.1.6	Galactonate dehydratase	David et al. (2003), Elshafei et al. (1995, A. terreus)	ANIG, ANID	An04g02760	50500
r182	: 2D3DGALT \rightleftharpoons PYR + GLYAL	No EC	2-Dehydro-3-deoxy-D- galactonate aldolase	David et al. (2003), Elshafei et al. (1995, A. terreus)	ANIG		
Galacturonate degradation							
r1215	: ATP + GALUNT \rightleftharpoons GALUNTP + ADP	2.7.1.44	Galacturonokinase	Witteveen et al. (1990, Inferred)	ANEW		
r1216	: GALUNTP + UTP \rightleftharpoons UDPGALU + PPI	No EC	Galacturonate-1- phosphate uridylyl trans- ferase		ANEW		
r1217	: UDPGALU + 2 NADH \rightleftharpoons UDPGAL + 2 NAD + H ₂ O	1.1.1.-	UDP-D-galactose dehydro- genase		ANEW		
Rhamnose metabolism							
r1218	: RHA \rightleftharpoons RHAMN	5.3.1.14	L-Rhamnose isomerase	de Vries et al. (2002); Fries and Kallstromer (1965)	ANEW		
r1219	: ATP + RHAMN \rightleftharpoons ADP + RHAMNP	2.7.1.5	L-Rhamnulose kinase	Fries and Kallstromer (1965, In- ferred)	ANEW		
r1220	: RHAMNP \rightleftharpoons T3P2 + LACAL	4.1.2.19	Rhamnulose phosphate al- dolase	Fries and Kallstromer (1965, In- ferred)	ANEW		
Mannose/Mannitol, Fructose and Sorbose/Sorbitol metabolism							
r184	: ATP + MAN \Rightarrow ADP + MAN6P	2.7.1.1	Hexokinase (hxx) (man- nokinase)	Martinelli and Kinghorn (1994); Panneman et al. (1998)	ANIG, ANID	An02g14380; An06g00380; An13g00510 50817	55651; 134301; 50817
r185	: MAN6P \rightleftharpoons F6P	5.3.1.8	Mannose-6-phosphate iso- merase	Martinelli and Kinghorn (1994)	ANIG, ANID	An08g06350; An04g03200 44098	55763; 44098
r186	: ATP + FRU \Rightarrow ADP + F6P	2.7.1.1	Hexokinase (hxx)	Martinelli and Kinghorn (1994); Panneman et al. (1998); Karafa et al. (2001)	ANIG, ANID	An02g14380; An06g00380; An13g00510 50817	55651; 134301; 50817
r187	: F6P + NADH \rightleftharpoons MNT1P + NAD	1.1.1.17	Mannitol-1-phosphate 5-dehydrogenase	Kiser and Niehaus Jr. (1981); Mar- tinelli and Kinghorn (1994)	ANIG, ANID	An02g05830	55560

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r188	$\text{MNTIP} + \text{H}_2\text{O} \Rightarrow \text{MNT} + \text{PI}$	3.1.3.22	Mannitol-1-phosphatase (Mannitol-1-phosphate phosphatase)	Hult et al. (1980)	ANIG, ANID		
r189	$\text{MNT} + \text{NADP} \rightleftharpoons \text{FRU} + \text{NADPH}$	1.1.1.138	Mannitol 2-dehydrogenase (NADP+)	Martinelli and Kinghorn (1994)	ANIG, ANID, ANEW	An06g00750	177668
r190	$\text{MNT} + \text{ATP} \Rightarrow \text{MNTIP} + \text{ADP}$	3.1.3.22	Mannitol kinase	Martinelli and Kinghorn (1994)	ANID	An07g06780; An18g06500	209558; 132771
r191	$\text{MANIP} \rightleftharpoons \text{MAN6P}$	5.4.2.8	Phosphomannomutase		ANID	An11g02380; An04g04990	55950; 204833
r192	$\text{GTP} + \text{MANIP} \Rightarrow \text{PPI} + \text{GDPMAN}$	2.7.7.13	Mannose-1-phosphate guanylyltransferase		ANID	An07g02100; An15g00200	128609; 209963
r193	$\text{ATP} + \text{F6P} \Rightarrow \text{ADP} + \text{F26P}$	2.7.1.105	6-Phosphofructo-2-kinase (Phosphofructokinase 2)	Kubicek-Pranz et al. (1990); Harnsen et al. (1992); Karaffa et al. (2001)	ANIG, ANID		
r194	$\text{F26P} + \text{H}_2\text{O} \Rightarrow \text{F6P} + \text{PI}$	3.1.3.46	D-Fructose-2,6-bisphosphate 2-phosphohydrolase		ANID	An07g02100; An15g00200	128609; 209963
r195	$\text{IDOL} + \text{NAD} \Rightarrow \text{SOR} + \text{NADH}$	1.1.1.14	L-Iditol 2-dehydrogenase (NAD-dependent sorbitol dehydrogenase)	Desai et al. (1969c)	ANID	An09g03900; An12g00030; An16g01700; An16g01710	188914; 203198; 183939; 183900
r196	$\text{SOR} + \text{NADH} \Rightarrow \text{SOT} + \text{NAD}$	1.1.99.21	D-Sorbitol dehydrogenase (acceptor)	Desai et al. (1967)	ANIG, ANID	An01g03480; An01g10920; An03g05190; An14g03510	206203; 46405; 50731; 185262
r197	$\text{SOT} + \text{NAD} \rightleftharpoons \text{FRU} + \text{NADH}$	1.1.1.19	Sorbitol (glucitol) dehydrogenase (NAD+)	Desai et al. (1967, 1969b,c); Witteveen et al. (1994)	ANIG, ANID	An05g02260; An08g09380; An15g04610	212968; 37988; 48775
DISACCHARIDES METABOLISM							
Trehalose Biosynthesis							
r198	$\text{UDPG} + \text{G6P} \Rightarrow \text{UDP} + \text{TRE6P}$	2.4.1.15	Alpha, alpha-trehalose-phosphate synthase (UDP-forming) 1 (tpsA, tpsB)	Wolschek and Kubicek (1997); Karaffa et al. (2001)	ANIG, ANID	An07g08710; An08g10510; An14g02180	55704; 211004
Hydrolysis							
r199	$\text{TRE6P} + \text{H}_2\text{O} \Rightarrow \text{TRE} + \text{PI}$	3.1.3.12	Trehalose-phosphatase	Arisan-Atac et al. (1996)	ANIG, ANID	An11g10990	119446
r200	$\text{TRE} + \text{H}_2\text{O} \Rightarrow 2 \text{ DGLC}$	3.2.1.28	Alpha, alpha-trehalase	David et al. (2003), d'Enfert and Fontaine (1997, A. nidulans)	ANIG, ANID	An01g01540	52061
Maltose							
r201	$\text{MLT} + \text{H}_2\text{O} \Rightarrow 2 \text{ GLC}$	3.2.1.20	Alpha-glucosidase (Maltase) (agIA)	Smirnov and Chubova (1965); Rudick et al. (1979); den Herder et al. (1992); Martinelli and Kinghorn (1994)	ANIG, ANID	An13g03710; An01g04880; An07g00350; An09g05880	50927; 55419; 40261; 128654
r202	$\text{MLTe} + \text{H}_2\text{Oe} \Rightarrow 2 \text{ GLCe}$	3.2.1.20	Alpha-glucosidase (Maltase) (agIA/agIU)	Smirnov and Chubova (1965); Rudick et al. (1979); den Herder et al. (1992); Martinelli and Kinghorn (1994)	ANIG, ANID	An04g06920	214233
Lactose							
r203	$\text{LACT} + \text{H}_2\text{O} \Rightarrow \text{GLC} + \text{GLAC}$	3.2.1.23	Beta-galactosidase	Martinelli and Kinghorn (1994)	ANID	An01g10350; An06g00290	46429; 177434

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r204	: LACTe + H ₂ Oe \Rightarrow GLCe + GLACe	3.2.1.23	Beta-galactosidase (lacA)	Widmer and Leuba (1979); Sykes et al. (1983); Martinelli and Kinghorn (1994); Manzanares et al. (1998); de Vries et al. (1999)	ANIG, ANID	An01g12150; An07g04420; An14g05820	51764; 180727; 41910
Melibiase							
r205	: MELIe + H ₂ Oe \Rightarrow GLCe + GLACe	3.2.1.22	Alpha-galactosidase (melbiase) (agIA, agC)	Manzanares et al. (1998); de Vries and Visser (2001); Wallis et al. (2001)	ANID	An09g00260; An09g00270; An01g01320; An02g11150; An06g00170; An11g06330; An14g01800	212736; 212736; 172232; 207264; 37736; 39180; 185285
Stachyose / Raffinose / Sucrose degradation							
r228	: STACe + H ₂ Oe \rightleftharpoons RAFFe + GLACe	3.2.1.22	alpha-galactosidase	Knap et al. (1994); Manzanares et al. (1998); de Vries and Visser (2001)	ANEW	An09g00260; An09g00270; An01g01320; An02g11150; An06g00170; An11g06330; An14g01800	212736; 212736; 172232; 207264; 37736; 39180; 185285
r229	: RAFFe + H ₂ Oe \rightleftharpoons SUCe + GLACe	3.2.1.22	alpha-galactosidase	Adva and Elbein (1977); Boddy et al. (1993); Knap et al. (1994); Manzanares et al. (1998); Wallis et al. (2001)	ANEW	An09g00260; An09g00270; An01g01320; An02g11150; An06g00170; An11g06330; An14g01800	212736; 212736; 172232; 207264; 37736; 39180; 185285
r230	: SUCe + H ₂ Oe \Rightarrow FRUe + GLCe	3.2.1.26	Invertase (sucI)	Schreier-Kunar et al. (1989); Berges et al. (1993); Boddy et al. (1993); Martinelli and Kinghorn (1994); L'Hocine et al. (2000); Yanai et al. (2001)	ANIG	An08g11070; An15g00320	198063; N/A
METABOLISM OF AROMATICS							
Phenylalanine/phenylacetate degradation							
r386	: PHPYR \Rightarrow PHAL + CO ₂			Kishore et al. (1976) Kishore et al. (1976)	ANEW		
r387	: PHAL + NAD + H ₂ O \rightleftharpoons PHAC + NADH	4.1.1.43	Phenylpyruvate decarboxylase	Kishore et al. (1976)	ANEW		
r388	: PHAC + O ₂ + NADP \Rightarrow 2HPAC + H ₂ O + NADP	1.2.1.39	Phenylacetaldehyde dehydrogenase	Kishore et al. (1976, Inferred)	ANEW	An02g04110	175251
r389	: 2HPAC + O ₂ + NADP \Rightarrow HOMOG + H ₂ O + NADP	No EC	Phenylacetate hydroxylase	Kishore et al. (1976)	ANEW		
r390	: HOMOG + O ₂ \rightleftharpoons MACAC	1.13.11.5	Homogentisate oxygenase	Kishore et al. (1976); Sugumaran and Vaidyanathan (1978)	ANID	An11g00430	178499
r391	: MACAC \rightleftharpoons FUACAC	5.2.1.2	Maleylacetate isomerase	Sugumaran et al. (1973)	ANID	An07g06280	180792
r392	: FUACAC + H ₂ O \Rightarrow FUM + ACTAC	3.7.1.2	Fumarylacetoacetase	Sugumaran et al. (1973)	ANID	An02g10000; An04g04150	37286; N/A
r393	: PHAC + O ₂ + NADP \Rightarrow 4HPAC + H ₂ O + NADP	No EC	Phenylacetate hydroxylase	Kishore et al. (1976)	ANEW		
r394	: 4HPAC + NADP + O ₂ \rightleftharpoons 4HMAND + H ₂ O + NADP	No EC	4-hydroxyphenylacetic acid monooxygenase	Kishore et al. (1976, Inferred)	ANEW		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r395	4HMAND + NADP \Rightarrow 4HBFOR + NADPH	No EC	4-hydroxymandelate dehydrogenase	Kishore et al. (1976)	ANW		
r396	4HMAND + NAD \Rightarrow 4HBFOR + NADH	No EC	4-hydroxymandelate dehydrogenase	Kishore et al. (1976)	ANW		
r397	4HBFOR \Rightarrow 4HBAL + CO ₂	No EC	4-hydroxybenzoylformic acid decarboxylase	Kishore et al. (1976)	ANW		
r398	4HBAL + NAD + H ₂ O \rightleftharpoons 4HBA + NADH	No EC	4-hydroxybenzaldehyde dehydrogenase	Kishore et al. (1976)	ANW		
r399	4HBA + NADPH + O ₂ \rightleftharpoons PCC + NADP + H ₂ O	1.14.13.33	hydroxylase	Kishore et al. (1976); Shailubhai et al. (1982); Boschloo et al. (1990); Martinelli and Kinghorn (1994)	ANW		
Coumarate degradation							
r1192	COUM + H ₂ O \rightleftharpoons AC + 4HBAL	No EC	Inferred reaction from Milstein et al. (1988)	Milstein et al. (1988)	ANW		
Dimethylterephthalate degradation							
r1193	DMT + H ₂ O \rightleftharpoons MTPPTH + METHOL		Dimethylterephthalate esterase	Ganji et al. (1995)	ANW		
r1194	MTPPTH + H ₂ O \rightleftharpoons TPPTH + METHOL		Dimethylterephthalate esterase	Ganji et al. (1995)	ANW		
r1195	TPPTH + NADPH + O ₂ \rightleftharpoons DHCHDDC + NADP	1.14.12.15	1,4-dicarboxybenzoate 1,2-dioxygenase	Kanehisa et al. (2002); Ganji et al. (1995, Inferred)	ANW		
r1196	DHCHDDC + NADP \rightleftharpoons PCC + CO ₂ + NADPH	1.3.1.61	cis-4,5-dihydroxycyclohexa-1(6),2-diene-1,4-dicarboxylate:NADP+oxidoreductase (decarboxylating)	Kanehisa et al. (2002); Ganji et al. (1995, Inferred)	ANW		
3-hydroxybenzoate degradation							
r1210	3HBA + O ₂ + NADPH \rightleftharpoons PCC + NADP + H ₂ O	1.14.13.23	3-hydroxybenzoate hydroxylase	Premkumar et al. (1969); Kumar et al. (1973); Sugumaran et al. (1973); Faber et al. (2001)	ANW	An02g13270; An01g08690; An01g15110; An04g08410; An08g06250; An09g01850; An09g03500; An12g04510	37516; 172555; 171519; 51444; 175996; 43449; 212897; 42416
Ferulic acid degradation							
r1268	FER + ATP + COA \Rightarrow AMP + PPI + FERCOA	6.2.1.12	Ferulate:CoA ligase (AMP-forming)	Milstein et al. (1988, Inferred)	ANW	An04g04330; An08g06100; An09g01820; An12g02430; An14g05630	44006; 38230; 188806; 43775; 184942
r1269	FERCOA + H ₂ O \rightleftharpoons FERHCOA	4.2.1.101	trans-feruloyl-CoA hydratase	Milstein et al. (1988, Inferred)	ANW		
r1270	FERHCOA \rightleftharpoons VANIN + ACCOA	4.1.2.41	vanillin synthase	Milstein et al. (1988, Inferred)	ANW		
r1271	VANIN + NAD + H ₂ O \rightleftharpoons VAN + NADH	1.2.1.67	vanillin dehydrogenase	Milstein et al. (1988, Inferred)	ANW		
Vanillate degradation							
r1200	VAN \Rightarrow GUA + CO ₂	No EC	vanillate decarboxylase	Milstein et al. (1988); Lesage-Meessen et al. (1996)	ANW		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1201	GUA + NADPH + O ₂ ⇌ CCL + NADP + H ₂ O + FALD	2.1.1.6	S-adenosyl-L-methionine:catechol O-methyltransferase	Milstein et al. (1988, Inferred)	ANEW	An04g04700; An15g02990; An17g00200	190631; 40535; N/A
Benzonitrile degradation							
r958	BN + 2 H ₂ O ⇌ BA + NH ₃	3.5.5.1	benzonitrilase	Snajdrova et al. (2004)	ANEW	An16g00550; An01g07510; An01g12090; An06g01960; An08g08940; N/A; An08g10150; An12g01260; An16g06210; An18g01740	41410; 35944; 170270; 175987; N/A; 52578; 141873; 40928; 211815
r959	BA + NADPH + O ₂ ⇒ 4HBA + NADP + H ₂ O	1.14.13.12	benzoate monooxygenase (benzoate-para-hydroxylase bphA)	Reddy and Vaidyanathan (1975); Boschloo et al. (1990); van Gorcom et al. (1990); Boschloo et al. (1991); Faber et al. (2001); Malonek et al. (2004)	ANEW	An02g13270; An01g08690; An01g15110; An04g08410; An08g06250; An09g01850; An09g03500; An12g04510	37516; 172555; 171519; 51444; 175996; 43449; 212597; 42416
Indole degradations							
r1206	IND + O ₂ + NADPH ⇌ 3HIND + H ₂ O + NADP	No EC	indole monooxygenase	Subba Rao et al. (1971); Kamath and Vaidyanathan (1990)	ANEW		
r1207	3HIND + O ₂ ⇌ NFAN	No EC	3-hydroxyindoxyl dioxygenase	Kamath and Vaidyanathan (1990)	ANEW		
r1208	NFAN + H ₂ O ⇌ FOR + AN	3.5.1.9	N-formylanthranilate deformylase	Kamath and Vaidyanathan (1990)	ANEW		
Tannic acid degradation							
r1222	TAN _{Ac} + 10 H ₂ O _e ⇒ 10 345THB _e + GLC _e	3.1.1.20	tannin acyl hydrolase (tannase)	Ramirez-Coronel et al. (2003); Bhardwaj et al. (2003); van Diepeningen et al. (2004)	ANEW	An01g02740; An01g11560; An02g14800; An02g00350; An03g05300; An04g04430; An08g08140; An08g09800; An09g00890; An10g00910; An10g00950; An11g01220; An11g03590; An12g10390; An13g03810; An17g00830	N/A; 35636; 35388; 172914; 44518; 191085; N/A; 175881; 189231; 50972; 50973; 178324; 38960; 51478; 131509; 45118
Tryptophan degradation							
r400	TRP + O ₂ ⇒ FKYN	1.13.11.11	Indoleamine dioxygenases, Tryptophan 2,3-dioxygenase	Subba Rao et al. (1971)	ANID	An04g07210	45277

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r401	: FKYN + H ₂ O ⇒ FOR + KYN	3.5.1.49	Kynurenine formamidase (formamidase)	Subba Rao et al. (1971)	ANID	An07g05830	180458
r402	: KYN + H ₂ O ⇒ ALA + AN	3.7.1.3	Kynureninase	Subba Rao et al. (1971); Shetty and Gaertner (1975)	ANID	An04g07200; An16g04630	45278; 210508
r403	: AN + NADPH + O ₂ ⇌ DHBA + NADP + NH ₃	1.14.13.35	anthranilate monooxygenase (deaminating)	Sreeleela et al. (1969); Subba Rao et al. (1971); Subramanian and Vaidyanathan (1984); Kamath and Vaidyanathan (1990)	ANEW		
r404	: DHBA ⇒ CCL + CO ₂	4.1.1.46	2,3-Dihydroxybenzoate carboxylase (dhbd)	Rao et al. (1967); Subba Rao et al. (1971); Ramachandran et al. (1979); Kamath et al. (1987); Kamath and Vaidyanathan (1990); Santha et al. (1995)	ANEW	An07g02050; An02g05560	209864; 36964
3-Hydroxykynurenine degradation							
r406	: HKYN + H ₂ O ⇒ HAN + ALA	3.7.1.3	Kynureninase	Shetty and Gaertner (1975)	ANEW	An04g07200; An16g04630	45278; 210508
Tyrosine degradation							
r411	: 4HPP + O ₂ ⇒ HOMOGEN + CO ₂	1.13.11.27	4-hydroxyphenylpyruvate dioxygenase	Utkin (1950)	ANEW	An04g01280; An07g01900	190603; 124205
Salicylic acid degradation							
r968	: SALI + NADPH + O ₂ ⇌ CCL + NADP + H ₂ O + CO ₂	1.14.13.1	Salicylate hydroxylase	Krupka et al. (1967); Shailubhai et al. (1982, 1983) Krupka et al. (1967); Shailubhai et al. (1982, 1983)	ANEW	An01g07130; An02g01050; An03g00530; An03g01540; An03g02130; An03g05310; An03g06690; An04g07370; An05g01200; An07g00550; An07g05650; An07g06800; An09g00590; An09g01840; An09g04390; An11g02480; An11g03060; An11g03150; An11g05130	172298; 36659; 45799; 133101; 194221; 191298; 191475; 45265; N/A; 181136; 46219; N/A; 50241; 188800; 189090; 178872; 178362; 38917; 208837
Benzoylamine degradation							
r979	: BAMN + H ₂ O + O ₂ ⇌ BAL + H ₂ O ₂ + NH ₃	1.4.3.6	Amine oxidase (AO-I and AO-II)	Schilling and Lerch (1995a); Fribort et al. (1999)	ANEW	An02g10920; An09g01550; An03g00730; An07g06400; An12g03290; An13g00710; An17g00010	37354; 54408; 45789; 120706; 57198; 204355
Mandelate degradation							
r974	: DMAND + NAD ⇌ NADH + BFOR	DMAN	D-mandelate dehydrogenase	Jamaluddin et al. (1970) Jamaluddin et al. (1970); Ramarayanan and Vaidyanathan (1973)	ANEW ANEW	An03g05150	50728

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r975	: LMAND + NAD \rightleftharpoons NADH + BFOR	LMAN	L-mandelate dehydrogenase	Jamaluddin et al. (1970)	ANEW		
r976	: BFOR \Rightarrow CO2 + BAL	4.1.1.7	benzoylformate decarboxylase	Jamaluddin et al. (1970)	ANEW	An02g05590	52239
r977	: BAL + NAD + H2O \Rightarrow BA + NADH	1.2.1.6	NAD-benzaldehyde dehydrogenase	Raman and Shammugasundaram (1962); Jamaluddin et al. (1970)	ANEW		
r978	: BAL + NADP + H2O \Rightarrow BA + NADPH	1.2.1.7	NADP-benzaldehyde dehydrogenase	Jamaluddin et al. (1970); Kishore et al. (1976)	ANEW		
Resorcinol degradation							
r971	: RES + O2 + NADPH \rightleftharpoons BTOL + NADP + H2O	1.3.1.32	Resorcinol hydroxylase	Shailubhai et al. (1982, 1983)	ANEW		
r972	: BTOL + O2 \rightleftharpoons 2MAC	1.13.11.37	hydroxyquinol dioxygenase	Shailubhai et al. (1982, 1983)	ANEW	An01g12310	46358
Hydroxyquinol pathway							
r973	: 2MAC + NADPH \rightleftharpoons 3OA + NADP	1.3.1.32	maleylacetate reductase	Shailubhai et al. (1982, 1983)	ANEW	An03g05490; An07g09360	44532; 48257
Gentisate pathway							
r980	: HOMOGEN + O2 \Rightarrow GNTAL + CO2 + H2O	1.13.12.-	Homogentisate monooxidase	Kanehisa et al. (2002); Yogambal and Karegoudar (1997, Inferred)	ANEW		
r981	: GNTAL + H2O + O2 \Rightarrow GEN + H2O2	1.2.3.1	gentisate 1,2-dioxygenase	Yogambal and Karegoudar (1997); Kishore et al. (1976, Inferred)	ANEW	An02g12800; An11g10310; An18g01020	135462; 125331; 187293
r982	: GEN + O2 \rightleftharpoons 3MPYR	1.13.11.4					
r983	: 3MPYR \rightleftharpoons 3FPYR	5.2.1.4	maleylpyruvate isomerase	Yogambal and Karegoudar (1997); Kishore et al. (1976, Inferred)	ANEW		
r984	: 3FPYR + H2O \rightleftharpoons FUM + PYR	3.7.1.5	acetylpyruvate hydrolase	Yogambal and Karegoudar (1997); Kishore et al. (1976, Inferred)	ANEW		
Catechol and protocatechuate pathways							
r960	: CCL + O2 \rightleftharpoons MUCO	1.13.11.1	catechol 1,2-dioxygenase	Cook and Cain (1977); Martinelli and Kinghorn (1994); Mazur et al. (1994); Kuswandi and Roberts (1992, A. nidulans)	ANEW		
r961	: MUCO \rightleftharpoons MUCL	5.5.1.1	muconate cycloisomerase	Shailubhai et al. (1983); Sa-harabudhe et al. (1986); Milstein et al. (1988); Kamath and Vaidyanathan (1990)	ANEW		
r962	: MUCL \rightleftharpoons OAEL	5.3.3.4	muconolactone delta-isomerase	Thatcher and Cain (1972)	ANEW	An01g14730	205361
r963	: DHSK \rightleftharpoons PCC + H2O	4.2.1.10	5-dehydroshikimate dehydratase	Cain (1972b)	ANEW	An08g06800	207929
r964	: PCC + O2 \rightleftharpoons 3CMUCO	1.13.11.3	protocatechuate 3,4-dioxygenase	Milstein et al. (1988); Martinelli and Kinghorn (1994)	ANEW		
r965	: 3CMUCO \rightleftharpoons 4CMUCL	5.5.1.2	3-Carboxy-cis-muconate cycloisomerase	Halsall et al. (1969); Thatcher and Cain (1972); Cook and Cain (1977); Mazur et al. (1994)	ANEW	An14g01340	185353
r966	: 4CMUCL \Rightarrow OAEL + CO2	4.1.1.44	4-carboxymuconolactone decarboxylase	Thatcher and Cain (1972)	ANEW	An03g06020	191430
r967	: OAEL + H2O \rightleftharpoons 3OA	3.1.1.24	3-oxoadipate enol-lactonase	Halsall et al. (1969)	ANEW	An13g01940; An07g07290	44810; 180211

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r969	: 3OAm + SUCCOAm \rightleftharpoons SUCCm + 3OACOAm	2.8.3.6	3-oxoadipate transferase	Halsall et al. (1969)	ANEW	An01g00200; An06g01370	172302; 55680
r970	: 3OACOAm + COAm \rightleftharpoons ACCOAm + SUCCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Halsall et al. (1969)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
METABOLISM OF AMINES							
Butylamine							
r1188	: BUTN + H ₂ O + O ₂ \rightleftharpoons BUTAL + H ₂ O ₂ + NH ₃	1.4.3.6	Amine oxidase (maoN, AO-I, AO-II)	Frebort et al. (1996); Schilling and Lerch (1995a)	ANEW	An02g10920; An09g01550; An03g00730; An07g06400; An12g03290; An13g00710; An17g00010	37354; 54408; 45789; 120706; 57198; 204355
r1189	: BUTAL + COA + NAD \rightleftharpoons C40COA + NADH	1.2.1.57	Butanal dehydrogenase	Frebort et al. (1996, Inferred)	ANEW		
Pentylamine							
r1202	: PENN + H ₂ O + O ₂ \rightleftharpoons PENAL + H ₂ O ₂ + NH ₃	1.4.3.6	Amine oxidase (maoN, AO-I, AO-II)	Frebort et al. (1996); Schilling and Lerch (1995a)	ANEW	An02g10920; An09g01550; An03g00730; An07g06400; An12g03290; An13g00710; An17g00010	37354; 54408; 45789; 120706; 57198; 204355
POLYSACCHARIDES METABOLISM							
CELL WALL COMPONENTS							
Glucan Biosynthesis							
r206	: UDPG \Rightarrow UDP + 13GLUCAN	2.4.1.34	1,3-beta-Glucan synthase	David et al. (2003)	ANIG, ANID	An17g02120	54934
r207	: UDPG \Rightarrow UDP + 14GLUCAN	2.4.1.18	1,4-alpha-Glucan branching enzyme	Stagg and Feather (1973)	ANEW	An14g04190	211162
r208	: UDPG \Rightarrow UDP + PSNIG	2.4.1.-	1,3-alpha-Glucan (Pseudonigeran) synthase	Horisberger et al. (1972); Damveld et al. (2005)	ANEW	An01g06120; An02g03260; An04g09890; An09g03070; An12g02450; An14g04190; An15g07810	46621; 36809; 55204; 54378; 212915; 211162; 40878
r209	: UDPG \Rightarrow UDP + NIG	2.4.1.-	1,3-alpha-1,4-alpha-Glucan (Nigeran) synthase	Bobbitt et al. (1977, Inferred)	ANEW	An01g06120; An02g03260; An04g09890; An09g03070; An12g02450; An14g04190; An15g07810	46621; 36809; 55204; 54378; 212915; 211162; 40878
Chitin Biosynthesis							

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r210	: $\text{GLN} + \text{F6P} \Rightarrow \text{GLU} + \text{GA6P}$	2.6.1.16	Glutamine-fructose-6-phosphate transaminase (isomerizing)	Ram et al. (2004)	ANIG, ANID	An03g05940; An18g06820	13927; N/A
r211	: $\text{ACCOA} + \text{GA6P} \rightleftharpoons \text{COA} + \text{NAGA6P}$	2.3.1.4	Glucosamine-phosphate N-acetyltransferase	David et al. (2003)	ANIG, ANID	An12g07840	49553
r212	: $\text{NAGA6P} \rightleftharpoons \text{NAGA1P}$	5.4.2.3	Phosphoacetylglucosamine mutase	David et al. (2003)	ANIG, ANID	An18g05160; An18g05170 An12g00480	212120; 212120; 54451
r213	: $\text{UTP} + \text{NAGA1P} \rightleftharpoons \text{PPI} + \text{UDPNAG}$	2.7.7.23	UDP-N-acetylglucosamine pyrophosphorylase	David et al. (2003)	ANIG, ANID	An03g06360; An07g05570; An08g05290; An09g02290; An09g04010; An12g10380; An14g00660	44589; 53259; 38285; 50188; 56923; 45992; 49223
r214	: $\text{UDPNAG} \Rightarrow \text{UDP} + \text{CHIT}$	2.4.1.16	Chitin synthase (chs1, chs2)	Gomez et al. (1977)	ANIG, ANID	An01g05360; An02g07020; An14g07420; An01g05160; An02g13580; An04g04670; An08g09030; An11g01160; An12g02920; An12g05330; An13g00840; An19g00100 An01g01920; An09g02240	170148; 197446; N/A; 196559; 129219; 190616; 38015; 119587; 127214; 189361; N/A; 40367; 122923 36363; 121359 and 54398
r215	: $\text{CHIT} + \text{H}_2\text{O} \Rightarrow \text{NAG}$	3.2.1.14	Chitinase (Endochitinase)	Gomez et al. (1977); Fukazawa et al. (2004)	ANID	An11g00920; An18g04560 An02g14380; An06g00380; An13g00510	199058; 126860 55651; 134301; 50817
r216	: $\text{CHIT} + \text{H}_2\text{O} \Rightarrow \text{NAG}$	3.2.1.52	N-Acetyl-beta-glucosaminidase	Gomez et al. (1977); Pera et al. (1997); Jones and Kosman (1980)	ANID	An04g07110; An02g13530; An12g04480	45285; 173767; 186040
r217	: $\text{NAG} + \text{H}_2\text{O} \Rightarrow \text{GLCN} + \text{AC}$	3.5.1.33	N-acetylglucosamine deacetylase		ANID		
r218	: $\text{ATP} + \text{GLCN} \Rightarrow \text{ADP} + \text{GA6P}$	2.7.1.1	Hexokinase (hxk)	Panneman et al. (1998)	ANID		
r219	: $\text{CHIT} + \text{H}_2\text{O} \Rightarrow \text{CHITO} + \text{AC}$	3.5.1.41	Chitin deacetylase		ANID		
Galactosaminogalactan r220	: $\text{UDPNAG} \rightleftharpoons \text{UDPNAGAL}$	5.1.3.7	UDP-N-acetylglucosamine 4-epimerase	Bardalaye and Nordin (1976, Inferred)	ANEW		
r221	: $0.754 \text{ UDPGAL} + 0.181 \text{ UDPNAGAL} + 0.065 \text{ UDPG} \Rightarrow \text{GAG} + \text{UDP}$	No EC	Lumped reaction for biosynthesis of galactosaminogalactan	Bardalaye and Nordin (1976, Inferred)	ANEW		
Galactoglucomanan r222	: $0.435 \text{ UDPGAL} + 0.435 \text{ GDPMAN} + 0.13 \text{ UDPG} \Rightarrow \text{GGM} + 0.565 \text{ UDP} + 0.435 \text{ GDP}$	No EC	Lumped reaction for biosynthesis of galactoglucomanan	Bardalaye and Nordin (1977, Inferred)	ANEW		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
ENERGY METABOLISM							
r235	$\text{NADHm} + \text{Qm} \Rightarrow \text{QH2m} + \text{NADm}$	1.6.5.3	NADH-ubiquinone oxidoreductase (nad5, nuo51, nd4L)	Promper et al. (1993); Juhász et al. (2004)	ANIG, ANID *	An02g05470; An02g05880; An02g09730; An02g11200; An04g00060; An04g00110; An04g05640; An06g01390; An07g04180; An08g04240; An08g04910; An08g10690; An09g06850; An11g06200; An11g08840; An11g09350; An11g09390; An12g04780; An12g07520; An14g00060	206795; 55562; 174046; 207272; 54674; 213396; 55011; 37834; 209689; 208150; 52695; 207707; 56863; 208884; 143222; 208985; 199481; 56704; 201966; 201294
r236	$\text{PPI} + \text{H2O} \Rightarrow 2 \text{PI}$	3.6.1.1	Inorganic diphosphatase	Pathak and Sreenivasan (1955); Rama and Shammugasundaram (1985)	ANIG, ANID	An02g12010	207331
r237	$\text{PPIIm} + \text{H2O} \Rightarrow 2 \text{PIIm}$	3.6.1.1	Inorganic diphosphatase	David et al. (2003)	ANIG, ANID	An02g12010	207331
r238	$\text{QH2m} + 0.5 \text{O2m} \Rightarrow \text{Qm} + \text{H2Om}$	UBIOX	Ubiquinol oxidase (mitochondrial alternative oxidase (aox))	Kirimura et al. (1999, 2006)	ANIG	An11g04810	47967
r239	$\text{NADHm} + \text{Qm} + 4 \text{H} + \text{P} \text{Om} \Rightarrow \text{NADm} + \text{QH2m} + 4 \text{H} + \text{P} \text{O}$	1.6.5.3	Respiratory-chain NADH dehydrogenase (nad5, nuo51, nd4L)	Promper et al. (1993); Juhász et al. (2004)	ANIG, ANID *	An02g05470; An02g05880; An02g09730; An02g11200; An04g00060; An04g00110; An04g05640; An06g01390; An07g04180; An08g04240; An08g04910; An08g10690; An09g06850; An11g06200; An11g08840; An11g09350; An11g09390; An12g04780; An12g07520; An14g00060	206795; 55562; 174046; 207272; 54674; 213396; 55011; 37834; 209689; 208150; 52695; 207707; 56863; 208884; 143222; 208985; 199481; 56704; 201966; 201294

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r240	$\text{NADH} + \text{Qm} + 4 \text{H} + {}_P\text{Om} \Rightarrow \text{NAD} + \text{QH2m} + 4 \text{H} + {}_P\text{O}$	1.6.5.3	Proton pumping Mitochondrial NADH dehydrogenase that catalyzes the oxidation of cytosolic NADH	Promper et al. (1993)	ANEW *	An02g05470; An02g05880; An02g09730; An02g11200; An04g00060; An04g00110; An04g05640; An06g01390; An07g04180; An08g04240; An08g04910; An08g10690; An09g06850; An11g06200; An11g08840; An11g08840; An11g09350; An11g09390; An12g04780; An12g07520; An12g07520; An14g00060	206795; 55562; 174046; 207272; 54674; 213396; 55011; 37834; 209689; 208150; 52695; 207707; 56863; 208884; 143222; 208985; 199481; 56704; 201966; 201294
r241	$\text{NADH} + \text{Qm} \Rightarrow \text{QH2m} + \text{NAD}$	1.6.5.3	NADH-ubiquinone oxidoreductase (nad5, nuo51, nd4L)	Promper et al. (1993); Juhász et al. (2004)	ANIG, ANID	An02g05470; An02g05880; An02g09730; An02g11200; An04g00060; An04g00110; An04g05640; An06g01390; An07g04180; An08g04240; An08g04910; An08g04910; An08g10690; An09g06850; An11g06200; An11g08840; An11g09350; An11g09390; An12g04780; An12g07520; An14g00060	206795; 55562; 174046; 207272; 54674; 213396; 55011; 37834; 209689; 208150; 52695; 207707; 56863; 208884; 143222; 208985; 199481; 56704; 201966; 201294
r242	$\text{NADPH} + 2 \text{FERIm} \Rightarrow \text{NADP} + 2 \text{FEROm}$	1.6.2.4	NADPH-ferrihemoprotein reductase (cprA)	van den Brink et al. (1996)	ANID	An04g06960; An05g00510; An08g07840	54972; 49744; 198350
r243	$\text{QH2m} + 2 \text{FERIm} + 4 \text{H} + {}_P\text{Om} \Rightarrow \text{Qm} + 2 \text{FEROm} + 4 \text{H} + {}_P\text{O}$	1.10.2.2	Ubiquinol-cytochrome c reductase	David et al. (2003)	ANIG, ANID	An01g12210; An01g06180; An04g05220; An08g06550; An14g04080	205553; 205959; 57369; 177548; 211145

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r244	$2 \text{ FEROm} + 0.5 \text{ O}_2\text{m} + 4 \text{ H} + \text{P} \text{Om} \Rightarrow 2 \text{ FERIm} + \text{H}_2\text{Om} + 4 \text{ H} + \text{P} \text{O}$	1.9.3.1	Cytochrome c oxidase subunit I (cox5)	Kirmura et al. (2000); Juhász et al. (2004)	ANIG, ANID	An02g01720; An02g0930; An04g01560; An07g07390; An08g01550; An09g03990; N/A; An11g10200; An14g04170	206489; 207204; 213247; 199998; 175806; N/A; 209100; 211156
r245	$\text{ADPm} + \text{PIm} + 3.88 \text{ H} + \text{P} \text{O} \Rightarrow \text{ATPm} + \text{H}_2\text{Om} + 3.88 \text{ H} + \text{P} \text{Om}$	3.6.3.14	F1F0-ATPase complex	David et al. (2003), Blair et al. (1996, A. nidulans)	ANIG, ANID	An01g04630; An01g04930; An01g10880; An02g04520; An02g06240; N/A; An07g06560; N/A; An12g00640; 138230; An12g04950; 128507; An14g04180; An16g07290; An16g07410 An12g08760	36164; 206061; 196131; 206734; N/A; N/A; 138230; 128507; 211159; 214565; 204982 201858
r246	$\text{ATPm} + \text{H}_2\text{Om} + 3.88 \text{ H} + \text{P} \text{Om} \Rightarrow \text{ADPm} + \text{PIm} + 3.88 \text{ H} + \text{P} \text{O}$	3.6.3.6	Mitochondrial ATPase 1	Jernejc and Legisa (2001)	ANID	An01g05670	171582
r257	$\text{ATP} + \text{H}_2\text{O} + 3.88 \text{ H} + \text{P} \text{O} \Rightarrow \text{ADP} + \text{PI} + 3.88 \text{ H} + \text{e}$	3.6.3.6	Plasma membrane ATPase 1		ANID	An02g06350; An02g09470; An02g09480; An08g03090; An12g04500; An17g02310; An19g00350	55567; 207175; 207175; 38450; 54015; 214148; 138839
r247	$\text{ATP} + \text{H}_2\text{O} + \text{H} + \text{Ke} \Rightarrow \text{ADP} + \text{PI} + \text{H} + \text{e} + \text{K}$	3.6.3.10	Potassium-transporting ATPase		ANID	An02g06350; An02g09470; An02g09480; An08g03090; An12g04500; An17g02310; An19g00350	55567; 207175; 207175; 38450; 54015; 214148; 138839
r248	$\text{ATP} + \text{H}_2\text{O} + \text{H} + \text{Cae} \Rightarrow \text{ADP} + \text{PI} + \text{H} + \text{e} + \text{Ca}$	3.6.3.8	Calcium-transporting ATPase		ANID	An02g06350; An02g09470; An02g09480; An08g03090; An12g04500; An17g02310; An19g00350	55567; 207175; 207175; 38450; 54015; 214148; 138839
r249	$2 \text{ FERIm} + \text{LLACm} \Rightarrow \text{PYRm} + 2 \text{ FEROm}$	1.1.2.3	Lactic acid dehydrogenase		ANID	An04g02840; An04g08560; An11g03500; An12g06530; An14g02250	213113; 45912; 140694; 186062; 211015
r250	$2 \text{ FERIm} + \text{LACm} \Rightarrow \text{PYRm} + 2 \text{ FEROm}$	1.1.2.4	Mitochondrial enzyme D-lactate ferricytochrome c oxidoreductase		ANID	An02g10670; An12g06290	47113; 186792
r251	$\text{ADP} + \text{PI} + \text{ATPm} + \text{H}_2\text{Om} + \text{H} + \text{P} \text{O} \Rightarrow \text{ADPm} + \text{PIm} + \text{ATP} + \text{H}_2\text{O} + \text{H} + \text{P} \text{Om}$	MCF	ADP/ATP translocase	David et al. (2003)	ANIG, ANID	An18g04220	212044
r252	$\text{NADPH} + \text{O}_2 \Rightarrow \text{NADP} + \text{H}_2\text{O}_2$	1.6.3.1	NADPH oxidase		ANID	An08g10000	52585
r253	$\text{NADPH} + \text{Qm} \Rightarrow \text{QH}_2\text{m} + \text{NADP}$	1.6.99.1	NADPH dehydrogenase (quinone) (NADPH oxidase)	David et al. (2003)	ANIG, ANID	An11g08510	39329

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r254	: FADH ₂ m + Qm \Rightarrow FADm + QH ₂ m	1.5.5.1	Electron-transferring-flavoprotein dehydrogenase		ANID	An16g03910	210584
Oxygen metabolism							
r255	: 2 H ₂ O ₂ \Rightarrow 2 H ₂ O + O ₂	1.11.1.6	Catalase (catR)	Horie et al. (1976); Gruft et al. (1978); Kikuchi-Torii et al. (1982); Witteveen et al. (1992); Fowler et al. (1993); Fiedurek (2000); Martinelli and Kinghorn (1994)	ANIG, ANID	An01g01820; An03g05660; An01g01550	206342; 213578; 55494
r256	: 2 H ₂ O ₂ e \Rightarrow 2 H ₂ Oe + O ₂ e	1.11.1.6	Catalase (catR)	Martinelli and Kinghorn (1994); Witteveen et al. (1992); Rogalski et al. (1998)	ANIG, ANID	An03g05660; An01g01550	213578; 55494
AMINO ACID METABOLISM							
Alanine, aspartate and asparagine biosynthesis							
r258	: OA + GLU \rightleftharpoons ASP + AKG	2.6.1.1	Aspartate transaminase	Kanehisa et al. (2002) Patil and Ramakrishnan (1966); Alvarez-Vasquez et al. (2000)	ANID	An03g00050; An03g01120; An04g05130; An09g02390; An12g07870; An16g05570	141281; 45764; 214397; 50187; 186098; 56390
r263	: ASP + ATP + GLN + H ₂ O \Rightarrow GLU + ASN + AMP + PPI	6.3.5.4	Asparagine synthase		ANID	An01g07910; An04g01340; An12g07660; An11g02620	131513; 57091; 186429; 208695
r259	: PYR + GLU \rightleftharpoons AKG + ALA	2.6.1.2	Alanine transaminase	Patil and Ramakrishnan (1966)	ANID		
r261	: PYR + NH ₃ + NADPH \Rightarrow ALA + H ₂ O + NADP	1.4.1.1	Alanine dehydrogenase (NADPH)	Hoshino et al. (1962); Savov et al. (1986)	ANEW		
r262	: PYR + NH ₃ + NADH \Rightarrow ALA + H ₂ O + NAD	1.4.1.1	Alanine dehydrogenase (NADH)	Savov et al. (1986)	ANEW		
r259m	: PYRm + GLUm \rightleftharpoons AKGm + ALAm	2.6.1.2	Alanine transaminase	Alvarez-Vasquez et al. (2000)	ANID	An11g02620	208695
r258m	: OAm + GLUm \rightleftharpoons ASPm + AKGm	2.6.1.1	Aspartate transaminase	Patil and Ramakrishnan (1966); Alvarez-Vasquez et al. (2000)	ANID	An04g06380	214270
Aspartate degradation							
r265	: ASP + H ₂ O + O ₂ \Rightarrow OA + NH ₃ + H ₂ O ₂	1.4.3.2	L-amino acid oxidase	Oganesyan et al. (1998)	ANEW	An08g10800	176790
Asparagine degradation							
r266	: ASN + H ₂ O \Rightarrow ASP + NH ₃	3.5.1.1	Asparaginase	Wriston, Jr. and Yelling (1973)	ANID	An01g14960; An18g03190	51685; 187609
Arginine metabolism							
r267	: ORN + AKG \Rightarrow GLUGSAL + GLU	2.6.1.13	Ornithine transaminase	Kanehisa et al. (2002)	ANEW	An04g04130; An11g08870	54525; 48081
r271	: SAM \rightleftharpoons DSAM + CO ₂	4.1.1.50	S-adenosylmethionine decarboxylase		ANID	An09g06050	54311

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r274	: GBAD \Rightarrow GBAT + NH ₃	3.5.1.4	Amidase/acetamidase		ANID	An16g07500; An01g12500; An02g00190; An02g00340; An03g05880; An07g00100; An07g03960; An09g01020; An09g04990; An11g02980; An11g08900; An12g01020; An14g00670; An15g00290; An02g07250	194059; 35556; 36604; 121987; 191243; 181662; 40014; 121710; 188491; 38912; 48084; 54468; 210891; 181881 55582
r275	: ARG + H ₂ O \Rightarrow ORN + UREA	3.5.3.1	Arginase (argA)	Kiesel (1922); Sukhenko and Podgainaya (1959)	ANID		
Urea cycle							
r268m	: CITRm + ASPm + ATPm \rightleftharpoons AMPm + PPIIm + ARGSUCCm	6.3.4.5	Argininosuccinate synthase		ANID	An12g01280; An15g02340	43683; 40489
r269m	: ARGSUCCm \rightleftharpoons FUMm + ARGm	4.3.2.1	Argininosuccinate lyase		ANID	An01g06560	51912
r275m	: ARGm + H ₂ Om \Rightarrow ORNm + UREA	3.5.3.1	Arginase	Kiesel (1922); Sukhenko and Podgainaya (1959)	ANID	An14g01190	41557
r282m	: ORNm + CAPm \Rightarrow CITRm + PIm	2.1.3.3	Ornithine carbanoyltransferase (argB)	Buxton et al. (1987); Swart et al. (1992); Lenouvel et al. (2002)	ANID	An14g03400	N/A
Ornithine cycle							
r277	: GLUm + ACCOAm \Rightarrow COAm + NAGLUm	2.3.1.1	Amino-acid acetyltransferase		ANID	An03g02930	194534
r278	: NAGLUm + ATPm \Rightarrow ADPm + NAGLUPm	2.7.2.8	Acetylglutamate kinase		ANID	An03g01910	194591
r279	: NAGLUPm + NADPHm \Rightarrow NADPm + PIm + NAGLUm	1.2.1.38	N-Acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) and acetylglutamate kinase (EC 2.7.2.8)		ANID	An12g07580	211485
r280	: NAGLUm + GLUm \Rightarrow AKGm + NAORNm	2.6.1.11	Acetylornithine aminotransferase		ANID	An15g02360	35307
r281	: NAORNm + GLUm \Rightarrow ORNm + NAGLUm	2.3.1.35	Glutamate acetyltransferase		ANID	An03g04330	50689
Cysteine biosynthesis							
r283	: SER + ACCOA \Rightarrow COA + ASER	2.3.1.30	Serine transacetylase/serine O-acetyltransferase	Stepien et al. (1975); Sienko and Paszewski (1999; A. nidulans)	ANID	An09g02800	212646 and 54391
r284	: ASER + H ₂ S \Rightarrow AC + CYS	2.5.1.47	Cysteine synthase (cysB) (O-acetylserine sulphydrylase)	Pieniazek et al. (1973); Stepien et al. (1975); Topczewski et al. (1997; A. nidulans)	ANID	An02g10750; An12g09880; An14g00960; An15g05170; An16g07520	207249; N/A; 184767; 181861; 193596
Cysteine degradation							
r285	: 2 CYS + O ₂ \Rightarrow CYST + H ₂ O ₂	1.8.3.3	Sulphydryl oxidase (Sox)	Vignaud et al. (2002)	ANEW	An09g05940; An16g02470	189206; 183599
r286	: 2 CYS + NAD \Rightarrow CYST + NADH	1.8.1.6	Cystine reductase	Kasaikina and Zheltova (1963)	ANEW		
Glutamate and glutamine metabolism							

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r289	: $\text{GLU} + \text{H}_2\text{O} + \text{NAD} \Rightarrow \text{AKG} + \text{NH}_3 + \text{NADH}$	1.4.1.2	Glutamate dehydrogenase	Patil and Ramakrishnan (1966); Punekar et al. (1985); Savov et al. (1986)	ANID	An02g14590	37620
r290	: $\text{AKG} + \text{NH}_3 + \text{NADPH} \Rightarrow \text{GLU} + \text{H}_2\text{O} + \text{NADP}$	1.4.1.4	Glutamate dehydrogenase (gdhA)	Punekar et al. (1985); Savov et al. (1986); Noor and Punekar (2005)	ANID	An04g00990	203758
r291	: $\text{GLU} + \text{NH}_3 + \text{ATP} \Rightarrow \text{GLN} + \text{ADP} + \text{PI}$	6.3.1.2	Glutamate-ammonia ligase	Kim (1981); Punekar et al. (1985); Savov et al. (1986)	ANID	An14g01460; An15g01850; An02g06720; An11g07960	49256; 48679; 197415; 208953
r292	: $\text{GLN} \Rightarrow \text{GLU} + \text{NH}_3$	3.5.1.2	Glutaminase A	Shi et al. (1996)	ANID	An01g08800	196278
r287	: $\text{AKG} + \text{GLN} + \text{NADPH} \Rightarrow \text{NADP} + 2 \text{GLU}$	1.4.1.14	Glutamate synthase (NADPH)	Savov et al. (1986)	ANEW	An07g09920	209263
r288	: $\text{AKG} + \text{GLN} + \text{NADH} \Rightarrow \text{NAD} + 2 \text{GLU}$	1.4.1.13	Glutamate synthase (NADH)	Savov et al. (1986)	ANEW	An02g02290; An11g06140	52149; 208879
r293	: $\text{GLUGSALm} + \text{NADPm} + 2 \text{H}_2\text{Om} \Rightarrow \text{NADPHm} + \text{GLUm}$	1.5.1.12	Delta-1-pyrroline-5-carboxylate dehydrogenase		ANID	An02g02290; An11g06140	52149; 208879
r294	: $\text{P5Cm} + \text{NADm} + 2 \text{H}_2\text{Om} \Rightarrow \text{NADHm} + \text{GLUm}$	1.5.1.12	Delta-1-pyrroline-5-carboxylate dehydrogenase		ANID	An11g09770	179814
r295	: $3\text{PG} + \text{NAD} \Rightarrow \text{NADH} + \text{PHP}$	1.1.1.95	Phosphoglycerate dehydrogenase	Pei et al. (2003, A. nidulans)	ANID	An11g01390; An12g01580; An17g02330	38797; 128882; 57311
r296	: $\text{PHP} + \text{GLU} \Rightarrow \text{AKG} + 3\text{PSER}$	2.6.1.52	Phosphoserine transaminase		ANID	An02g00890	206447
r297	: $3\text{PSER} + \text{H}_2\text{O} \Rightarrow \text{PI} + \text{SER}$	3.1.3.3	Phosphoserine phosphatase		ANID	An11g09770	179814
r298	: $\text{THF} + \text{SER} \rightleftharpoons \text{GLY} + \text{METHF} + \text{H}_2\text{O}$	2.1.2.1	Glycine hydroxymethyltransferase/serine hydroxymethyltransferase	Lewandowska et al. (1996, A. nidulans)	ANID	An05g00410; An16g02970	211700; 56462
r301	: $\text{GLY} + \text{ACAL} \Rightarrow \text{THR}$	4.1.2.5	Threonine aldolase		ANID	An15g03260; An03g01360; An03g02300; An07g00680	40551; 194373; 45688; 56260
r311	: $\text{THR} + \text{NAD} + \text{H}_2\text{O} \Rightarrow \text{GLY} + \text{AC} + \text{NADH}$	1.1.1.103	Threonine dehydrogenase		ANID	An05g02000	189384
r306	: $\text{HSER} + \text{ATP} \Rightarrow \text{ADP} + \text{PHSER}$	2.7.1.39	Homoserine kinase		ANID	An17g02090	214104
r307	: $\text{PHSER} + \text{H}_2\text{O} \Rightarrow \text{PI} + \text{THR}$	4.2.3.1	Threonine synthase		ANID	An16g02520	183233
r299	: $\text{GLY} + \text{THF} + \text{NAD} \Rightarrow \text{METHF} + \text{NADH} + \text{CO}_2 + \text{NH}_3$	2.1.2.10	Aminomethyltransferase (2.1.2.10, 1.4.4.2 and 1.8.1.4 lumped)		ANID	An14g01150; An08g03070	210951; 122951
Homoserine biosynthesis							
r302	: $\text{ASP} + \text{ATP} \Rightarrow \text{ADP} + \text{BASP}$	2.7.2.4	Aspartate kinase		ANID	An17g02280	54942
r303	: $\text{BASP} + \text{NADPH} \Rightarrow \text{NADP} + \text{PI} + \text{ASPSA}$	1.2.1.11	Aspartic beta semi-aldehyde dehydrogenase, aspartate semialdehyde dehydrogenase I		ANID	An11g09510	209010
r304	: $\text{ASPSA} + \text{NADH} \Rightarrow \text{NAD} + \text{HSER}$	1.1.1.3	Homoserine dehydrogenase I		ANID	An02g07430	52305
r300	: $\text{ALA} + \text{GLX} \rightleftharpoons \text{PYR} + \text{GLY}$	2.6.1.44	Alanine-glyoxylate transaminase	Oganesyan et al. (2004)	ANID	An09g03830	50140

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r308a	: GLYm + HPLYSm \rightleftharpoons HPSAMLYSm + CO ₂ m	2.1.2.10	Aminomethyltransferase (2.1.2.10, 1.4.4.2 and 1.8.1.4 lumped)		ANEW	An14g01150; An08g03070	210951; 122951
r308b	: HPSAMLYSm + THFm \rightleftharpoons NH ₃ m + METTHFm + DHPLYSm	2.1.2.1	Glycine hydroxymethyltransferase/serine hydroxymethyltransferase		ANEW	An05g00410; An16g02970	211700; 56462
r308c	: DHPLYSm + NADm \rightleftharpoons HPLYSm + NADHm	1.4.4.2	Glycine dehydrogenase (decarboxylating) / glycine decarboxylase complex (P-subunit), glycine synthase (P-subunit), glycine cleavage system (P-subunit)		ANEW	An14g01150	210951
Threonine and serine degradation							
r312	: SER \Rightarrow PYR + NH ₃	4.3.1.17	L-Serine ammonia-lyase		ANID	An04g02220	213166
r313	: THR \Rightarrow NH ₃ + OBUT	4.3.1.19	Threonine dehydratase	MacDonald et al. (1974, A. nidulans)	ANID	An04g02580	190860
r313m	: THRm \Rightarrow NH ₃ m + OBUTm	4.3.1.19	Threonine dehydratase		ANID	An04g02580	190860
r316	: R5P + ATP \rightleftharpoons PRPP + AMP	2.7.6.1	Ribose-phosphate pyrophosphokinase	Foley et al. (1965); Nielsen et al. (2004, A. nidulans)	ANID	An02g09240; An04g05860; An07g02210	52363; 204746; 209842
r317	: PRPP + ATP \Rightarrow PPI + PRBAMP	2.4.2.17	ATP phosphoribosyltransferase	Busch et al. (2001, A. nidulans)	ANID	An13g01080	54800
r318	: PRBAMP + H ₂ O \Rightarrow PPI + PRBAMP	3.6.1.31	phosphoribosyl-ATP diphosphatase	Berlyn (1967); Busch et al. (2001, A. nidulans)	ANID	An01g12570	205513
r319	: PRBAMP + H ₂ O \Rightarrow PRFP	3.5.4.19	phosphoribosyl-AMP cyclohydrolase	Berlyn (1967); Busch et al. (2001, A. nidulans)	ANID	An01g12570	205513
r320	: PRFP \Rightarrow PRLP	5.3.1.16	1-(5-phosphoribosyl)-5-[(6-phosphoribosylamino)methyl]-4-carboxamide isomerase	Busch et al. (2001, A. nidulans)	ANID	An17g01640	51056
r321	: PRLP + GLN \Rightarrow GLU + AICAR + DIMGP	2.4.2.-	Glutamine amidotransferase/cyclase/imidazole glycerol phosphate synthase	Valerius et al. (2001, A. nidulans)	ANID	An02g14890	198031
r322	: DIMGP \Rightarrow IMACP + H ₂ O	4.2.1.19	Imidazoleglycerol-phosphate dehydratase	Berlyn (1967); Busch et al. (2001, A. nidulans)	ANID	An15g00610	200493
r323	: IMACP + GLU \Rightarrow AKG + HISOLP	2.6.1.9	Histidinol-phosphate aminotransferase	Pain et al. (2004, A. fumigatus)	ANID	An01g11930	171507
r324	: HISOLP + H ₂ O \Rightarrow PI + HISOL	3.1.3.15	Histidinol phosphatase		ANID	An14g00840	56528
r325	: HISOL + 2 NAD + H ₂ O \Rightarrow HIS + 2 NADH	1.1.1.23	Histidinol dehydrogenase	Berlyn (1967); Creaser and Varela-Torres (1971, A. nidulans)	ANID	An14g07210	56640
Histidine degradation							
r326	: HIS \Rightarrow HISN + CO ₂	4.1.1.22	histidine decarboxylase	Tanaka et al. (1977)	ANEW		
r327	: ACCOA + HISN \rightleftharpoons COA + NAHISN	No EC	histamine N-acetyltransferase	Tanaka et al. (1977)	ANEW		
r328	: 2 PYRm \Rightarrow CO ₂ m + ACLACm	2.2.1.6	Acetolactate synthase		ANID	An01g09250; An03g00480; An16g01310; An16g04170	35805; 51385; 139646; 210558

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r329	: ACLACm + NADPHm \Rightarrow NADPm + DHVALm	1.1.1.86	Ketol-acid merase		ANID	An09g03940	212581
r330	: DHVALm \Rightarrow OIVALm + H2Om	4.2.1.9	Dihydroxy acid dehydratase		ANID	An07g09870; An11g09270; An15g06700; An18g02550; An18g04160	181283; 179001; 53523; 42733; 54174
r331	: OIVALm + GLUm \rightleftharpoons AKGm + VALm	2.6.1.42	Branched chain amino acid aminotransferase		ANEW	An12g02890; An02g06150; An04g00430; An09g01990	43811; 197362; 190990; 124698
r337	: OIVALm + ACCOAm + IPPMALm \Rightarrow COAm + IPPMALm	2.3.3.13	Alpha-isopropylmalate synthase (2-isopropylmalate synthase)		ANID	An01g13160; An09g00170	205459; 203189
r338	: IPPMALm + NADm \Rightarrow NADHm + OICAPm + CO2m	1.1.1.85	Beta-IPM (isopropylmalate) dehydrogenase (leu2A and leu2B)	Williams et al. (1996); Kohlhaw (2003)	ANID	An04g10130; An01g14130	205291; 205395
r339	: OICAPm + GLUm \rightleftharpoons AKGm + LEUm	2.6.1.42	Branched chain amino acid aminotransferase		ANID	An12g02890; An02g06150; An04g00430; An09g01990	43811; 197362; 190990; 124698
r339m	: OICAP + GLU \rightleftharpoons AKG + LEU	2.6.1.42	Branched chain amino acid aminotransferase		ANID	An12g02890; An02g06150; An04g00430; An09g01990	43811; 197362; 190990; 124698
Isoleucine biosynthesis							
r332	: OBUTm + PYRm \Rightarrow ABUTm + CO2m	2.2.1.6	Acetolactate synthase		ANID	An01g09250; An03g00480; An16g01310; An16g04170	35805; 51385; 139646; 210558
r333	: ABUTm + NADPHm \Rightarrow NADPm + DHMVAm	1.1.1.86	Ketol-acid merase		ANID	An09g03940	212581
r334	: DHMVAm \Rightarrow OMVALm + H2Om	4.2.1.9	Dihydroxy acid dehydratase		ANID	An07g09870; An11g09270; An15g06700; An18g02550; An18g04160	181283; 179001; 53523; 42733; 54174
r335	: OMVALm + GLUm \rightleftharpoons AKGm + ILEm	2.6.1.42	Branched chain amino acid aminotransferase		ANID	An12g02890; An02g06150; An04g00430; An09g01990	43811; 197362; 190990; 124698
r335m	: OMVAL + GLU \rightleftharpoons AKG + ILE	2.6.1.42	Branched chain amino acid aminotransferase		ANID	An12g02890; An02g06150; An04g00430; An09g01990	43811; 197362; 190990; 124698
Lysine biosynthesis							
r341	: ACCOAm + H2Om + AKGm \Rightarrow HC-ITm + COAm	2.3.3.14	Homocitrate synthase	Garrad and Bhattacharjee (1992, A. Fungi)	ANID	An04g06210	54991
r351	: HCITm \rightleftharpoons HACNm + H2Om	4.2.1.79	2-methylcitrate dehydratase	Garrad and Bhattacharjee (1992, A. fumigatus) Weidner et al. (1997, A. nidulans)	ANID	An15g01780	53423

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r352	: $\text{HACNm} + \text{H}_2\text{Om} \rightleftharpoons \text{HICITm}$	4.2.1.36	Homocitronate hydratase	Weidner et al. (1997); Zabriske and Jackson (2000, A. nidulans)	ANID	An15g00350	56275
r353	: $\text{HICITm} + \text{NADm} \rightleftharpoons \text{OXAm} + \text{CO}_2\text{m} + \text{NADHm}$	1.1.1.87	Homocitronate dehydrogenase	Garrad and Bhattacharjee (1992, A. fumigatus), Zabriske and Jackson (2000); Weidner et al. (1997, A. nidulans)	ANID		
NE3	: $\text{OXAm} \rightleftharpoons \text{CO}_2\text{m} + \text{AKAm}$	Non enzymatic step	Non enzymatic reaction		ANID		
r346	: $\text{AKAm} + \text{GLUm} \rightleftharpoons \text{AMAm} + \text{AKGm}$	2.6.1.39	2-aminoacidate transaminase	Garrad and Bhattacharjee (1992, A. fumigatus), Weidner et al. (1997); Zabriske and Jackson (2000, A. nidulans)	ANID		
r347	: $\text{AMAm} + \text{NADPHm} \rightleftharpoons \text{AMASAm} + \text{NADPm} + \text{H}_2\text{Om}$	1.2.1.31	L-aminoacidate-semialdehyde dehydrogenase	Garrad and Bhattacharjee (1992, A. fumigatus), Zabriske and Jackson (2000, A. nidulans)	ANID	An04g05420; An11g04250; An12g10090; An11g05500; 39114	55018; 129526; 194895; 39114
r348	: $\text{AMAm} + \text{NADHm} \rightleftharpoons \text{AMASAm} + \text{NADm} + \text{H}_2\text{Om}$	1.2.1.31	L-aminoacidate-semialdehyde dehydrogenase	Garrad and Bhattacharjee (1992, A. fumigatus), Zabriske and Jackson (2000, A. nidulans)	ANID	An04g05420; An11g04250; An12g10090; An11g05500; 39114	55018; 129526; 194895; 39114
r349	: $\text{GLUm} + \text{AMASAm} + \text{NADPHm} \rightleftharpoons \text{SACPm} + \text{NADPm} + \text{H}_2\text{Om}$	1.5.1.10	Saccharopine dehydrogenase (NADP ⁺ , L-glutamate forming)	Garrad and Bhattacharjee (1992, A. fumigatus), Zabriske and Jackson (2000, A. nidulans)	ANID	An01g13590; An04g05260	35485; 214383
r350	: $\text{SACPm} + \text{NADm} + \text{H}_2\text{Om} \rightleftharpoons \text{LYSm} + \text{AKGm} + \text{NADHm}$	1.5.1.7	Saccharopine dehydrogenase (NAD ⁺ , L-lysine forming)	Garrad and Bhattacharjee (1992, A. fumigatus), Zabriske and Jackson (2000, A. nidulans)	ANID	An02g07500	207003
Methionine metabolism							
r354	: $\text{SAM} + \text{HCYS} \rightleftharpoons \text{SAH} + \text{MET}$	2.1.1.10	Homocysteine methyltransferase	Stepien et al. (1975, A. nidulans)	ANID	An15g07110	210376
r355	: $\text{ACCOA} + \text{HSER} \rightleftharpoons \text{COA} + \text{OAHSER}$	2.3.1.31	O-homoserine acetyltransferase	Stepien et al. (1975); Sienko and Paszewski (1999); Grynberg et al. (2001, A. nidulans)	ANID	An17g00630	213962
r356	: $\text{OAHSER} + \text{CYS} \rightleftharpoons \text{LLCT} + \text{AC}$	2.5.1.48	Cystathionine gamma-synthase	Paszewski and Grabski (1975); Stepien et al. (1975); Sienko and Paszewski (1999, A. nidulans)	ANEW	An12g01110	128744
r357	: $\text{OAHSER} + \text{METH} \rightleftharpoons \text{MET} + \text{AC}$	2.5.1.49	O-acetylhomoserine (thiol)-lyase		ANID	An09g06710	54281
r358	: $\text{OAHSER} + \text{H}_2\text{S} \rightleftharpoons \text{AC} + \text{HCYS}$	2.5.1.47	Cysteine synthase (O-acetylhomoserine sulphydrylase)	Pieniazek et al. (1974); Paszewski and Grabski (1975); Stepien et al. (1975); Sienko and Paszewski (1999, A. nidulans)	ANID	An02g10750; An12g09880; An14g00960; An15g05170; An16g07520	207249; N/A; 184767; 181861; 193596
r359	: $\text{HCYS} + \text{SER} \rightleftharpoons \text{LLCT} + \text{H}_2\text{O}$	4.2.1.22	Cystathionine beta-synthase	Pieniazek et al. (1974); Paszewski and Grabski (1975); Stepien et al. (1975, A. nidulans)	ANEW	An05g00160	49760
r360	: $\text{LLCT} \rightleftharpoons \text{CYS} + \text{NH}_3 + \text{OBUT}$	4.4.1.1	Cystathionine gamma-lyase	Pieniazek et al. (1974); Stepien et al. (1975); Sienko and Paszewski (1999, A. nidulans)	ANID	An04g04720; An16g08720	190884; 194072
r361	: $\text{LLCT} + \text{H}_2\text{O} \rightleftharpoons \text{HCYS} + \text{PYR} + \text{NH}_3$	4.4.1.8	Cystathionine-b-lyase	Stepien et al. (1975); Sienko and Paszewski (1999, A. nidulans)	ANID	An14g00930	201388

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r362	: HCYS + MTHF \Rightarrow THF + MET	2.1.1.13	Methionine synthase	Balinska and Paszewski (1979); Paszewski and Grabski (1975, A. nidulans)	ANID	An04g01750	203669
r363	: MET + ATP + H ₂ O \Rightarrow PPI + PI + SAM	2.5.1.6	S-adenosylmethionine synthetase	Martinelli and Kinghorn (1994, A. nidulans) *	ANID	An02g10660; An08g02700	175387; 208283
r364	: SAM + CALH \Rightarrow SAH + DPTH	2.1.1.98	Diphthine synthase	Martinelli and Kinghorn (1994, A. nidulans), Pain et al. (2004, A. fumigatus)	ANID	An08g07220	47429
r365	: SAH + H ₂ O \Rightarrow HCYS + ADN	3.3.1.1	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase)	David et al. (2003), Sienko and Paszewski (1999, A. nidulans)	ANIG, ANID	An08g01960	208343
Phenylalanine, tyrosine and tryptophan biosynthesis (aromatic amino acids)							
r367	: E4P + PEP + H ₂ O \Rightarrow PI + 3DDAH7P	2.5.1.54	3-deoxy-7-phosphoheptulonate synthase	Hartmann et al. (2001, A. nidulans)	ANID	An01g06150	196476
r368	: 3DDAH7P \Rightarrow DQT + PI	4.2.3.4	Pentafunctional arom polypeptide (contains: 3-dehydroquinase, 3-dehydroquinatase, 3-dehydroquinase), shikimate 5-dehydrogenase, shikimate kinase, and EPSP synthase	Hawkins (1987); Nichols et al. (2004, A. nidulans)	ANID	An08g06800; An08g06810	207929; 207929
r369	: DQT \Rightarrow DHSK + H ₂ O	4.2.1.10	Catabolic dehydroquinase (3-dehydroquinatase)	Cain (1972a)	ANID	An08g06800; An08g06810	207929; 207929
r370	: QT + NAD \rightleftharpoons DQT + NADH	1.1.1.24	Quinate 5-dehydrogenase	Cain (1972a)	ANID	An03g03710; An04g08100	44404; 51457
r371	: DHSK + NADH \Rightarrow SME + NAD	1.1.1.24	Quinate 5-dehydrogenase	Cain (1972a)	ANEW	An03g03710; An04g08100	44404; 51457
r372	: DHSK + NADPH \Rightarrow SME + NADP	1.1.1.25	dehydroshikimate dehydrogenase	Cain (1972a)	ANID	An08g06800; An08g06810	207929; 207929
r373	: SME + ATP \Rightarrow ADP + SME3P	2.7.1.71	Shikimate kinase I, II	Hawkins (1987, A. nidulans)	ANID	An08g06800; An08g06810	207929; 207929
r374	: SME3P + PEP \Rightarrow 3PSME + PI	2.5.1.19	3-phosphoshikimate-1-carboxyvinyltransferase	Hawkins (1987, A. nidulans)	ANID	An08g06800; An08g06810	207929; 207929
r375	: 3PSME \Rightarrow PI + CHOR	4.2.3.5	Chorismate synthase	Martinelli and Kinghorn (1994, A. nidulans)	ANID		
r376	: CHOR \Rightarrow PHEN	5.4.99.5	Chorismate mutase	Yelton et al. (1983); Krappmann et al. (1999, A. nidulans)	ANID	An14g06010	41927
r377	: PHEN \Rightarrow CO ₂ + H ₂ O + PHPYR	4.2.1.51	Prephenate dehydratase	Alvarez-Vasquez et al. (2000)	ANID	An17g02200	54937
r378	: PHPYR + GLU \rightleftharpoons AKG + PHE	2.6.1.1	Phenylalanine:alpha-ketoglutarate aminotransferase		ANID	An03g00050; An03g01120; An04g05130; An04g06380; An09g02390; An12g07870; An16g05570	141281; 45764; 214397; 214270; 50187; 186098; 56390
r379	: PHEN + NADP \Rightarrow 4HPP + CO ₂ + NADPH	1.3.1.13	Prephenate dehydrogenase (NADP+)		ANID	An02g06120	46999

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r380	4HPP + GLU \rightleftharpoons AKG + TYR	2.6.1.1	Aspartate transaminase	Alvarez-Vasquez et al. (2000)	ANID	An03g00050; An03g01120; An04g05130; An04g06380; An09g02390; An12g07870; An16g05570	141281; 45764; 214397; 214270; 50187; 186098; 56390
r381	CHOR + GLN \Rightarrow GLU + PYR + AN	4.1.3.27	Anthranelate synthase (trpC)	Kos et al. (1985); Horng et al. (1989); Adams and Royer (1990)	ANID	An08g06080	52668
r382	AN + PRPP \Rightarrow PPI + NPRAN	2.4.2.18	Anthranelate phosphoribosyl transferase		ANID	An01g07260	51886
r383	NPRAN \Rightarrow CPAD5P	5.3.1.24	N-(5-phosphoribosyl)-anthranilate isomerase (trpC)	Kos et al. (1985); Horng et al. (1989); Adams and Royer (1990)	ANID	An08g06080	52668
r384	CPAD5P \Rightarrow CO ₂ + IGP + H ₂ O	4.1.1.48	Indoleglycerol phosphate synthase (trpC)	Kos et al. (1985); Horng et al. (1989); Adams and Royer (1990)	ANID	An08g06080	52668
r385	IGP + SER \Rightarrow T3P1 + TRP + H ₂ O	4.2.1.20	Tryptophan synthetase		ANID	An02g02170; An12g03230; An16g02500	52146; 43841; 183278
Proline biosynthesis							
r412	GLU + NADH \Rightarrow NAD + GLUGSAL + 2 H ₂ O	1.5.1.12	1-pyrroline-5-carboxylate dehydrogenase	Jones et al. (1981); Hull et al. (1989, A. nidulans)	ANEW	An02g02290; An07g05000; An11g06140	52149; 181275; 208879
NE4	GLUGSAL \rightleftharpoons P5C + H ₂ O	Non enzymatic step	Non enzymatic reaction		ANID		
r413	P5C + NADPH \rightleftharpoons PRO + NADP	1.5.1.2	Pyrroline-5-carboxylate reductase	Jones et al. (1981); Hull et al. (1989, A. nidulans)	ANID	An07g05050; An01g01520; An04g02800	136532; 36398; 57044
r414	GLU + ATP \Rightarrow ADP + GLUP	2.7.2.11	Gamma-glutamyl kinase, glutamate kinase		ANID	An05g00120	124391
r415	PROm + NADm \Rightarrow P5Cm + NADHm	1.5.99.8	Proline dehydrogenase		ANID	An01g01530; An11g06160	132598; 179947
NE5	GLUGSALm \rightleftharpoons P5Cm	Non enzymatic step	Non enzymatic reaction		ANID		
Proline degradation							
r416	P5C + NAD + 2 H ₂ O \Rightarrow GLU + NADH	1.5.1.12	1-pyrroline-5-carboxylate dehydrogenase	Jones et al. (1981); Hull et al. (1989, A. nidulans)	ANEW	An02g02290; An07g05000; An11g06140	52149; 181275; 208879
METABOLISM OF OTHER AMINO ACIDS							
Beta-alanine biosynthesis							
r417	ASP \Rightarrow CO ₂ + bALA	4.1.1.11	Aspartate decarboxylase	Kanehisa et al. (2002); Jerebzooff and Jerebzooff-Quintin (1971)	ANID		
Cyanocamino acid metabolism							

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r418	: APROP \Rightarrow ALA + NH ₃	3.5.5.1	Nitrilase	Snajdrova et al. (2004)	ANID	An16g00550; An01g07510; An01g12090; An06g01960; An08g08940; N/A; An08g10150; An12g01260; An16g06210; An18g01740	41410; 35944; 170270; 175987; N/A; 52578; 141873; 40928; 211815
r419	: ACYBUT \Rightarrow GLU + NH ₃	3.5.5.1	Nitrilase	Snajdrova et al. (2004)	ANID	An16g00550; An01g07510; An01g12090; An06g01960; An08g08940; N/A; An08g10150; An12g01260; An16g06210; An18g01740	41410; 35944; 170270; 175987; N/A; 52578; 141873; 40928; 211815
Glutathione biosynthesis							
r420	: CYS + GLU + ATP \Rightarrow GC + PI + ADP	6.3.2.2	Gamma-glutamylcysteine synthetase		ANID	An08g01270	38585
r421	: GLY + GC + ATP \Rightarrow RGT + PI + ADP	6.3.2.3	Glutathione synthetase	Murata et al. (1989)	ANID	An01g13620; An09g03030	170255; 50166
r422	: OGT + O ₂ \Rightarrow RGT + H ₂ O ₂	1.11.1.9	Glutathione peroxidase	Vignaud et al. (2002); Kuzniak et al. (2006)	ANID	An02g02750	206591
r423	: NADPH + OGT \Rightarrow NADP + RGT	1.8.1.7	glutathione-disulfide reductase		ANID	An03g03660	213429
NUCLEOTIDE METABOLISM							
Purine Biosynthesis (ATP, dATP, IMP, XMP, GTP, dGTP)							
r424	: PRPP + GLN + H ₂ O \Rightarrow PPI + GLU + PRAM	2.4.2.14	Phosphoribosylpyrophosphat amidotransferase/amidophosphoribosyltransferase	Foley et al. (1965, A. nidulans) Foley et al. (1965, A. nidulans)	ANID	An15g01760	129349
r425	: PRAM + ATP + GLY \rightleftharpoons ADP + PI + GAR	6.3.4.13	Glycinamide ribotide synthetase and aminimidazole ribotide synthetase/phosphoribosyl-amine-glycine ligase	Foley et al. (1965, A. nidulans)	ANID	An15g00570	53390
r426	: GAR + FTHF \Rightarrow THF + FGAR	2.1.2.2	Phosphoribosylglycinamide formyltransferase	Foley et al. (1965, A. nidulans)	ANID	An02g02700	36764
r427	: FGAR + ATP + GLN + H ₂ O \Rightarrow GLU + ADP + PI + FGAM	6.3.5.3	5-phosphoribosylformyl-glycinamide synthetase	Foley et al. (1965, A. nidulans)	ANID	An02g09960	37283
r428	: FGAM + ATP \Rightarrow ADP + PI + AIR	6.3.3.1	Phosphoribosylformyl-glycinamide cyclo-ligase	Foley et al. (1965, A. nidulans)	ANID	An15g00570	53390
r429	: AIR + CO ₂ \rightleftharpoons CAIR	4.1.1.21	Phosphoribosylaminoimidazole carboxylase (Ade2 homolog)	Jin et al. (2004, A. oryzae)	ANID	An01g08090	55358
r430	: CAIR + ATP + ASP \Rightarrow ADP + PI + SAICAR	6.3.2.6	Phosphoribosyl aminoimidazolesuccinocarboxamide synthetase (Ade1 homolog)	Jin et al. (2004, A. oryzae)	ANID	An11g10150	48145

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r431	: SAICAR \rightleftharpoons FUM + AICAR	4.3.2.2	5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminimidazole lyase	Jin et al. (2004, A. oryzae)	ANID	An02g04020	206692
r432	: AICAR + FTHF \rightleftharpoons THF + PRFICA	2.1.2.3	5-aminimidazole-4-carboxamide ribonucleotide (AICAR) trans-formylase / IMP cyclohydrolase	Jin et al. (2004, A. oryzae)	ANID	An04g02060	57068
r433	: PRFICA \rightleftharpoons IMP + H ₂ O	3.5.4.10	5-aminimidazole-4-carboxamide ribonucleotide (AICAR) trans-formylase / IMP cyclohydrolase	Jin et al. (2004, A. oryzae)	ANID	An04g02060	57068
r434	: IMP + GTP + ASP \Rightarrow GDP + PI + ASUC	6.3.4.4	Adenylosuccinate synthetase	Foley et al. (1965); Ribard et al. (2001, A. nidulans)	ANID	An01g13920	51711
r435	: ASUC \Rightarrow FUM + AMP	4.3.2.2	5'-phosphoribosyl-4-(N-succinocarboxamide)-5-aminimidazole lyase	Foley et al. (1965); Ribard et al. (2001, A. nidulans)	ANID	An02g04020	206692
r436	: ATP + AMP \rightleftharpoons 2 ADP	2.7.4.3	Adenylate kinase	Perl (1982)	ANIG, ANID	An01g04710; An07g10100	46678; 56109
r437	: ADP + RTHIO \Rightarrow DADP + OTHIO + H ₂ O	1.17.4.1	Ribonucleotide reductase	Hockertz et al. (1987)	ANID *	An04g01080; An14g06870	57102; 56635
r438	: DAMP + ATP \rightleftharpoons DADP + ADP	2.7.4.11	Adenylate kinase, dAMP kinase		ANID	An01g04710	46678
r439	: DADP + ATP \rightleftharpoons DATP + ADP	2.7.4.6	Nucleoside-diphosphate kinase	Lin et al. (2003, A. nidulans)	ANID	An09g05870	212435
r440	: IMP + NAD \Rightarrow NADH + XMP	1.1.1.205	Inosine-5'-monophosphate dehydrogenase		ANID	An07g08170	53197
r441	: XMP + ATP + GLN + H ₂ O \Rightarrow GLU + AMP + PPi + GMP	6.3.5.2	GMP synthase		ANID	An02g14520	37616
r442	: GMP + ATP \rightleftharpoons GDP + ADP	2.7.4.8	Guanylate kinase		ANID	An01g07070; An08g00300	143052; 130364
r443	: GDP + ATP \rightleftharpoons GTP + ADP	2.7.4.6	Nucleoside-diphosphate kinase	Lin et al. (2003, A. nidulans), David et al. (2003)	ANIG, ANID	An09g05870	212435
r444	: GTP + AMP \rightleftharpoons ADP + GDP	2.7.4.3	Adenylate kinase	Perl (1982)	ANIG, ANID	An01g04710; An07g10100	46678; 56109
r445	: GDP + RTHIO \Rightarrow DGDP + OTHIO + H ₂ O	1.17.4.1	Ribonucleotide reductase	Hockertz et al. (1987)	ANID *	An04g01080; An14g06870	57102; 56635
r446	: DGDP + ATP \rightleftharpoons DGTP + ADP	2.7.4.6	Nucleoside-diphosphate kinase	Lin et al. (2003, A. nidulans)	ANID	An09g05870	212435
r447	: DGDP + ADP \rightleftharpoons DGMP + ATP	2.7.4.8	Guanylate kinase		ANID	An01g07070; An08g00300	143052; 130364
r448	: ITP + AMP \rightleftharpoons ADP + IDP	2.7.4.6	Adenylate kinase	Perl (1982)	ANIG, ANID	An09g05870	212435
r449	: IDP + H ₂ O \Rightarrow IMP + PI	3.6.1.6	Inosine diphosphatase		ANID		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
Purine conversions							
r450	$\text{GMP} + \text{DATP} \rightleftharpoons \text{GDP} + \text{DADP}$	2.7.4.8	Guanylate kinase	Darlington et al. (1965); Scazzocchio et al. (1982, A. nidulans), Kanehisa et al. (2002); Elzainy et al. (1989)	ANID	An01g07070; An08g00300	143052; 130364
Purine degradation							
r451	$\text{AMP} + \text{H}_2\text{O} \Rightarrow \text{PI} + \text{ADN}$	3.1.3.5	5'-nucleotidase	Kuwahara and Fujii (1978); Elzainy et al. (1989); Elzainy and Ali (2000); Ali and Elzainy (2000)	ANID	An08g08080	128775
r452	$\text{AMP} + \text{H}_2\text{O} \rightleftharpoons \text{AD} + \text{R5P}$	3.2.2.4	AMP nucleosidase	Kuwahara and Fujii (1978)	ANEW		
r453	$\text{ADN} + \text{H}_2\text{O} \Rightarrow \text{AD} + \text{RIB}$	3.2.2.1	Purine nucleoside hydrolase	Kuwahara and Fujii (1978); Elzainy et al. (1978, 1989)	ANID	An08g03980	55818
r454	$\text{ADN} + \text{H}_2\text{O} \Rightarrow \text{INS} + \text{NH}_3$	3.5.4.4	Adenosine deaminase	Ribard et al. (2003, A. nidulans), Mitschell and McElroy (1946); Grosshans and Wolfenden (1993, A. oryzae), Abu-Shady et al. (1994, A. ferrocola)	ANID	An12g04800; An16g02890	49658; 183577
r455	$\text{AD} + \text{H}_2\text{O} \Rightarrow \text{NH}_3 + \text{HYXN}$	3.5.4.2	Adenine deaminase	Scazzocchio et al. (1982); Ribard et al. (2001, A. nidulans)	ANID	An12g04800; An16g02890	49658; 183577
r456	$\text{DAMP} + \text{H}_2\text{O} \Rightarrow \text{DA} + \text{PI}$	3.1.3.5	5'-nucleotidase	Rama and Shanmugasundaram (1985, A. nidulans)	ANID	An08g08080	128775
r457	$\text{DA} + \text{PI} \rightleftharpoons \text{AD} + \text{DR1P}$	2.4.2.1	Purine nucleotide phosphorylase, xanthosine phosphorylase		ANID	An11g06110	178461
r458	$\text{DA} + \text{H}_2\text{O} \Rightarrow \text{DIN} + \text{NH}_3$	3.5.4.4	Adenine deaminase/adenosine deaminase	Ribard et al. (2003, Inferred), Grosshans and Wolfenden (1993, A. oryzae)	ANID	An12g04800; An16g02890	49658; 183577
r459	$\text{DIN} + \text{PI} \rightleftharpoons \text{HYXN} + \text{DR1P}$	2.4.2.1	Purine nucleotide phosphorylase, xanthosine phosphorylase		ANID	An11g06110	178461
r460	$\text{IMP} + \text{H}_2\text{O} \Rightarrow \text{PI} + \text{INS}$	3.1.3.5	5'-nucleotidase	Kuwahara and Fujii (1978)	ANID	An08g08080	128775
r461	$\text{IMP} + \text{H}_2\text{O} \Rightarrow \text{HYXN} + \text{R5P}$	3.2.2.1	purine nucleosidase	Kuwahara and Fujii (1978)	ANEW	An08g03980	55818
r462	$\text{INS} + \text{PI} \Rightarrow \text{HYXN} + \text{R1P}$	2.4.2.1	Purine nucleotide phosphorylase, xanthosine phosphorylase	Kuwahara and Fujii (1978); Elzainy et al. (1978)	ANID	An11g06110	178461
r463	$\text{INS} + \text{H}_2\text{O} \Rightarrow \text{HYXN} + \text{RIB}$	3.2.2.1	Purine nucleosidase/purine nucleoside hydrolase	Kuwahara and Fujii (1978); Elzainy et al. (1978)	ANEW	An08g03980	55818
r464	$\text{HYXN} + \text{NAD} + \text{H}_2\text{O} \rightleftharpoons \text{XAN} + \text{NADH}$	1.17.1.4	Xanthine dehydrogenase	Darlington et al. (1965); Scazzocchio et al. (1982, A. nidulans)	ANEW	An03g01530	214667
r465	$\text{GMP} + \text{H}_2\text{O} \Rightarrow \text{PI} + \text{GSN}$	3.1.3.5	5'-nucleotidase	Elzainy et al. (1989); Ali and Elzainy (2000)	ANID	An08g08080	128775
r466	$\text{GSN} + \text{PI} \rightleftharpoons \text{GN} + \text{R5P}$	3.2.2.1	purine nucleosidase	Kuwahara and Fujii (1978)	ANEW	An08g03980	55818
r467	$\text{GSN} + \text{H}_2\text{O} \Rightarrow \text{GN} + \text{RIB}$	3.2.2.1	Purine nucleoside hydrolase	Kuwahara and Fujii (1978); Elzainy et al. (1978, 1989)	ANID	An08g03980	55818
r468	$\text{GN} + \text{H}_2\text{O} \rightleftharpoons \text{XAN} + \text{NH}_3$	3.5.4.3	Guanine aminohydrolase	Darlington et al. (1965, Inferred)	ANEW	An11g01070; An14g01140	38774; 184651

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r469	: DGMP + H ₂ O ⇒ DG + PI	3.1.3.5	5'-nucleotidase	Rama and Shamugasundaram (1985, A. nidulans)	ANID	An08g08080	128775
r470	: DG + PI ⇌ GN + DRIP	2.4.2.1	Purine nucleotide phosphorylase, xanthosine phosphorylase		ANID	An11g06110	178461
r471	: XMP + H ₂ O ⇒ PI + XTSINE	3.1.3.5	5'-nucleotidase	Rama and Shamugasundaram (1985, A. nidulans)	ANID	An08g08080	128775
r472	: PI + XTSINE ⇌ XAN + R1P	2.4.2.1	Purine nucleotide phosphorylase, xanthosine phosphorylase		ANID	An11g06110	178461
r473	: XAN + NAD + H ₂ O ⇌ URIC + NADH	1.17.1.4	Xanthine dehydrogenase (purine hydroxylase I)	Darlington et al. (1965); Arst and Cove (1969); Scazzocchio et al. (1982, A. nidulans)	ANEW	An03g01530	214667
r474	: URIC + O ₂ + H ₂ O ⇌ HIUR + H ₂ O ₂	1.7.3.3	Uricase	Ertan and Aksoz (2000)	ANEW	An02g06030; An03g02330	55563; 51359
r475	: HIUR + H ₂ O ⇒ ATN + CO ₂	3.5.2.17	Hydroxyisourate hydrolase + spontaneous conversion	Darlington et al. (1965, A. nidulans)	ANEW		
r476	: ATN + H ₂ O ⇌ ATT	3.5.2.5	Allantoinase	Darlington et al. (1965); Arst and Cove (1969); Scazzocchio et al. (1982, A. nidulans)	ANID	An14g03370	N/A
r477	: ATT + H ₂ O ⇌ UGC + UREA	3.5.3.4	Allantoicase	Darlington et al. (1965); Arst and Cove (1969); Scazzocchio et al. (1982, A. nidulans)	ANID	An02g08520	172988
r478	: UGC + H ₂ O ⇒ GLX + 2 NH ₃ + CO ₂	3.5.3.19	Ureidoglycolate hydrolase	Darlington et al. (1965, A. nidulans)	ANID	An16g08100	193909
Pyrimidine biosynthesis (UTP, CTP, dCTP, dUTP and dTTP)							
r479	: GLN + 2 ATP + CO ₂ + 2 H ₂ O ⇒ GLU + CAP + 2 ADP + PI	6.3.5.5	Carbamoyl-phosphate synthetase, aspartate transcarbamylase, and glutamine amidotransferase	Palmer et al. (1975); Aleksenko et al. (1999, A. nidulans)	ANID *	An16g04960; An16g04970; An17g00820	53574; 53574; 54890
r480	: CAP + ASP ⇒ CAASP + PI	2.1.3.2	Aspartate-carbamoyltransferase	Palmer et al. (1975, A. nidulans)	ANID	An08g07420	55738
r481	: CAASP ⇌ DOROA + H ₂ O	3.5.2.3	Dihydroorotase		ANID	An01g10650; An08g07420	205639; 55738
r482	: DOROA + O ₂ ⇒ H ₂ O ₂ + OROA	1.3.3.1	Dihydroorotate dehydrogenase	Gustafson and Waldron (1992, A. nidulans)	ANID	An02g02910	36779
r483	: OROA + PRPP ⇌ PPI + OMP	2.4.2.10	Orotate phosphoribosyltransferase 1		ANID	An04g08330	55173
r484	: OMP ⇒ CO ₂ + UMP	4.1.1.23	Orotidine-5'-phosphate decarboxylase (pyrA)	Goosen et al. (1987)	ANID	An12g03570	56726
r485	: ADP + UDP ⇌ ATP + UMP	2.7.4.14	Cytidylate kinase	David et al. (2003)	ANID	An13g00440	50815
r486	: UTP + AMP ⇌ UDP + ADP	2.7.4.3	Adenylate kinase		ANIG	An01g04710; An07g10100	46678; 56109
r487	: UDP + ATP ⇌ UTP + ADP	2.7.4.6	Nucleoside-diphosphate kinase	Lin et al. (2003, A. nidulans), David et al. (2003)	ANIG, ANID	An09g05870	212435

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r488	UTP + GLN + ATP + H ₂ O \Rightarrow GLU + CTP + ADP + PI	6.3.4.2	CTP synthase		ANID	An03g01310	57431
r489	ATP + UTP + NH ₃ \Rightarrow ADP + PI + CTP	6.3.4.2	CTP synthase		ANID	An03g01310	57431
r490	CTP + ADP \rightleftharpoons CDP + ATP	2.7.4.6	Nucleoside-diphosphate kinase	Lin et al. (2003, A. nidulans), David et al. (2003)	ANIG, ANID	An09g05870	212435
r491	CTP + AMP \rightleftharpoons CDP + ADP	2.7.4.3	Adenylyate kinase	David et al. (2003)	ANIG	An01g04710; An07g10100	46678; 56109
r492	ADP + CDP \rightleftharpoons CMP + ATP	2.7.4.14	Cytidylate kinase		ANID	An13g00440	50815
r493	CDP + RTHIO \Rightarrow DCDP + OTHIO + H ₂ O	1.17.4.1	Ribonucleotide reductase, small subunit (alt), beta chain	Hockertz et al. (1987)	ANID *	An04g01080; An14g06870	57102; 56635
r494	UDP + RTHIO \Rightarrow OTHIO + DUDP + H ₂ O	1.17.4.1	Ribonucleotide reductase, small subunit (alt), beta chain	Hockertz et al. (1987)	ANID *	An04g01080; An14g06870	57102; 56635
r495	DUMP + METHF \Rightarrow DHF + DTMP	2.1.1.45	Thymidylate synthase		ANID	An14g00570	49219
r496	DCDP + ATP \rightleftharpoons DCTP + ADP	2.7.4.6	Nucleoside-diphosphate kinase	Lin et al. (2003, A. nidulans)	ANID	An09g05870	212435
r497	DCMP + ATP \rightleftharpoons ADP + DCDP	2.7.4.14	Nucleoside-phosphate kinase/ATP:UMP-CMP phosphotransferase/-cytidylate kinase		ANID	An13g00440	50815
r498	DUDP + ATP \rightleftharpoons DUTP + ADP	2.7.4.6	Nucleoside-diphosphate kinase	Lin et al. (2003, A. nidulans)	ANID	An09g05870	212435
r499	DUMP + ATP \rightleftharpoons DUDP + ADP	2.7.4.9	Uridylate kinase		ANID	An09g05840	56895
r500	DTMP + ATP \rightleftharpoons ADP + DTDP	2.7.4.9	dTMP kinase/thymidylate kinase		ANID	An09g05840	56895
r501	DTDP + ATP \rightleftharpoons DTTP + ADP	2.7.4.6	Nucleoside-diphosphate kinase	Lin et al. (2003, A. nidulans)	ANID	An09g05870	212435
Pyrimidine conversions							
r502	URI + GTP \Rightarrow UMP + GDP	2.7.1.48	Uridine kinase		ANID	An11g09320	53035
r503	URI + ATP \Rightarrow ADP + UMP	2.7.1.48	Uridine kinase		ANID	An11g09320	53035
r504	CYTD + GTP \Rightarrow GDP + CMP	2.7.1.48	Uridine kinase		ANID	An11g09320	53035
r505	URA + PRPP \Rightarrow UMP + PPI	2.4.2.9	UPRTase, uracil phosphoribosyltransferase (furA)		ANID	An12g09660; An12g09670; An15g06580; An17g02370	42030; 49490; 53518; 54952
r506	DUTP + H ₂ O \Rightarrow PPI + DUMP	3.6.1.23	dUTP pyrophosphatase (dUTPase)		ANID	An01g05040	172313
r507	DORO + Qm \Rightarrow QH2m + OROA	1.3.1.14	Dihydroorotate dehydrogenase	Gustafson and Waldron (1992); Aleksenko et al. (1999, A. nidulans)	ANID	An02g02910	36779
r508	OTHIO + NADPH \Rightarrow NADP + RTHIO	1.8.1.9	Thioredoxin reductase		ANID	An12g02850	50359
r509	OTHIOm + NADPHm \Rightarrow NADPm + RTHIOm	1.8.1.9	Thioredoxin reductase		ANID	An12g02850	50359

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
Pyrimidine degradation							
r510	: UMP + H ₂ O ⇒ PI + URI	3.1.3.5	5'-nucleotidase	Darlington et al. (1965, A. nidulans), Kanehisa et al. (2002); Elzaïny et al. (1989)	ANID	An08g08080	128775
r511	: URI + H ₂ O ⇒ URA + RIB	3.2.2.3	Uridine hydrolase	Ali and Elzaïny (2000)	ANEW	An18g04340	42881
r512	: CMP + H ₂ O ⇒ CYTD + PI	3.1.3.5	5'-nucleotidase	Fukami (1961, A. nidulans)	ANEW	An18g04340	42881
r513	: CYTD + H ₂ O ⇒ URI + NH ₃	3.5.4.5	Cytidine deaminase	Elzaïny et al. (1989); Ali and Elzaïny (2000)	ANID	An08g08080	128775
r514	: CMP + H ₂ O ⇒ CYTS + R5P	3.2.2.10	CMP glycosylase	Elzaïny et al. (1989); Ali (1998)	ANID	An03g06870	50782
r515	: CYTS + H ₂ O ⇒ URA + NH ₃	3.5.4.1	Cytosine deaminase	Fukami (1961, A. nidulans)	ANID	An01g04260	206127
r516	: DCMP + H ₂ O ⇒ DC + PI	3.1.3.5	5'-nucleotidase	Rama and Shanmugasundaram (1985, A. nidulans)	ANID	An08g08080	128775
r517	: DC + H ₂ O ⇒ NH ₃ + DU	3.5.4.5	Deoxycytidine deaminase	Fukami (1961, A. nidulans)	ANID	An03g06870	50782
r518	: DUMP + H ₂ O ⇒ DU + PI	3.1.3.5	5'-nucleotidase	Rama and Shanmugasundaram (1985, A. nidulans)	ANID	An08g08080	128775
r519	: URA + DR1P ⇒ DU + PI	2.4.2.1	Purine-nucleoside phosphorylase		ANEW	An11g06110	178461
r520	: DTMP + H ₂ O ⇒ DT + PI	3.1.3.5	5'-nucleotidase	Rama and Shanmugasundaram (1985, A. nidulans)	ANID	An08g08080	128775
r521	: THY + DR1P ⇒ DT + PI	2.4.2.1	Purine-nucleoside phosphorylase		ANEW	An11g06110	178461
Salvage pathways for nucleotides							
r522	: HYN + PRPP ⇒ PPI + IMP	2.4.2.8	Hypoxanthine phosphoribosyltransferase		ANID	An14g00280	210854
r523	: GN + PRPP ⇒ PPI + GMP	2.4.2.8	Hypoxanthine phosphoribosyltransferase		ANID	An14g00280	210854
r524	: AD + PRPP ⇒ PPI + AMP	2.4.2.7	Adenine phosphoribosyltransferase	Ribard et al. (2001, A. nidulans)	ANID	An12g00320	54445
r525	: XAN + PRPP ⇒ XMP + PPI	2.4.2.22	Xanthine-guanine phosphoribosyltransferase		ANID	An14g00280	210854
r526	: PRPP + H ₂ O ⇒ PRCP + PI	No EC	Non Enz	Trembacz and Jezewska (1990)	ANEW		
r527	: PRCP + H ₂ O ⇒ RIP + PI	No EC	Non Enz	Trembacz and Jezewska (1990)	ANEW		
r528	: AD + RIP ⇒ PI + ADN	2.4.2.1	Purine nucleotide phosphorylase, xanthosine phosphorylase		ANID		
r529	: GN + RIP ⇒ PI + GSN	2.4.2.1	Purine nucleotide phosphorylase, xanthosine phosphorylase		ANID		
r531	: ADN + ATP ⇒ AMP + ADP	2.7.1.20	Adenosine kinase	David et al. (2003)	ANIG, ANID	An17g01330	214022
r532	: INS + ATP ⇒ IMP + ADP	2.7.1.73	Inosine kinase		ANID		
r533	: GSN + ATP ⇒ GMP + ADP	2.7.1.73	Inosine kinase		ANID		
r534	: ATP ⇒ cAMP + PPI	4.6.1.1	Adenylate cyclase	Wold and Suzuki (1974)	ANID	An11g01520	178015
r535	: cAMP ⇒ AMP	3.1.4.17	3',5'-cyclic-nucleotide phosphodiesterase	Wold and Suzuki (1974); Pall (1981)	ANID	An01g04450; An01g13010	36176; 195992
r536	: cdAMP ⇒ DAMP	3.1.4.17	3',5'-cyclic-nucleotide phosphodiesterase		ANID	An01g04450; An01g13010	36176; 195992

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r537	: cIMP \Rightarrow IMP	3.1.4.17	3'-5'-cyclic-nucleotide phosphodiesterase		ANID	An01g04450; An01g13010	36176; 195992
r538	: cGMP \Rightarrow GMP	3.1.4.17	3'-5'-cyclic-nucleotide phosphodiesterase, low affinity		ANID	An01g04450; An01g13010	36176; 195992
r539	: cCMP \Rightarrow CMP	3.1.4.17	3'-5'-cyclic-nucleotide phosphodiesterase, low affinity		ANID	An01g04450; An01g13010	36176; 195992
r540	: cAMPe \Rightarrow AMPe	3.1.4.17	3'-5'-cyclic-nucleotide phosphodiesterase	Wold and Suzuki (1974)	ANEW	An01g04450; An01g13010	36176; 195992
r541	: ATPm + AMPm \rightleftharpoons 2 ADPm	2.7.4.3	Adenylate kinase		ANIG, ANID	An01g04710; An07g10100	46678; 56109
r542	: GTPm + AMPm \rightleftharpoons ADPm + GDPm	2.7.4.3	Adenylate kinase		ANIG, ANID	An01g04710; An07g10100	46678; 56109
r543	: ITPm + AMPm \rightleftharpoons ADPm + IDPm	2.7.4.3	Adenylate kinase		ANID	An01g04710; An07g10100	46678; 56109
NAD and NADPH metabolism							
Nicotinate and Nicotinamide biosynthesis							
r544	: ASP + O ₂ \Rightarrow IMASP + H ₂ O ₂	1.4.3.16	L-aminoacid oxidase	Sarma et al. (1962, Inferred)	ANEW		
r1267	: IMASP + T3P1 \rightleftharpoons QUIN + 2 H ₂ O + PI	No Ec	quinolinate synthetase, NAD ⁺	Sarma et al. (1962, Inferred)	ANEW		
r545	: QUIN + PRPP \Rightarrow NAMN + PPI + CO ₂	2.4.2.19	Nicotinate mononucleotide pyrophosphorylase	Sarma et al. (1962, Inferred)	ANEW	An11g10910	56085
r546	: NICD + H ₂ O \rightleftharpoons NICA + NH ₃	3.5.1.19	nicotinamidase	Sarma et al. (1964); Kuwahara et al. (1983)	ANEW	An07g08360	48305
r547	: NICA + PRPP \Rightarrow NAMN + PPI	2.4.2.11	Nicotinate phosphoribosyltransferase	Sarma et al. (1962); Kuwahara et al. (1983, Inferred)	ANEW	An12g00760	50290
r548	: ATP + NAMN \Rightarrow PPI + DMNAD	2.7.7.1	Nicotinamide-nucleotide adenyllyltransferase	Kuwahara et al. (1983, Inferred)	ANEW	An11g06610	178093
r549	: ATP + DMNAD + GLN + H ₂ O \rightleftharpoons AMP + PPI + NAD + GLU	6.3.5.1	NAD synthetase	Kuwahara et al. (1983, Inferred)	ANEW	An09g05660	54326
r550	: ATP + NAD \Rightarrow ADP + NADP	2.7.1.23	NAD kinase	Kuwahara et al. (1982, Inferred)	ANEW	An03g05090; An14g06430	191587; 53896
NADP and NAD degradation							
r551	: NADP + H ₂ O \Rightarrow NAD + PI	No Ec	NADPH phosphatase	Kuwahara et al. (1982, Inferred)	ANEW		
r552	: NAD + H ₂ O \Rightarrow NAMR + ADP	No Ec	acid phosphatase	Elzainy and Ali (2000)	ANEW		
r553	: NAD + H ₂ O \Rightarrow ADPR + NICD	3.2.2.5	NAD-glycohydrolase	Sarma et al. (1964),	ANEW		
r554	: NAD + H ₂ O \Rightarrow AMP + NMN	3.6.1.22	NAD pyrophosphatase	Kuwahara et al. (1983, Inferred)	ANEW	An09g05670	212451
r555	: NMN + H ₂ O \Rightarrow NAMR + PI	3.1.3.5	5'-nucleotidase	Kuwahara et al. (1983, Inferred)	ANEW	An08g08080	128775
r556	: NAMR + H ₂ O \Rightarrow NAR + NH ₃	No Ec	nicotinate nucleotide amidase	Kuwahara et al. (1983)	ANEW		
r557	: NMN + H ₂ O \rightleftharpoons R5P + NICD	3.2.2.14	NMN nucleosidase	Kuwahara et al. (1983, Inferred)	ANEW		
r558	: NAMN + H ₂ O \Rightarrow NAR + PI	3.1.3.5	5'-nucleotidase	Kuwahara et al. (1982, 1983, Inferred)	ANEW	An08g08080	128775
3-Cyanopyridine degradation				Snajdrova et al. (2004)			

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1213	: 3CPYRD + 2 H ₂ O ⇒ NICA + NH ₃	3.5.5.1	benzonitrilase	Snajdrova et al. (2004)	ANEW	An16g00550; An01g07510; An01g12090; An06g01960; An08g08940; An08g10150; An12g01260; An16g06210; An18g01740	41410; 35944; 170270; 175987; N/A; 32578; 141873; 40928; 211815
LIPID METABOLISM							
FATTY ACIDS METABOLISM							
Formation of saturated cytosolic fatty acids (Even numbers)							
r559	: CBCCP + ACCOA ⇒ BCCP + MAL-CoA	6.4.1.2	Acetyl-CoA carboxylase (ACC) / biotin carboxylase	Schwenk and Bennett (1969)	ANID	An12g04020	56715
r560	: ATP + BCCP + CO ₂ + H ₂ O ⇌ ADP + PI + GBCCP	6.3.4.14	Biotin carboxylase	Schwenk and Bennett (1969)	ANEW	An12g04020	56715
r561	: MALCOA + ACP ⇌ MALACP + COA	2.3.1.39	Malonyl transferase		ANEW	An04g00040	190484
r562	: ACCOA + ACP ⇌ ACACP + COA	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r563	: ACACP + MALACP ⇒ AACACP + CO ₂ + ACP	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604
r564	: AACACP + NADPH ⇌ C4HACP + NADP	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r565	: C4HACP ⇌ C4DACP + H ₂ O	2.3.1.85	Fatty-acid synthase		ANEW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r566	: C4DACP + NADPH ⇌ C4OACP + NADP	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r568	: C4OACP + MALACP ⇒ C6OACP + CO ₂ + ACP	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r569	$\text{C6OACP} + \text{NADPH} \rightleftharpoons \text{C6HACP} + \text{NADP}$	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r570	$\text{C6HACP} \rightleftharpoons \text{C6DACP} + \text{H}_2\text{O}$	2.3.1.85	Fatty-acid synthase		ANW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r571	$\text{C6DACP} + \text{NADPH} \rightleftharpoons \text{C6OACP} + \text{NADP}$	1.3.1.9	Enoyl-ACP reductase		ANW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r573	$\text{C6OACP} + \text{MALACP} \rightleftharpoons \text{C8OACP} + \text{CO}_2 + \text{ACP}$	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANW	An02g14220; An14g01760	55650; 41604
r574	$\text{C8OACP} + \text{NADPH} \rightleftharpoons \text{C8HACP} + \text{NADP}$	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r575	$\text{C8HACP} \rightleftharpoons \text{C8DACP} + \text{H}_2\text{O}$	2.3.1.85	Fatty-acid synthase		ANW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r576	$\text{C8DACP} + \text{NADPH} \rightleftharpoons \text{C8OACP} + \text{NADP}$	1.3.1.9	Enoyl-ACP reductase		ANW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r578	$\text{C8OACP} + \text{MALACP} \rightleftharpoons \text{C10OACP} + \text{CO}_2 + \text{ACP}$	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANW	An02g14220; An14g01760	55650; 41604

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r579	$C10OACP + NADPH \rightleftharpoons C10HACP + NADP$	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r580	$C10HACP \rightleftharpoons C10DACP + H_2O$	2.3.1.85	Fatty-acid synthase		ANEW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r581	$C10DACP + NADPH \rightleftharpoons C10OACP + NADP$	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r583	$C10OACP + MALACP \rightleftharpoons C12OACP + CO_2 + ACP$	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604
r584	$C12OACP + NADPH \rightleftharpoons C12HACP + NADP$	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r585	$C12HACP \rightleftharpoons C12DACP + H_2O$	2.3.1.85	Fatty-acid synthase		ANEW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r586	$C12DACP + NADPH \rightleftharpoons C12OACP + NADP$	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r588	$C12OACP + MALACP \rightleftharpoons C14OACP + CO_2 + ACP$	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r589	C14OACP + NADPH \rightleftharpoons C14HACP + NADP	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An01g14000; An03g02840; An05g02050; An06g02000; An06g02610; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An16g07090; An18g00290	35566; 172477; 45652; 43929; 37709 and 47218; 137016; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 45606; 187979
r590	C14HACP \rightleftharpoons C14DACP + H2O	4.2.1.61	Long chain beta-hydroxypalmitoyl thioester dehydratase		ANEW	An12g01990	43740
r591	C14DACP + NADPH \rightleftharpoons C14OACP + NADP	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r598	C14OACP + MALACP \rightleftharpoons C16OACP + CO2 + ACP	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604
r599	C16OACP + NADPH \rightleftharpoons C16HACP + NADP	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An01g14000; An03g02840; An05g02050; An06g02000; An06g02610; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An16g07090; An18g00290	35566; 172477; 45652; 43929; 37709 and 47218; 137016; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 45606; 187979
r600	C16HACP \rightleftharpoons C16DACP + H2O	4.2.1.61	Long chain beta-hydroxypalmitoyl thioester dehydratase		ANEW	An12g01990	43740
r601	C16DACP + NADPH \rightleftharpoons C16OACP + NADP	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r608	C16OACP + MALACP \rightleftharpoons C18OACP + CO2 + ACP	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r609	$C18OACP + NADPH \rightleftharpoons C18HACP + NADP$	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An01g14000; An03g02840; An05g02050; An06g02000; An06g02610; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An16g07090; An18g00290	35566; 172477; 45652; 43929; 37709 and 47218; 137016; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 45606; 187979
r610	$C18HACP \rightleftharpoons C18DACP + H_2O$	4.2.1.61	Long chain beta-hydroxypalmitoyl thioester dehydratase		ANEW	An12g01990	43740
r611	$C18DACP + NADPH \rightleftharpoons C18OACP + NADP$	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r618	$C18OACP + MALACP \rightleftharpoons C20OACP + CO_2 + ACP$	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604
r619	$C20OACP + NADPH \rightleftharpoons C20HACP + NADP$	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An01g14000; An03g02840; An05g02050; An06g02000; An06g02610; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An16g07090; An18g00290	172477; 45652; 43929; 37709 and 47218; 137016; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 45606; 187979
r620	$C20HACP \rightleftharpoons C20DACP + H_2O$	4.2.1.61	Long chain beta-hydroxypalmitoyl thioester dehydratase		ANEW	An12g01990	43740
r621	$C20DACP + NADPH \rightleftharpoons C20OACP + NADP$	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r1224	Formation of saturated cytosolic fatty acids (Odd numbers) $PROPCOA + ACP \rightleftharpoons PROPACP + COA$	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1225	: PROPACP + MALACP \Rightarrow C5OACP + CO ₂ + ACP	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604
r1226	: C5OACP + NADPH \rightleftharpoons C5HACP + NADP	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709; and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r1227	: C5HACP \rightleftharpoons C5DACP + H ₂ O	2.3.1.85	Fatty-acid synthase		ANEW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r1228	: C5DACP + NADPH \rightleftharpoons C5OACP + NADP	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r1230	: C5OACP + MALACP \Rightarrow C7OACP + CO ₂ + ACP	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604
r1231	: C7OACP + NADPH \rightleftharpoons C7HACP + NADP	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709; and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r1232	: C7HACP \rightleftharpoons C7DACP + H ₂ O	2.3.1.85	Fatty-acid synthase		ANEW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r1233	: C7DACP + NADPH \rightleftharpoons C7OACP + NADP	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r1235	: C7OACP + MALACP \Rightarrow C9OACP + CO ₂ + ACP	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1236	$C9OACP + NADPH \rightleftharpoons C9HACP + NADP$	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r1237	$C9HACP \rightleftharpoons C9DACP + H_2O$	2.3.1.85	Fatty-acid synthase		ANEW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r1238	$C9DACP + NADPH \rightleftharpoons C9OACP + NADP$	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r1240	$C9OACP + MALACP \rightleftharpoons C11OACP + CO_2 + ACP$	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604
r1241	$C11OACP + NADPH \rightleftharpoons C11HACP + NADP$	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r1242	$C11HACP \rightleftharpoons C11DACP + H_2O$	2.3.1.85	Fatty-acid synthase		ANEW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r1243	$C11DACP + NADPH \rightleftharpoons C11OACP + NADP$	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r1245	$C11OACP + MALACP \rightleftharpoons C13OACP + CO_2 + ACP$	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1246	: C13OACP + NADPH \rightleftharpoons C13HACP + NADP	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; and An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r1247	: C13HACP \rightleftharpoons C13DACP + H ₂ O	2.3.1.85	Fatty-acid synthase		ANW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r1248	: C13DACP + NADPH \rightleftharpoons C13OACP + NADP	1.3.1.9	Enoyl-ACP reductase		ANW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r1250	: C13OACP + MALACP \rightleftharpoons C15OACP + CO ₂ + ACP	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANW	An02g14220; An14g01760	55650; 41604
r1251	: C15OACP + NADPH \rightleftharpoons C15HACP + NADP	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; and An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r1252	: C15HACP \rightleftharpoons C15DACP + H ₂ O	2.3.1.85	Fatty-acid synthase		ANW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r1253	: C15DACP + NADPH \rightleftharpoons C15OACP + NADP	1.3.1.9	Enoyl-ACP reductase		ANW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r1255	: C15OACP + MALACP \rightleftharpoons C17OACP + CO ₂ + ACP	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANW	An02g14220; An14g01760	55650; 41604

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1256	$C17OACP + NADPH \rightleftharpoons C17HACP + NADP$	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r1257	$C17HACP \rightleftharpoons C17DACP + H_2O$	2.3.1.85	Fatty-acid synthase		ANEW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r1258	$C17DACP + NADPH \rightleftharpoons C17OACP + NADP$	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
r1260	$C17OACP + MALACP \rightleftharpoons C19OACP + CO_2 + ACP$	2.3.1.41	3-oxoacyl-[acyl-carrier-protein] synthase		ANEW	An02g14220; An14g01760	55650; 41604
r1261	$C19OACP + NADPH \rightleftharpoons C19HACP + NADP$	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase		ANEW	An01g12400; An03g02840; An05g02050; An06g02000; An08g01930; An11g00760; An12g02320; An12g05100; An13g01130; An14g01270; An14g06740; An18g00290	35566; 45652; 43929; 37709 and 47218; 177736; 124830; 189865; 49639; 44744; 124614; 185180; 187979
r1262	$C19HACP \rightleftharpoons C19DACP + H_2O$	2.3.1.85	Fatty-acid synthase		ANEW *	An08g10930; An09g02010; An12g01980	47227; 188253; 189622
r1263	$C19DACP + NADPH \rightleftharpoons C19OACP + NADP$	1.3.1.9	Enoyl-ACP reductase		ANEW	An07g03290; An16g05340; An04g02300	209754; 56395; 190311
Formation of unsaturated cytosolic fatty acids							
r623	$C19OACP + NADH + 2 H_2O \rightleftharpoons C191ACP + NAD + 2 H_2O$	1.14.19.1	C190-CoA 9-desaturase	Chattopadhyay et al. (1985b,a) Chattopadhyay et al. (1985b)	ANEW	An07g01960; An12g09940	209875; 195065
r624	$C191ACP + NADH + 2 H_2O \rightleftharpoons C192ACP + NAD + 2 H_2O$	1.14.19.3	C190-CoA 12-desaturase	Chattopadhyay et al. (1985a)	ANEW	An07g06770; An16g06350	209561; 48908
r625	$C18OACP + NADH + 2 H_2O \rightleftharpoons C181ACP + NAD + 2 H_2O$	1.14.19.1	stearoyl-CoA 9-desaturase	Chattopadhyay et al. (1985b)	ANEW	An07g01960; An12g09940	209875; 195065
r626	$C181ACP + NADH + 2 H_2O \rightleftharpoons C182ACP + NAD + 2 H_2O$	1.14.19.3	stearoyl-CoA desaturase	Chattopadhyay et al. (1985a)	ANEW	An07g06770; An16g06350	209561; 48908

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r627	: C182ACP + NADH + O2 \rightleftharpoons C183ACP + NAD + 2 H2O	No EC	stearoyl-CoA desaturase	15- Chattopadhyay et al. (1985a)	ANEW		
r988	: C170ACP + NADH + O2 \rightleftharpoons C171ACP + NAD + 2 H2O	No EC	C170-CoA 9-desaturase	Levery et al. (2000, Inferred)	ANEW		
r628	: C160ACP + NADH + O2 \rightleftharpoons C161ACP + NAD + 2 H2O	1.14.19.1	C160-CoA 9-desaturase	Chattopadhyay et al. (1985b, Inferred)	ANEW	An07g01960; An12g09940	209875; 195065
r629	: C161ACP + NADH + O2 \rightleftharpoons C162ACP + NAD + 2 H2O	1.14.19.3	C160-CoA 12-desaturase	Chattopadhyay et al. (1985a, Inferred)	ANEW	An07g06770; An16g06350	209561; 48908
r630	: C140ACP + NADH + O2 \rightleftharpoons C141ACP + NAD + 2 H2O	1.14.19.1	C160-CoA 9-desaturase	Chattopadhyay et al. (1985a, Inferred)	ANEW	An07g01960; An12g09940	209875; 195065
Removal of ACPs							
r936	: C40ACP + H2O \Rightarrow C40 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r937	: C60ACP + H2O \Rightarrow C60 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r938	: C80ACP + H2O \Rightarrow C80 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r939	: C100ACP + H2O \Rightarrow C100 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r940	: C120ACP + H2O \Rightarrow C120 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r941	: C140ACP + H2O \Rightarrow C140 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r942	: C141ACP + H2O \Rightarrow C141 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r943	: C150ACP + H2O \Rightarrow C150 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r944	: C160ACP + H2O \Rightarrow C160 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r945	: C161ACP + H2O \Rightarrow C161 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r946	: C162ACP + H2O \Rightarrow C162 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r947	: C170ACP + H2O \Rightarrow C170 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r987	: C171ACP + H2O \Rightarrow C171 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r948	: C180ACP + H2O \Rightarrow C180 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r949	: C181ACP + H2O \Rightarrow C181 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r950	: C182ACP + H2O \Rightarrow C182 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r951	: C183ACP + H2O \Rightarrow C183 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r952	: C190ACP + H2O \Rightarrow C190 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r953	: C191ACP + H2O \Rightarrow C191 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r954	: C192ACP + H2O \Rightarrow C192 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
r955	: C200ACP + H2O \Rightarrow C200 + ACP	3.1.2.14	Acyl-ACP-hydrolase		ANEW		
Transfer of ACP-Acyls to CoA for transport and biosynthesis							
r631	: C40ACP + CoA \rightleftharpoons C40CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r617	: C60ACP + CoA \rightleftharpoons C60CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW		
r632	: C80ACP + CoA \rightleftharpoons C80CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r633	: C80ACP + CoA \rightleftharpoons C80CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r634	: C100ACP + CoA \rightleftharpoons C100CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r635	: C120ACP + CoA \rightleftharpoons C120CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r636	: C140ACP + CoA \rightleftharpoons C140CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r637	: C141ACP + CoA \rightleftharpoons C141CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r638	: C150ACP + CoA \rightleftharpoons C150CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r639	: C160ACP + CoA \rightleftharpoons C160CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r640	: C161ACP + CoA \rightleftharpoons C161CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r641	: C162ACP + CoA \rightleftharpoons C162CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r642	: C170ACP + CoA \rightleftharpoons C170CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r985	: C171ACP + CoA \rightleftharpoons C171CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r643	: C180ACP + CoA \rightleftharpoons C180CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r644	: C181ACP + CoA \rightleftharpoons C181CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r645	: C182ACP + CoA \rightleftharpoons C182CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r646	: C183ACP + CoA \rightleftharpoons C183CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r647	: C190ACP + CoA \rightleftharpoons C190CoA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r648	: C191ACP + COA \rightleftharpoons C191COA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r649	: C192ACP + COA \rightleftharpoons C192COA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
r650	: C200ACP + COA \rightleftharpoons C200COA + ACP	2.3.1.38	[ACP]acetyltransferase		ANEW	An12g01990	43740
Transfer of Acyls to CoA for transport and biosynthesis							
r651	: C40 + COA + ATP \Rightarrow C40COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An18g03800	187366
r652	: C60 + COA + ATP \Rightarrow C60COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An18g03800	187366
r653	: C80 + COA + ATP \Rightarrow C80COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An18g03800	187366
r654	: C100 + COA + ATP \Rightarrow C100COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An18g03800	187366
r655	: C120 + COA + ATP \Rightarrow C120COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An18g03800; 188673	187366; 188673
r656	: C140 + COA + ATP \Rightarrow C140COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An18g03800; 188673	187366; 188673
r657	: C141 + COA + ATP \Rightarrow C141COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An18g03800; 188673	187366; 188673
r658	: C150 + COA + ATP \Rightarrow C150COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An18g03800; 188673	187366; 188673
r659	: C160 + COA + ATP \Rightarrow C160COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r660	: C161 + COA + ATP \Rightarrow C161COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r661	: C162 + COA + ATP \Rightarrow C162COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r662	: C170 + COA + ATP \Rightarrow C170COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r686	: C171 + COA + ATP \Rightarrow C171COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r663	: C180 + COA + ATP \Rightarrow C180COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r664	: C181 + COA + ATP \Rightarrow C181COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r665	: C182 + COA + ATP \Rightarrow C182COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r666	: C183 + COA + ATP \Rightarrow C183COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r667	: C190 + COA + ATP \Rightarrow C190COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r668	: C191 + COA + ATP \Rightarrow C191COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r669	: C192 + COA + ATP \Rightarrow C192COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
r670	: C200 + COA + ATP \Rightarrow C200COA + PPI + AMP	6.2.1.3	Acyl-CoA synthetase	Baltazar et al. (1999)	ANEW	An09g06740	188673
Fatty acids conversions							
r671	: 2 ACCOA \rightleftharpoons COA + AACCOA	2.3.1.9	Acetyl-CoA acetyltransferase, acetoacetyl-CoA lase	Kanehisa et al. (2002)	ANID	An16g09190	214441

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r672	: ACTAC + ATP + COA \rightleftharpoons ADP + AACCOA + PI	6.4.1.2, 6.3.4.14	Acetyl-CoA carboxylase (ACC) / biotin carboxylase	Inferred for ACTAC connection	ANEW		
Baltazar et al. (1999)							
Carnitine shuttle							
r678	: C120COA + CAR \rightleftharpoons COA + C120CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r679	: C140COA + CAR \rightleftharpoons COA + C140CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r680	: C141COA + CAR \rightleftharpoons COA + C141CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r681	: C150COA + CAR \rightleftharpoons COA + C150CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r682	: C160COA + CAR \rightleftharpoons COA + C160CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r683	: C161COA + CAR \rightleftharpoons COA + C161CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r684	: C162COA + CAR \rightleftharpoons COA + C162CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r685	: C170COA + CAR \rightleftharpoons COA + C170CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r1211	: C171COA + CAR \rightleftharpoons COA + C171CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r686	: C180COA + CAR \rightleftharpoons COA + C180CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r687	: C181COA + CAR \rightleftharpoons COA + C181CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r688	: C182COA + CAR \rightleftharpoons COA + C182CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r689	: C183COA + CAR \rightleftharpoons COA + C183CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r690	: C190COA + CAR \rightleftharpoons COA + C190CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r691	: C191COA + CAR \rightleftharpoons COA + C191CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r692	: C192COA + CAR \rightleftharpoons COA + C192CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r693	: C200COA + CAR \rightleftharpoons COA + C200CAR	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r699	: CARm + C120CAR \Rightarrow CAR + C120CARm		Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r700	: CARm + C140CAR \Rightarrow CAR + C140CARm		Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r701	: CARm + C141CAR \Rightarrow CAR + C141CARm		Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r702	: CARm + C150CAR \Rightarrow CAR + C150CARm		Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r703	CARm + C160CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r704	CARm + C161CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r705	CARm + C162CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r706	CARm + C170CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r989	CARm + C171CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r707	CARm + C180CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r708	CARm + C181CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r709	CARm + C182CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r710	CARm + C183CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r711	CARm + C190CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r712	CARm + C191CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r713	CARm + C192CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r714	CARm + C200CARm	+	Carnitine transport reaction	Jernejc and Legisa (1996)	ANEW		
r720	C120CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r721	C140CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r722	C141CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r723	C150CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r724	C160CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r725	C161CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r726	C162CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r727	C170CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r990	C171CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r728	C180CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r729	C181CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r730	C182CARm + COAm	⇌	Carnitine acetyltransferase	Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r731	: C183COAm + COAm \rightleftharpoons CARm +	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r732	: C190COAm + COAm \rightleftharpoons CARm +	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r733	: C191COAm + COAm \rightleftharpoons CARm +	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r734	: C192COAm + COAm \rightleftharpoons CARm +	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
r735	: C200COAm + COAm \rightleftharpoons CARm +	2.3.1.7	Carnitine acetyltransferase	O- Jernejc and Legisa (1996); Baltazar et al. (1999)	ANEW	An08g04990; An18g01590	198577; 120926
Oxidation of fatty acids (even numbers)							
r736	: C200COAm + FADm \Rightarrow C20DCOAm + FADH2m	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914
r737	: C200COAm + FADm \Rightarrow C20DCOAm + FADH2m	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r738	: C20DCOAm + H2Om \rightleftharpoons C20HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00090; An02g02820; An02g05840; N/A; An02g07320	201398; 36773; 197480
r739	: C20HCOAm + NADm \rightleftharpoons C20OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00090; An12g03260	201398; 43844
r740	: C20OCOAm + COAm \Rightarrow ACCOAm + C18OCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r746	: C180COAm + FADm \Rightarrow C18DCOAm + FADH2m	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914
r747	: C180COAm + FADm \Rightarrow C18DCOAm + FADH2m	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r748	: C18DCOAm + H2Om \rightleftharpoons C18HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00090; An02g02820; An02g05840; N/A; An02g07320	201398; 36773; 197480
r749	: C18HCOAm + NADm \rightleftharpoons C18OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00090; An12g03260	201398; 43844
r750	: C18OCOAm + COAm \Rightarrow ACCOAm + C16OCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r756	: C160COAm + FADm \Rightarrow C16DCOAm + FADH2m	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914
r757	: C160COAm + FADm \Rightarrow C16DCOAm + FADH2m	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r758	: C16DCOAm + H2Om \rightleftharpoons C16HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00090; An02g02820; An02g05840; N/A; An02g07320	201398; 36773; 197480
r759	: C16HCOAm + NADm \rightleftharpoons C16OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00090; An12g03260	201398; 43844

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r760	: C16OCOAm + COAm \Rightarrow ACOCOAm + C14OCOAm FADH _{2m}	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r766	: C14OCOAm + FADm \Rightarrow C14DCOAm + FADH _{2m}	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914
r767	: C14OCOAm + FADm \Rightarrow C14DCOAm + FADH _{2m}	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r768	: C14DCOAm + H ₂ Om \rightleftharpoons C14HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00990; An02g02820; An02g05840; N/A; An02g07320	201398; 36773; N/A; 197480
r769	: C14HCOAm + NADm \rightleftharpoons C14OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00990; An12g03260	201398; 43844
r770	: C14OCOAm + COAm \Rightarrow ACOCOAm + C12OCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r771	: C12OCOAm + FADm \Rightarrow C12DCOAm + FADH _{2m}	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914
r772	: C12OCOAm + FADm \Rightarrow C12DCOAm + FADH _{2m}	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r773	: C12DCOAm + H ₂ Om \rightleftharpoons C12HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00990; An02g02820; An02g05840; N/A; An02g07320	201398; 36773; N/A; 197480
r774	: C12HCOAm + NADm \rightleftharpoons C12OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00990; An12g03260	201398; 43844
r775	: C12OCOAm + COAm \Rightarrow ACOCOAm + C10OCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r776	: C10OCOAm + FADm \Rightarrow C10DCOAm + FADH _{2m}	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914
r777	: C10OCOAm + FADm \Rightarrow C10DCOAm + FADH _{2m}	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r778	: C10DCOAm + H ₂ Om \rightleftharpoons C10HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00990; An02g02820; An02g05840; N/A; An02g07320	201398; 36773; N/A; 197480
r779	: C10HCOAm + NADm \rightleftharpoons C10OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00990; An12g03260	201398; 43844
r780	: C10OCOAm + COAm \Rightarrow ACOCOAm + C8OCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r781	: C8OCOAm + FADm \Rightarrow C8DCOAm + FADH _{2m}	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r782	: C8OCOAm + FADm \Rightarrow C8DCOAm + FADH ₂ m	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r783	: C8DCOAm + H ₂ Om \rightleftharpoons C8HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00090; An02g02820; An02g05840; An02g07320	201398; 36773; N/A; 197480
r784	: C8HCOAm + NADm \rightleftharpoons C8OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00090; An12g03260	201398; 43844
r785	: C8OCOAm + COAm \Rightarrow ACCOAm + C6OCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r786	: C6OCOAm + FADm \Rightarrow C6DCOAm + FADH ₂ m	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r787	: C6DCOAm + H ₂ Om \rightleftharpoons C6HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00090; An02g02820; An02g05840; An02g07320	201398; 36773; N/A; 197480
r788	: C6HCOAm + NADm \rightleftharpoons C6OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00090; An12g03260	201398; 43844
r789	: C6OCOAm + COAm \Rightarrow ACCOAm + C4OCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r790	: C4OCOAm + FADm \Rightarrow C4DCOAm + FADH ₂ m	1.3.99.3	Acyl-CoA dehydrogenase	Kazimirova and Novotel'nov (1956, Inferred)	ANEW	An17g01150	128861
r791	: C4DCOAm + H ₂ Om \rightleftharpoons C4HCOAm	4.2.1.17	Enoyl-CoA hydratase	Kazimirova and Novotel'nov (1956, Inferred)	ANEW	An14g00090; An02g02820; An02g05840; An02g07320	201398; 36773; N/A; 197480
r792	: C4HCOAm + NADm \rightleftharpoons AACCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Kazimirova and Novotel'nov (1956, Inferred)	ANEW	An14g00090; An12g03260	201398; 43844
r793	: AACCOAm + COAm \Rightarrow 2 ACCOAm	2.3.1.9	Acetyl-CoA acetyltransferase, acetoacetyl-CoA thiolase		ANEW	An13g01920	44808
Oxidation of fatty acids (odd chains)							
r741	: C19OCOAm + FADm \Rightarrow C19DCOAm + FADH ₂ m	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914
r742	: C19DCOAm + FADm \Rightarrow C19DCOAm + FADH ₂ m	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r743	: C19DCOAm + H ₂ Om \rightleftharpoons C19HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00090; An02g02820; An02g05840; An02g07320	201398; 36773; N/A; 197480
r744	: C19HCOAm + NADm \rightleftharpoons C19OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00090; An12g03260	201398; 43844

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r745	: C19OCOAm + COAm \Rightarrow ACCOAm + C17OCOAm FADH _{2m}	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r751	: C17OCOAm + FADm \Rightarrow C17DCOAm + FADH _{2m}	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914
r752	: C17OCOAm + FADm \Rightarrow C17DCOAm + FADH _{2m}	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r753	: C17DCOAm + H ₂ Om \rightleftharpoons C17HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00990; An02g02820; An02g05840; N/A; An02g07320	201398; 36773; N/A; 197480
r754	: C17HCOAm + NADm \rightleftharpoons C17OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00990; An12g03260	201398; 43844
r755	: C17OCOAm + COAm \Rightarrow ACCOAm + C15OCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r761	: C15OCOAm + FADm \Rightarrow C15DCOAm + FADH _{2m}	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914
r762	: C15OCOAm + FADm \Rightarrow C15DCOAm + FADH _{2m}	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r763	: C15DCOAm + H ₂ Om \rightleftharpoons C15HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00990; An02g02820; An02g05840; N/A; An02g07320	201398; 36773; N/A; 197480
r764	: C15HCOAm + NADm \rightleftharpoons C15OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An12g03260	201398; 43844
r765	: C15OCOAm + COAm \Rightarrow ACCOAm + C13OCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r593	: C13OCOAm + FADm \Rightarrow C13DCOAm + FADH _{2m}	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914
r594	: C13OCOAm + FADm \Rightarrow C13DCOAm + FADH _{2m}	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r595	: C13DCOAm + H ₂ Om \rightleftharpoons C13HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00990; An02g02820; An02g05840; N/A; An02g07320	201398; 36773; N/A; 197480
r596	: C13HCOAm + NADm \rightleftharpoons C13OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00990; An12g03260	201398; 43844
r597	: C13OCOAm + COAm \Rightarrow ACCOAm + C11OCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r603	: C11OCOAm + FADm \Rightarrow C11DCOAm + FADH _{2m}	1.3.99.13	Long-chain-acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An04g03290; An13g03940	57034; 191914

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r604	: C110COAm + FADm \Rightarrow C11DCOAm + FADH ₂ m	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r605	: C11DCOAm + H ₂ Om \rightleftharpoons C11HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00090; An02g02820; An02g05840; An02g07320	201398; 36773; N/A; 197480
r606	: C11HCOAm + NADm \rightleftharpoons C11OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00090; An12g03260	201398; 43844
r607	: C11OCOAm + COAm \Rightarrow ACCOAm + C90COAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r613	: C90COAm + FADm \Rightarrow C9DCOAm + FADH ₂ m	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r614	: C9DCOAm + H ₂ Om \rightleftharpoons C9HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00090; An02g02820; An02g05840; An02g07320	201398; 36773; N/A; 197480
r615	: C9HCOAm + NADm \rightleftharpoons C9OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00090; An12g03260	201398; 43844
r616	: C9OCOAm + COAm \Rightarrow ACCOAm + C70COAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r673	: C70COAm + FADm \Rightarrow C7DCOAm + FADH ₂ m	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r674	: C7DCOAm + H ₂ Om \rightleftharpoons C7HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00090; An02g02820; An02g05840; An02g07320	201398; 36773; N/A; 197480
r675	: C7HCOAm + NADm \rightleftharpoons C7OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00090; An12g03260	201398; 43844
r676	: C7OCOAm + COAm \Rightarrow ACCOAm + C50COAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823
r694	: C50COAm + FADm \Rightarrow C5DCOAm + FADH ₂ m	1.3.99.3	Acyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An17g01150	128861
r695	: C5DCOAm + H ₂ Om \rightleftharpoons C5HCOAm	4.2.1.17	Enoyl-CoA hydratase	Baltazar et al. (1999)	ANEW	An14g00090; An02g02820; An02g05840; An02g07320	201398; 36773; N/A; 197480
r696	: C5HCOAm + NADm \rightleftharpoons C5OCOAm + NADHm	1.1.1.35	3-hydroxyacyl-CoA dehydrogenase	Baltazar et al. (1999)	ANEW	An14g00090; An12g03260	201398; 43844
r697	: C5OCOAm + COAm \Rightarrow ACCOAm + PROPCOAm	2.3.1.16	3-ketoacyl-CoA thiolase	Baltazar et al. (1999)	ANEW	An02g03320; An04g05720; An08g05400; An13g00590	46947; 55007; 38275; 50823

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
PHOSPHOLIPID BIOSYNTHESIS							
Phosphatidylserine							
r794	$\begin{aligned} & \text{GL3P} + 0.022 \text{ C120ACP} + 0.031 \\ & \text{C140ACP} + 0.022 \text{ C141ACP} + 0.214 \\ & \text{C160ACP} + 0.045 \text{ C161ACP} + 0.016 \\ & \text{C162ACP} + 0.045 \text{ C170ACP} + 0.08 \\ & \text{C180ACP} + 0.2 \text{ C181ACP} + 0.183 \\ & \text{C182ACP} + 0.081 \text{ C183ACP} + 0.061 \\ & \text{C200ACP} \Rightarrow \text{PSAGL3P} + \text{ACP} \end{aligned}$	2.3.1.15	Glycerol-3-phosphate acyl-transferase	Chopra and Khuller (1984); Kanehisa et al. (2002)	ANID	An18g01960	188006
r795	$\begin{aligned} & \text{T3P2} + 0.022 \text{ C120ACP} + 0.031 \\ & \text{C140ACP} + 0.022 \text{ C141ACP} + 0.214 \\ & \text{C160ACP} + 0.045 \text{ C161ACP} + 0.016 \\ & \text{C162ACP} + 0.045 \text{ C170ACP} + 0.08 \\ & \text{C180ACP} + 0.2 \text{ C181ACP} + 0.183 \\ & \text{C182ACP} + 0.081 \text{ C183ACP} + 0.061 \\ & \text{C200ACP} \Rightarrow \text{PSAT3P2} + \text{ACP} \end{aligned}$	2.3.1.15	Glycerol-3-phosphate acyl-transferase	Chopra and Khuller (1984, Inferred)	ANID	An18g01960	188006
r796	$\begin{aligned} & \text{PSAT3P2} + \text{NADPH} \Rightarrow \text{PSAGL3P} + \\ & \text{NADP} \end{aligned}$	1.1.1.101	Acylidihydroxyacetonephosphoreductase/ acylglycerone-phosphate reductase	Chopra and Khuller (1984, Inferred)	ANID	An16g06470	184098
r797	$\begin{aligned} & \text{PSAGL3P} + 0.022 \text{ C120ACP} + 0.031 \\ & \text{C140ACP} + 0.022 \text{ C141ACP} + 0.214 \\ & \text{C160ACP} + 0.045 \text{ C161ACP} + 0.016 \\ & \text{C162ACP} + 0.045 \text{ C170ACP} + 0.08 \\ & \text{C180ACP} + 0.2 \text{ C181ACP} + 0.183 \\ & \text{C182ACP} + 0.081 \text{ C183ACP} + 0.061 \\ & \text{C200ACP} \Rightarrow \text{PSPA} + \text{ACP} \end{aligned}$	2.3.1.51	1-acylglycerol-3-phosphate acyltransferase	Chopra and Khuller (1984, Inferred)	ANID	An13g00040	126602
r798	$\begin{aligned} & \text{PSPA} + \text{CTP} \rightleftharpoons \text{PSCDPPDG} + \text{PPI} \end{aligned}$	2.7.7.41	Cdp-diacylglycerol synthetase (phosphatidate cytidylyltransferase)	Chopra and Khuller (1984, Inferred)	ANID	An07g09570	181254
r799	$\text{PSCDPPDG} + \text{SER} \rightleftharpoons \text{CMP} + \text{PS}$	2.7.8.8	Phosphatidylserine synthase	Chopra and Khuller (1984, Inferred)	ANID	An17g01120	51030
Phosphatidylethanolamine							
r800	$\begin{aligned} & \text{GL3P} + 0.03 \text{ C120ACP} + 0.015 \\ & \text{C140ACP} + 0.011 \text{ C141ACP} + 0.001 \\ & \text{C150ACP} + 0.24 \text{ C160ACP} + 0.046 \\ & \text{C161ACP} + 0.039 \text{ C162ACP} + 0.041 \\ & \text{C170ACP} + 0.093 \text{ C180ACP} + 0.135 \\ & \text{C181ACP} + 0.282 \text{ C182ACP} + 0.065 \\ & \text{C183ACP} + 0.002 \text{ C200ACP} \Rightarrow \\ & \text{PEAGL3P} + \text{ACP} \end{aligned}$	2.3.1.15	Glycerol-3-phosphate acyl-transferase	Chopra and Khuller (1984, Inferred)	ANID	An18g01960	188006
r801	$\begin{aligned} & \text{T3P2} + 0.03 \text{ C120ACP} + 0.015 \\ & \text{C140ACP} + 0.011 \text{ C141ACP} + 0.001 \\ & \text{C150ACP} + 0.24 \text{ C160ACP} + 0.046 \\ & \text{C161ACP} + 0.039 \text{ C162ACP} + 0.041 \\ & \text{C170ACP} + 0.093 \text{ C180ACP} + 0.135 \\ & \text{C181ACP} + 0.282 \text{ C182ACP} + 0.065 \\ & \text{C183ACP} + 0.002 \text{ C200ACP} \Rightarrow \\ & \text{PEAT3P2} + \text{ACP} \end{aligned}$	2.3.1.15	Glycerol-3-phosphate acyl-transferase	Chopra and Khuller (1984, Inferred)	ANID	An18g01960	188006
r802	$\begin{aligned} & \text{PEAT3P2} + \text{NADPH} \Rightarrow \text{PEAGL3P} + \\ & \text{NADP} \end{aligned}$	1.1.1.101	Acylidihydroxyacetonephosphoreductase/ acylglycerone-phosphate reductase	Chopra and Khuller (1984, Inferred)	ANID	An16g06470	184098

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r803	PEAGL3P + 0.03 C120ACP + 0.015 C140ACP + 0.011 C141ACP + 0.001 C150ACP + 0.24 C160ACP + 0.046 C161ACP + 0.039 C162ACP + 0.041 C170ACP + 0.093 C180ACP + 0.135 C181ACP + 0.282 C182ACP + 0.065 C183ACP + 0.002 C200ACP \Rightarrow PEPA + ACP	2.3.1.51	1-acylglycerol-3-phosphate acyltransferase	Chopra and Khuller (1984, ferred)	ANID	An13g00040	126602
r804	PEPA + CTP \rightleftharpoons PCDDPDG + PPI	2.7.7.41	Cdp-diacylglycerol synthetase (phosphatidate cytidyltransferase)	Chopra and Khuller (1984, ferred)	ANID	An07g09570	181254
r805	PCDDPDG + SER \rightleftharpoons CMP + PEPS	2.7.8.8	Phosphatidylserine synthase	Chopra and Khuller (1984, ferred)	ANID	An17g01120	51030
r806	PEPS \Rightarrow PE + CO2	4.1.1.65	Phosphatidylserine decarboxylase	Chopra and Khuller (1984, ferred)	ANID	An03g02830; An01g14110; An04g10280; N/A; An09g04710; An12g00910; An14g01880	194479; 35440; N/A; 202968; 50299; 41614
Phosphatidylcholine							
r807	GL3P + 0.01 C120ACP + 0.044 C140ACP + 0.077 C141ACP + 0.224 C160ACP + 0.039 C161ACP + 0.018 C162ACP + 0.048 C170ACP + 0.068 C180ACP + 0.131 C181ACP + 0.308 C182ACP + 0.021 C183ACP + 0.012 C200ACP \Rightarrow PCAGL3P + ACP	2.3.1.15	Glycerol-3-phosphate acyltransferase	Chopra and Khuller (1984, ferred)	ANID	An18g01960	188006
r808	T3P2 + 0.01 C120ACP + 0.044 C140ACP + 0.077 C141ACP + 0.224 C160ACP + 0.039 C161ACP + 0.018 C162ACP + 0.048 C170ACP + 0.068 C180ACP + 0.131 C181ACP + 0.308 C182ACP + 0.021 C183ACP + 0.012 C200ACP \Rightarrow PCAT3P2 + ACP	2.3.1.15	Glycerol-3-phosphate acyltransferase	Chopra and Khuller (1984, ferred)	ANID	An18g01960	188006
r809	PCAT3P2 + NADPH \Rightarrow PCAGL3P + NADP	1.1.1.101	Acylidihydroxyacetonephosphoreductase/ acylglycerone-phosphate reductase	Chopra and Khuller (1984, ferred)	ANID	An16g06470	184098
r810	PCAGL3P + 0.01 C120ACP + 0.044 C140ACP + 0.077 C141ACP + 0.224 C160ACP + 0.039 C161ACP + 0.018 C162ACP + 0.048 C170ACP + 0.068 C180ACP + 0.131 C181ACP + 0.308 C182ACP + 0.021 C183ACP + 0.012 C200ACP \Rightarrow PCPA + ACP	2.3.1.51	1-acylglycerol-3-phosphate acyltransferase	Chopra and Khuller (1984, ferred)	ANID	An13g00040	126602
r811	PCPA + CTP \rightleftharpoons PCDDPDG + PPI	2.7.7.41	Cdp-diacylglycerol synthetase (phosphatidate cytidyltransferase)	Chopra and Khuller (1984, ferred)	ANID	An07g09570	181254
r812	PCDDPDG + SER \rightleftharpoons CMP + PCPS	2.7.8.8	Phosphatidylserine synthase	Chopra and Khuller (1984, ferred)	ANID	An17g01120	51030

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r813	PCPS \Rightarrow PCPE + CO ₂	4.1.1.65	Phosphatidylserine decarboxylase	Chopra and Khuller (1984, ferred)	ANID	An03g02830; An01g14110; An04g10280; An09g04710; An12g00910; An14g01880 An15g06310	19479; 35440; N/A; 202968; 50299; 41614 53511
r814	PCPE + SAM \Rightarrow SAH + PCPMME	2.1.1.17	Phosphatidylethanolamine N-methyltransferase		ANID		
r815	PCPMME + SAM \Rightarrow SAH + PCPDME	2.1.1.71	Methylene-fatty-acyl-phospholipid synthase		ANID		208474
r816	PCPDME + SAM \Rightarrow PC + SAH	2.1.1.71	Methylene-fatty-acyl-phospholipid synthase		ANID	An08g00560 An08g00560	208474
Cardiolipin							
r817	GL3P + 0.024 C120ACP + 0.032 C140ACP + 0.017 C141ACP + 0.232 C160ACP + 0.027 C161ACP + 0.009 C162ACP + 0.017 C170ACP + 0.081 C180ACP + 0.124 C181ACP + 0.326 C182ACP + 0.111 C183ACP \Rightarrow CLAGL3P + ACP	2.3.1.15	Glycerol-3-phosphate acyltransferase	Chopra and Khuller (1984, ferred)	ANID	An18g01960	188006
r818	CLAGL3P + 0.024 C120ACP + 0.032 C140ACP + 0.017 C141ACP + 0.232 C160ACP + 0.027 C161ACP + 0.009 C162ACP + 0.017 C170ACP + 0.081 C180ACP + 0.124 C181ACP + 0.326 C182ACP + 0.111 C183ACP \Rightarrow CLPA + ACP	2.3.1.51	1-acylglycerol-3-phosphate acyltransferase	Chopra and Khuller (1984, ferred)	ANID	An13g00040	126602
r819	CLPA + CTP \rightleftharpoons CLCDPDG + PPI	2.7.7.41	Cdp-diacylglycerol synthetase (phosphatidate cytidyltransferase)	Chopra and Khuller (1984, ferred)	ANID	An07g09570	181254
r820	CLCDPDG + GL3P \Rightarrow CMP + CLPIGP	2.7.8.5	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	Chopra and Khuller (1984, ferred)	ANID	An17g01120	51030
r821	CLPIGP + H ₂ O \Rightarrow PG + PI	3.1.3.27	Phosphatidylglycerophosphatase	Chopra and Khuller (1984, ferred)	ANID		
r822	CLCDPDG + PG \Rightarrow CMP + CL	CRD1	Cardiolipin synthase/CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	Chopra and Khuller (1984, ferred)	ANID	An15g01020	126969
PHOSPHOLIPID DEGRADATION							
r823	PC \Rightarrow LPC + 0.01 C120 + 0.044 C140 + 0.077 C141 + 0.224 C160 + 0.039 C161 + 0.018 C162 + 0.048 C170 + 0.088 C180 + 0.131 C181 + 0.308 C182 + 0.021 C183 + 0.012 C200	3.1.1.4	Phospholipase A2/lecithinase a/phosphatidase/phosphatidolipase/phospholipase A	Chopra and Khuller (1984); Kanehisa et al. (2002) Mustranta et al. (1995)	ANIG, ANID ANID	An02g04040; An04g03360; An08g08490; An08g12250; N/A; An12g06690 An15g05710	52198; 44084; 176070; N/A; N/A 56347

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r824	PE \Rightarrow LPE + 0.03 C120 + 0.015 C140 + 0.011 C141 + 0.001 C150 + 0.24 C160 + 0.046 C161 + 0.039 C162 + 0.041 C170 + 0.093 C180 + 0.135 C181 + 0.282 C182 + 0.065 C183 + 0.002 C200	3.1.1.14	Phospholipase A2/lecithinase A/phosphatidase/phosphatidolipase/phospholipase a		ANID	An02g04040; An04g03360; An08g08490; An08g12250; N/A; An12g06690 An15g05710	52198; 44084; 176070; N/A; N/A; 56347
GLYCOSPHINGOLIPID METABOLISM							
Biosynthesis of precursors							
r825	G6P \rightleftharpoons MI1P	5.5.1.4	Myo-inositol-1-phosphate synthase	Memon et al. (1983) Kanehisa et al. (2002)	ANID	An10g00530	54854
r826	MI1P \Rightarrow MYOI + PI	3.1.3.25	Myo-inositol-1(or 4)-monophosphatase	Neuwald et al. (1991, A. nidulans)	ANID	An03g03700	54687
r827	0.25 CLCDPDG + 0.25 PCDDPDG + 0.25 PECDDPDG + 0.25 PSCDDPDG \Rightarrow CDDPDG	No EC	Artificial reaction for TGDMPIC		ANEW		
r828	CDDPDG + MYOI \Rightarrow CMP + PINS	2.7.8.11	Phosphatidylinositol synthase	Chopra and Khuller (1984, In-ferred)	ANID	An01g14140	55234
r829	ATP + PINS \Rightarrow ADP + PINS	2.7.1.137	1-phosphatidylinositol 3-kinase/phosphoinositide 3-kinase	Ibrahim-Granet et al. (2003, A. fumigatus)	ANID	An07g04820; An16g04720	39962; 53581
r830	C160COA + SER \Rightarrow COA + C18DHSPH + CO2	2.3.1.50	Serine palmitoyltransferase	Mandala et al. (1994, A. fumigatus)	ANID	An08g04100; An18g03820 An01g06830	208165; 202464 51907
r831	C18DHSPH + NADPH \Rightarrow C18SPH + NADP	1.1.1.102	3-dehydrophinganine reductase		ANID	An01g10030	51801
r832	C18SPH + O2 + NADPH \Rightarrow C18PSPH + NADP + H2O	SUR2	Sphingosine hydroxylase/syngomyacin response protein 2		ANID		
r833	C180COA + SER \Rightarrow COA + C20DHSPH + CO2	2.3.1.50	Serine palmitoyltransferase	Mandala et al. (1994, A. fumigatus)	ANEW	An08g04100; An18g03820 An01g06830	208165; 202464 51907
r834	C20DHSPH + NADPH \Rightarrow C20SPH + NADP	1.1.1.102	3-dehydrophinganine reductase		ANEW		
r835	C20SPH + O2 + NADPH \Rightarrow C20PSPH + NADP + H2O	SUR2	Sphingosine hydroxylase/syngomyacin response protein 2		ANEW	An01g10030	51801
r836	C171COA + SER \Rightarrow COA + C191DHSPH + CO2	2.3.1.50	Serine palmitoyltransferase	Mandala et al. (1994, A. fumigatus)	ANEW	An08g04100; An18g03820 An01g06830	208165; 202464 51907
r837	C191DHSPH + NADPH \Rightarrow C191SPH + NADP	1.1.1.102	3-dehydrophinganine reductase		ANEW		
Biosynthesis of Cerebrin 1							
r838	C18PSPH + C180COA \Rightarrow CERB1A + COA	2.3.1.24	Ceramide synthase	Wagner and Fiebert (1969); Kanehisa et al. (2002)	ANEW	An11g00090	52868
r839	C18PSPH + C181COA \Rightarrow CERB1B + COA	2.3.1.24	Ceramide synthase	Wagner and Fiebert (1969, In-ferred)	ANEW	An11g00090	52868
r840	C20PSPH + C180COA \Rightarrow CERB1C + COA	2.3.1.24	Ceramide synthase	Wagner and Fiebert (1969, In-ferred)	ANEW	An11g00090	52868
r841	C20PSPH + C181COA \Rightarrow CERB1D + COA	2.3.1.24	Ceramide synthase	Wagner and Fiebert (1969, In-ferred)	ANEW	An11g00090	52868

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r842	: 0.25 CERB1A + 0.25 CERB1B + 0.25 CERB1C + 0.25 CERB1D \Rightarrow CERB1	NO EC	Artificial reaction		ANEW		
Biosynthesis of Cerebrin 2							
r843	: C18SPH + C180COA \Rightarrow CERB2A + COA	2.3.1.24	Ceramide synthase	Wagner and Fiegert (1969); Kanehisa et al. (2002)	ANEW	An11g00990	52868
r844	: C18SPH + C181COA \Rightarrow CERB2B + COA	2.3.1.24	Ceramide synthase	Wagner and Fiegert (1969, Inferred)	ANEW	An11g00990	52868
r845	: C20SPH + C180COA \Rightarrow CERB2C + COA	2.3.1.24	Ceramide synthase	Wagner and Fiegert (1969, Inferred)	ANEW	An11g00990	52868
r846	: C20SPH + C181COA \Rightarrow CERB2D + COA	2.3.1.24	Ceramide synthase	Wagner and Fiegert (1969, Inferred)	ANEW	An11g00990	52868
r847	: 0.25 CERB2A + 0.25 CERB2B + 0.25 CERB2C + 0.25 CERB2D \Rightarrow CERB2	NO EC	Artificial reaction		ANEW		
Biosynthesis of Galactocerebroside							
r848	: UDPGAL + CERB2A \Rightarrow UDP + GAL-CERA	2.4.1.45	2-hydroxyacylsphingosine 1-beta-galactosyltransferase	Wagner and Fiegert (1969); Kanehisa et al. (2002)	ANEW	An04g08370	45922
r849	: UDPGAL + CERB2B \Rightarrow UDP + GAL-CERB	2.4.1.45	2-hydroxyacylsphingosine 1-beta-galactosyltransferase	Wagner and Fiegert (1969, Inferred)	ANEW	An04g08370	45922
r850	: 0.5 GALCERA + 0.5 GALCERB \Rightarrow GALCER	NO EC	Artificial reaction		ANEW		
Biosynthesis of Glucocerebroside 1							
r851	: C191SPH + C180COA \Rightarrow CEREB1 + COA	2.3.1.24	Ceramide synthase	Levery et al. (2000); Kanehisa et al. (2002)	ANEW	An11g00990	52868
r852	: UDPG + CEREB1 \Rightarrow UDP + GLUCER1	2.4.1.80	2-hydroxyacylsphingosine 1-beta-glucosyltransferase	Levery et al. (2000, Inferred)	ANEW	An07g03380	209752
Biosynthesis of Glucocerebroside 2							
r853	: C191SPH + C181COA \Rightarrow CEREB2 + COA	2.3.1.24	Ceramide synthase	Levery et al. (2000, Inferred)	ANEW	An11g00990	52868
r854	: UDPG + CEREB2 \Rightarrow UDP + GLUCER2	2.4.1.80	2-hydroxyacylsphingosine 1-beta-glucosyltransferase	Levery et al. (2000, Inferred)	ANEW	An07g03380	209752
Biosynthesis of ceramide-P-inositol and trigalactosyldimannosylinositolphosphorylceramide (GPSL G)							
r855	: CERB2 + PINS \Rightarrow IPC + H2O	2.-.-	IPC synthase, mannosyl diphosphorylinositol ceramide synthase	Byrne and Brennan (1976); Kanehisa et al. (2002)	ANID		
r856	: IPC + GDPMAN \Rightarrow MIPC + GDP	SUR1	MIPC synthase	Zhong et al. (2000)	ANID		
r857	: MIPC + GDPMAN \Rightarrow DMIPC + GDP	SUR1	MIPC synthase	Byrne and Brennan (1976, Inferred)	ANID *	An05g02310; An09g00100; An15g00630	189424; 43578; 210021
r858	: UDPGAL + DMIPC \Rightarrow GDMIPC + UDP	2.4.1.-	Galactosyltransferase	Byrne and Brennan (1976, Inferred)	ANID *	An05g02310; An09g00100; An15g00630	189424; 43578; 210021
r859	: UDPGAL + GDMIPC \Rightarrow DGDMPIC + UDP	2.4.1.-	Galactosyltransferase	Byrne and Brennan (1976, Inferred)	ANEW	An01g09810	170454
				Byrne and Brennan (1976, Inferred)	ANEW	An01g09810	170454

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r860	: UDPGAL + DGDMPIC \Rightarrow TGDMPIC + UDP	2.4.1.-	Galactosyltransferase	Byrne and Brennan (1976, Inferred)	ANEW	An01g09810	170454
BIOSYNTHESIS OF LANOSTEROL							
r861	: ACCOA + AACCOA + H ₂ O \rightleftharpoons H ₃ MCOA + COA	2.3.3.10	3-hydroxy-3-methylglutaryl coenzyme A synthase	Servouse and Karst (1986); Kanehisa et al. (2002); Nemeć and Jernejc (2002)	ANIG, ANID	An02g06320; An07g04260	55566; 56215
r862	: H ₃ MCOA + 2 NADPH \rightleftharpoons MVL + COA + 2 NADP	1.1.1.34	3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase isozyme	Evans and Gealt (1988, A. nidulans)	ANID	An04g00610; An07g08280; An09g03240; An13g04000	213343; 209439; 188317; 44946
r863	: ATP + MVL \Rightarrow ADP + PMVL	2.7.1.36	Mevalonate kinase	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An04g02190	213169
r864	: ATP + PMVL \Rightarrow ADP + PPMVL	2.7.4.2	Phosphomevalonate kinase	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An14g04010	211137
r865	: ATP + PPMVL \Rightarrow ADP + PI + IPPP + CO ₂	4.1.1.33	Diphosphomevalonate decarboxylase	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An04g01540	203692
r866	: IPPP \rightleftharpoons DMPP	5.3.3.2	Isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP isomerase)	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An08g07570	52621
r867	: DMPP + IPPP \Rightarrow GPP + PPI	2.5.1.1	Prenyltransferase	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An11g02500	38877
r868	: GPP + IPPP \Rightarrow FPP + PPI	2.5.1.10	Farnesyl diphosphate synthetase (FPP synthetase)	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An16g01670; An04g04640	125382; 134931
r869	: 2 FPP + NADPH \Rightarrow NADP + SQL + 2 PPI	2.5.1.21	Squalene synthase	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An02g11000	130900
r870	: SQL + O ₂ + NADPH \Rightarrow S ₂ 3E + NADP + H ₂ O	1.14.99.7	Squalene monooxygenase	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANEW	An03g03770	213441
r871	: S ₂ 3E \Rightarrow LNST	5.4.99.7	2,3-oxidosqualene-lanosterol cyclase	Nemeć and Jernejc (2002, Inferred), Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An07g06150; An09g01330	181224; 189003
BIOSYNTHESIS OF ZYMOSTEROL AND ERGOSTEROL							
r872	: LNST + 3 NADPH + 3 O ₂ \Rightarrow DCTOL + FOR + 3 NADP + 4 H ₂ O	ERG11	Cytochrome p450 lanosterol 14A-demethylase (ERG11)	Servouse and Karst (1986); Kanehisa et al. (2002); Cherry et al. (1998) van den Brink et al. (1996)	ANID	An11g00270; An11g02230	38711; 55947
r873	: DCTOL + NADPH \Rightarrow DCDOL + NADP	ERG24	C-14 sterol reductase (ERG24)	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An01g07000	51895
r874	: DCDOL + 3 O ₂ + 3 NADPH \Rightarrow DCDA + 3 NADP + 4 H ₂ O	ERG25	C-4 sterol methyl oxidase (ERG25)	Chopra and Khuller (1984, Inferred), Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANEW	An03g06410	44595
r875	: DCDA \Rightarrow CDOL + CO ₂	ERG26	C-4 sterol decarboxylase (ERG26)	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANEW	An15g03090	200652
r876	: CDOL + 3 O ₂ + 3 NADPH \Rightarrow CDA + 3 NADP + 4 H ₂ O	ERG25	C-4 sterol methyl oxidase (ERG25)	Chopra and Khuller (1984, Inferred), Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANEW	An03g06410	44595
r877	: CDA \Rightarrow ZYMST + CO ₂	ERG25	C-4 sterol decarboxylase (ERG26)	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANEW	An15g03090	200652

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r879	: ZYMST + SAM \Rightarrow FEST + SAH	2.1.1.41	S-adenosyl-methionine delta-24-sterol-C- methyltransferase (ERG6)	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An04g04210; An14g01590	213016; 56548
r880	: FEST \rightleftharpoons EPST	ERG2	C-8 sterol isomerase (ERG1)	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANID	An01g03350	206219
r881	: EPST + O ₂ + NADPH \Rightarrow NADP + ER-GOD + 2 H ₂ O	ERG3	C-5 sterol desaturase (ERG3)	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANEW	An15g00150; An16g02930	200430; 53645
r882	: ERGOD + O ₂ + NADPH \Rightarrow NADP + ERGOT + 2 H ₂ O	ERG5	C-22 sterol desaturase (ERG5)	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANEW	An01g02810; An11g03230	206266; 55967
r883	: ERGOT + NADPH \Rightarrow ERGOST + NADP	ERG4	C-24 sterol reductase (ERG4)	Ferreira et al. (2005, A. nidulans, A. fumigatus, A. oryzae)	ANEW	An14g05780	49423
METABOLISM OF ERGOSTEROL ESTERS							
r884	: 0.074 C160ACP + 0.222 C181ACP + 0.704 C182ACP + GL3P \Rightarrow ACP + SEMAGP	2.3.1.15	Glycerol-3-phosphate O-acyltransferase		ANEW	An18g01960	188006
r885	: 0.074 C160ACP + 0.222 C181ACP + 0.704 C182ACP + SEMAGP \Rightarrow ACP + SEDAGP	2.3.1.51	1-acylglycerol-3-phosphate O-acyltransferase		ANEW	An13g00040	126602
r886	: SEDAGP + H ₂ O \Rightarrow SEDAG + PI	3.1.3.4	phosphatidate phatase		ANEW		
r887	: SEDAG + ERGOST \Rightarrow SEMAG + ER-GOSE	2.3.1.73	sterol O-acyltransferase		ANEW	An18g04660	54192
r888	: ERGOSE + H ₂ O \Rightarrow ERGOST + 0.074 C160 + 0.222 C181 + 0.704 C182	3.1.1.13	sterol esterase		ANEW		
r889	: SEMAG + H ₂ O \Rightarrow 0.074 C160 + 0.222 C181 + 0.704 C182 + GL	3.1.1.23	Acylglycerol lipase		ANEW		
METABOLISM OF COMPLEX LIPIDS							
Glycerolipid biosynthesis							
r890	: 0.024 C120ACP + 0.013 C140ACP + 0.012 C141ACP + 0.002 C150ACP + 0.154 C160ACP + 0.02 C161ACP + 0.008 C162ACP + 0.002 C170ACP + 0.026 C180ACP + 0.374 C181ACP + 0.327 C182ACP + 0.032 C183ACP + 0.006 C200ACP + GL3P \Rightarrow ACP + MAGLYP	2.3.1.15	Glycerol-3-phosphate O-acyltransferase	David et al. (2003)	ANIG, ANID, ANIG, ANID, ANEW	An18g01960	188006
r896	: MAGLYP + H ₂ O \Rightarrow MAGLY + PI	3.1.3.4	phosphatidate phatase		ANEW		
r891	: 0.024 C120ACP + 0.013 C140ACP + 0.012 C141ACP + 0.002 C150ACP + 0.154 C160ACP + 0.02 C161ACP + 0.008 C162ACP + 0.002 C170ACP + 0.026 C180ACP + 0.374 C181ACP + 0.327 C182ACP + 0.032 C183ACP + 0.006 C200ACP + MAGLYP \Rightarrow ACP + DAGLYP	2.3.1.51	Glycerol-3-phosphate O-acyltransferase	Kanehisa et al. (2002)	ANEW	An13g00040	126602
r892	: DAGLYP + H ₂ O \Rightarrow DAGLY + PI	3.1.3.4	phosphatidate phatase		ANEW		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r893	: 0.024 C120ACP + 0.013 C140ACP + 0.012 C141ACP + 0.002 C150ACP + 0.154 C160ACP + 0.02 C161ACP + 0.008 C162ACP + 0.002 C170ACP + 0.026 C180ACP + 0.374 C181ACP + 0.327 C182ACP + 0.032 C183ACP + 0.006 C200ACP + DAGLY \Rightarrow TAGLY + ACP	2.3.1.20	1-acylglycerol-3-phosphate acyltransferase	Tomoda et al. (1999)	ANID	An12g03600; An15g03770	186422; 181869
Glycerolipid degradation							
r894	: TAGLY + H ₂ O \Rightarrow DAGLY + 0.024 C120 + 0.013 C140 + 0.012 C141 + 0.002 C150 + 0.154 C160 + 0.02 C161 + 0.008 C162 + 0.002 C170 + 0.026 C180 + 0.374 C181 + 0.327 C182 + 0.032 C183 + 0.006 C200	3.1.1.3	Triacylglycerol lipase	Hannan (1959)	ANID	An13g01880; An03g06560; An03g06630; An06g00350; An07g00440; An07g04200; An09g02180; An09g02270; An09g03760; An09g05120; An12g06560; An12g06560; An13g00480; An14g00860; An16g08870	50877; N/A; 191506; 177254; 53361; 39997; 212664; 189135; 43311; 50087; 185927; 191767; 185301; 193610
r895	: DAGLY + H ₂ O \Rightarrow MAGLY + 0.024 C120 + 0.013 C140 + 0.012 C141 + 0.002 C150 + 0.154 C160 + 0.02 C161 + 0.008 C162 + 0.002 C170 + 0.026 C180 + 0.374 C181 + 0.327 C182 + 0.032 C183 + 0.006 C200	3.1.1.3	Triacylglycerol lipase	Hannan (1959)	ANID	An13g01880; An03g06560; An03g06630; An06g00350; An07g00440; An07g04200; An09g02180; An09g02270; An09g03760; An09g05120; An12g06560; An13g00480; An14g00860; An16g08870	50877; N/A; 191506; 177254; 53361; 39997; 212664; 189135; 43311; 50087; 185927; 191767; 185301; 193610
Glycolipids metabolism							
Mono- and di-galactosylglyceride biosynthesis							
r896	: DAGLY + UDPGAL \rightleftharpoons UDP + MGDG	2.4.1.46	UDPgalactose:1,2-diacylglycerol 3-beta-D-galactosyltransferase	David et al. (2003)	ANIG, ANID		
r897	: MGDG + UDPGAL \rightleftharpoons UDP + DGDG	2.4.1.184	Galactolipid galactosyltransferase		ANID		
Monoglucosyloxyoctadecenoic acid							
r898	: C18COA + UDPG + H ₂ O \rightleftharpoons MGC181 + UDP + COA	2.4.1.-	lipid galactosyltransferase		ANEW		
SECONDARY METABOLISM							
Ochratoxin A biosynthesis							

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1010	4 ACCOA + 1 MALCOA + 1 PHE \Rightarrow 5 COA + OTA	No EC	Artificial reaction, chlor left out	Abarca et al. (1994); Varga et al. (2003); O'Callaghan et al. (2003); Samson et al. (2004); Blumenthal (2004)	ANEW	An10g00140	44965
PROTEIN PRODUCTION							
Glucosylase production							
r1266	0.951 ALA + 0.307 ARG + 0.366 ASN + 0.644 ASP + 0.146 CYS + 0.249 GLN + 0.38 GLU + 0.687 GLY + 0.059 HIS + 0.351 ILE + 0.702 LEU + 0.190 LYS + 0.044 MET + 0.322 PHE + 0.322 PRO + 1.272 SER + 1.082 THR + 0.278 TRP + 0.395 TYR + 0.614 VAL + 40.39 ATP \Rightarrow 40.39 ADP + 40.49 PI + GAMYLE	No EC	Artificial protein synthesis reaction		ANEW		
Alphaamylase production							
r1265	0.622 ALA + 0.226 ARG + 0.452 ASN + 0.773 ASP + 0.170 CYS + 0.283 GLN + 0.320 GLU + 0.754 GLY + 0.132 HIS + 0.509 ILE + 0.716 LEU + 0.189 LYS + 0.151 MET + 0.264 PHE + 0.358 PRO + 1.018 SER + 0.716 THR + 0.207 TRP + 0.660 TYR + 0.603 VAL + 39.37 ATP \Rightarrow 39.37 ADP + 39.37 PI + AAMYLE	No EC	Artificial protein synthesis reaction		ANEW		
Sulfur metabolism							
r899	H ₂ SO ₃ + 3 NADPH \rightleftharpoons H ₂ S + 3 NADP + 3 H ₂ O	1.8.1.2	Sulfite reductase	Sienko and Paszewski (1999, A. nidulans)	ANID	An11g06670	208898
r900	SLF + ATP \Rightarrow PPI + APS	2.7.7.4	ATP sulfurylase	Buxton et al. (1989)	ANID	An11g09790	209058
r901	APS + ATP \Rightarrow ADP + PAPS	2.7.1.25	Adenylylsulfate kinase	Borges-Walmsley et al. (1995); Clarke et al. (1997); Sienko and Paszewski (1999, A. nidulans)	ANID	An08g02990	208264
r902	PAPS + RTHIO \Rightarrow OTHIO + H ₂ SO ₃ + PAP	1.8.4.8	PAPS reductase	Borges-Walmsley et al. (1995); Sienko and Paszewski (1999, A. nidulans)	ANID	An11g09780	56053
r903	CHOSLF + H ₂ O \rightleftharpoons CHO + SLF	3.1.6.6	Choline sulphatase	Scott and Spencer (1968, A. nidulans)	ANEW	An08g08950	55721
r904	PAPS + CHO \rightleftharpoons PAP + CHOSLF	2.8.2.6	choline sulfotransferase	Hussey and Spencer (1966, A. nidulans)	ANEW		
r905	PAP + H ₂ O \Rightarrow AMP + PI	3.1.3.7	3' - 5' bisphosphate nucleotidase		ANID	An11g06820	208912
r112	H ₂ SO ₃ \rightleftharpoons S + O ₂ + H ₂ O	1.13.11.18	Sulfur dioxygenase	Tepper et al. (1966, Inferred)	ANEW		
Nitrogen metabolism							
r906	HNO ₃ + NADPH \Rightarrow HNO ₂ + NADP + H ₂ O	1.7.1.3	Nitrate reductase (niaD)	Unkles et al. (1992)	ANID	An08g05610	208048
r907	HNO ₂ + 3 NADPH \Rightarrow NH ₄ OH + 3 NADP + H ₂ O	1.7.1.4	Nitrite reductase	Unkles et al. (1992)	ANID	An08g05640	198539
r908	NH ₄ OH \rightleftharpoons NH ₃ + H ₂ O	Non enzymatic step	Non enzymatic reaction		ANEW		
r909	UREA + ATP \rightleftharpoons H ₂ O + CO ₂ \rightleftharpoons ADP + PI + UREAC	6.3.4.6	Urea carboxylase		ANID	An01g13810	172796
r910	UREAC \Rightarrow 2 NH ₃ + 2 CO ₂	3.5.1.54	Allophanate hydrolase		ANID		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r911	: ACNL \Rightarrow INAC + NH ₃	3.5.5.1	Nitrilase	Snajdova et al. (2004)	ANID	An16g00550; An01g07510; An01g12090; An06g01960; An08g08940; An08g10150; An12g01260; An16g06210; An18g01740	41410; 35944; 170270; 175987; N/A; 52578; 141873; 40928; 211815
r912	: UREA + H ₂ O \Rightarrow CO ₂ + 2 NH ₃	3.5.1.5	urease	Ivanov (1925); Smith et al. (1993)	ANEW	An01g03550; An15g00940	52004; 200521
BIOMASS REACTIONS							
POLYMERIZATION REACTIONS (PROTEINS, DNA, RNA)							
Protein formation							
PROTEIN	: 1.033 ALA + 0.413 ARG + 0.209 ASN + 0.628 ASP + 0.079 CYS + 0.899 GLU + 0.300 GLN + 0.862 GLY + 0.205 HIS + 0.396 ILE + 0.704 LEU + 0.651 LYS + 0.105 MET + 0.312 PHE + 0.441 PRO + 0.628 SER + 0.503 THR + 0.126 TRP + 0.205 TYR + 0.536 VAL + 39.729 ATP + 30.489 H ₂ O \Rightarrow 39.729 ADP + 39.729 PI + Protein	Artificial	Artificial reaction		ANEW		
RNA formation							
RNA	: 0.773 AMP + 0.931 GMP + 0.773 CMP + 0.616 UMP + 7.423 ATP + 4.330 H ₂ O \Rightarrow 7.424 ADP + 7.424 PI + RNA	2.7.7.6	DNA-directed RNA polymerase		ANEW *	An01g02200; An01g04380; An01g05740; An01g07250; An01g11950; An01g12710; An02g01800; An02g05460; An02g11470; An08g07050; An09g04100; An11g01770; An11g09370; An12g00720; An12g00780; An12g03900; An13g00280; An15g00700; An15g05780; An15g05790; An16g07430	196819; 36183; 171679; 143936; 205564; 205506; 52135; 206792; 128750; 176941; 128642; 55936; 39394; 54460; 190142; 211641; 57188; 40356; 48809; 48810; 55082
DNA formation							

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
DNA	0.794 DAMP + 0.826 DCMP + 0.794 DTMP + 0.826 DGMP + 11.019 ATP + 7.778 H ₂ O ⇒ 11.019 ADP + 11.019 PI + DNA	2.7.7.7	DNA-directed DNA polymerase		ANEW *	An02g02510; An02g14830; An04g02280; An08g02440; An11g00720; An11g09550; An14g06200; An14g06560; An15g07150; An16g03060	206569; 173303; 213157; 176678; 179102; 179788; 184522; 185612; 210383; 53636
Cell wall composition							
Cellwall	0.043 GAG + 0.254 NIG + 0.337 PSNIG + 0.381 GGM + 0.389 14GLUCAN + 2.726 13GLUCAN + 1.623 CHIT ⇒ CELLWALL	Artificial	Artificial reaction		ANEW		
Lipids:							
Lipidassemb	0.010083 TAGLY + 0.001009 DAGLY + 0.008912 MAGLY + 0.000223 C140 + 0.001480 C160 + 0.000245 C180 + 0.001678 C181 + 0.001664 C182 + 0.000047 C183 + 0.034062 ERGOST + 0.010038 ERGOSE + 0.030053 MGDG + 0.012374 MGC181 + 0.007859 DGDG + 0.000005 TGDMPIC + 0.000030 CERB1 + 0.000031 CERB2 + 0.000025 GALCER + 0.000024 GLUCER1 + 0.000024 GLUCER2 + 0.001746 CL + 0.015312 PC + 0.000359 PS + 0.034807 PE ⇒ LIPIDS	Artificial	Artificial reaction		ANEW		
Small molecules pool:							
Pool	0.00039 ICIT + 0.013 CIT + 0.00091 SUCC + 0.00007 FUM + 0.00065 MAL + 0.0017 NAD + 0.00018 NADH + 0.00014 NADP + 0.00008 NADPH + 0.04 TRE + 0.18 MNT + 0.46 GL + 0.3 EOL + 0.01 AOL ⇒ POOL	Artificial	Artificial reaction		ANEW		
Biomass formation							
GROWTH	0.263 Protein + 0.00244 DNA + 0.01814 RNA + LIPIDS + POOL + 0.38 CELLWALL + 61 ATP + 61 H ₂ O ⇒ 61 ADP + 61 PI + BIOMASS	Artificial	Artificial reaction		ANEW		
Maintenance requirements (non-growth associated)							
m _A TP	ATP + H ₂ O ⇒ ADP + PI	Artificial	Artificial reaction		ANIG, ANID		
TRANSPORT PROCESSES							
Non-carrier-mediated (free diffusion)							
Across the cytoplasmatic membrane							
Others:							
r1092	CO ₂ e ⇌ CO ₂			David et al. (2003)	ANIG, ANID		

Continues on next page

Continued from last page						
ID	Reaction	EC no	Enzyme	Source	Model	ATCC
r1093	: H ₂ O _e ⇌ H ₂ O			David et al. (2003)	ANIG, ANID	
r1094	: O ₂ e ⇌ O ₂			David et al. (2003)	ANIG, ANID	
r1091	: H ₂ O ₂ e ⇌ H ₂ O ₂			Pel et al. (2007)	ANEW	
Alcohols:						
r1071	: ETh _e ⇌ ETH			David et al. (2003)	ANIG, ANID	
r1141	: METHOL _e ⇌ METHOL			David et al. (2003)	ANIG, ANID	
Acids:						
r1069	: AC _e ⇌ AC			David et al. (2003)	ANIG, ANID	
r1142	: FOR _e ⇌ FOR			Hauge (1957, Inferred)	ANID	
r1066	: LAC _e ⇌ LAC			Netik et al. (1997)	ANIG, ANID	
r1065	: LLAC _e ⇌ LLAC			Netik et al. (1997)	ANIG, ANID	
Across the mitochondrial membrane						
Others:						
r1150	: H ₂ O ⇌ H ₂ O _m			David et al. (2003)	ANIG, ANID	
r1153	: O ₂ ⇌ O _{2m}			David et al. (2003)	ANIG, ANID	
r1152	: CO ₂ ⇌ CO _{2m}			David et al. (2003)	ANIG, ANID	
r1151	: NH ₃ ⇌ NH _{3m}			David et al. (2003)	ANIG, ANID	
Alcohols:						
r1149	: ETh ⇌ ETh _m				ANID	
Aldehydes:						
r1148	: ACAL ⇌ ACAL _m				ANID	
Acids:						
r1147	: AC ⇌ AC _m			David et al. (2003)	ANIG, ANID	
Fatty acids:						
r1014	: C ₄₀ e ⇌ C ₄₀			Chattopadhyay et al. (1985b)	ANEW	
r1015	: C ₆₀ e ⇌ C ₆₀			Chattopadhyay et al. (1985b)	ANEW	
r1016	: C ₈₀ e ⇌ C ₈₀			Chattopadhyay et al. (1985b)	ANEW	
r1017	: C ₁₀₀ e ⇌ C ₁₀₀			Chattopadhyay et al. (1985b)	ANEW	
r1018	: C ₁₂₀ e ⇌ C ₁₂₀			Chattopadhyay et al. (1985b)	ANEW	
r1019	: C ₁₄₀ e ⇌ C ₁₄₀			Chattopadhyay et al. (1985b)	ANEW	
r1020	: C ₁₄₁ e ⇌ C ₁₄₁			Chattopadhyay et al. (1985b)	ANEW	
r1021	: C ₁₅₀ e ⇌ C ₁₅₀			Chattopadhyay et al. (1985b)	ANEW	
r1022	: C ₁₆₀ e ⇌ C ₁₆₀			Chattopadhyay et al. (1985b)	ANEW	
r1023	: C ₁₆₁ e ⇌ C ₁₆₁			Chattopadhyay et al. (1985b)	ANEW	
r1024	: C ₁₆₂ e ⇌ C ₁₆₂			Chattopadhyay et al. (1985b)	ANEW	
r1025	: C ₁₇₀ e ⇌ C ₁₇₀			Chattopadhyay et al. (1985b)	ANEW	
r1026	: C ₁₇₁ e ⇌ C ₁₇₁			Chattopadhyay et al. (1985b)	ANEW	
r1027	: C ₁₈₀ e ⇌ C ₁₈₀			Chattopadhyay et al. (1985b)	ANEW	
r1028	: C ₁₈₁ e ⇌ C ₁₈₁			Chattopadhyay et al. (1985b)	ANEW	
r1029	: C ₁₈₂ e ⇌ C ₁₈₂			Chattopadhyay et al. (1985b)	ANEW	

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1030	: C183e \rightleftharpoons C183			Chattopadhyay et al. (1985b)	ANEW		
r1031	: C190e \rightleftharpoons C190			Chattopadhyay et al. (1985b)	ANEW		
r1032	: C191e \rightleftharpoons C191			Chattopadhyay et al. (1985b)	ANEW		
r1033	: C192e \rightleftharpoons C192			Chattopadhyay et al. (1985b)	ANEW		
r1034	: C200e \rightleftharpoons C200			Chattopadhyay et al. (1985b)	ANEW		
Carrier-mediated							
Across the cytoplasmatic membrane							
Nucleotide related							
r1124	: ATPe \rightleftharpoons ATP		ATP permease	Chowdhury et al. (1997)	ANEW		
r1123	: AMPe \rightleftharpoons AMP		AMP permease	Inferred	ANEW		
r1125	: ATNe \rightleftharpoons ATN		Allantoin permease	Arst and Cove (1969); Martinelli and Kinghorn (1994, A. nidulans)	ANEW		
r1119	: HYXNe \rightleftharpoons HYXN		Hypoxanthine permease	Arst and Cove (1969); Martinelli and Kinghorn (1994, A. nidulans)	ANEW		
r1120	: UR Ae \rightleftharpoons UR Ae		Uracil permease	Experimental	ANEW		
r1121	: URle \rightleftharpoons URle		Uridine permease	Experimental	ANEW		
r1180	: ADe \rightleftharpoons AD		adenine permease	Martinelli and Kinghorn (1994, A. nidulans)	ANEW		
r1129	: QUINe \rightleftharpoons QUIN		Quinolinate permease		ANEW		
r1126	: NICAe \rightleftharpoons NICA		Nicotinate permease		ANEW		
r1127	: NICDe \rightleftharpoons NICD		Nicotinamide permease		ANEW		
r1122	: XANe \rightleftharpoons XAN		Xanthine permease	Taha and Sharabash (1956, Inferred), Martinelli and Kinghorn (1994, A. nidulans)	ANEW		
r1128	: KYNe \rightleftharpoons KYN		L-Kynurenine permease		ANEW		
r1214	: 3CPYRDe \rightleftharpoons 3CPYRD			Snajdrova et al. (2004, Inferred)	ANEW		
Aromatics and catabolic products							
r1182	: ANe \rightleftharpoons AN				ANEW		
r1074	: PHACe \rightleftharpoons PHAC		Anthranilate transporter	Kanath et al. (1987, Inferred)	ANEW		
r1076	: DMANDe \rightleftharpoons DMAND		Phenylacetate transporter	Sugumaran et al. (1973, Inferred)	ANEW		
r1075	: LMANDe \rightleftharpoons LMAND		Mandelate-transporter	Jamaluddin et al. (1970, Inferred)	ANEW		
r1073	: PHALe \rightleftharpoons PHAL		Mandelate-transporter	Jamaluddin et al. (1970, Inferred)	ANEW		
r1078	: BAe \rightleftharpoons BA		benzoate transporter	Martinelli and Kinghorn (1994, Inferred)	ANEW		
r1077	: BNe \rightleftharpoons BN				ANEW		
r1084	: DHSKe \rightleftharpoons DHSK				ANEW		
r1082	: SALIe \rightleftharpoons SALI		salicylate transporter	Krupka et al. (1967); Martinelli and Kinghorn (1994, Inferred)	ANEW		
r1072	: PHPYRe \rightleftharpoons PHPYR				ANEW		
r1079	: BAMNe \rightleftharpoons BAMN				ANEW		
r1083	: RESe \rightleftharpoons RES				ANEW		
r1272	: COUMe \rightleftharpoons COUM			Milstein et al. (1988, Inferred)	ANEW		
r1197	: DMTe \rightleftharpoons DMT			Ganji et al. (1995, Inferred)	ANEW		
r1198	: TPHTHe \rightleftharpoons TPHTH			Ganji et al. (1995, Inferred)	ANEW		
r1199	: PCCe \rightleftharpoons PCC			Ganji et al. (1995, Inferred)	ANEW		
r1204	: FERe \rightleftharpoons FER				ANEW		
r1205	: VANE \rightleftharpoons VAN				ANEW		
r1209	: INDe \rightleftharpoons IND			Kamath and Vaidyanathan (1990, Inferred)	ANEW		
r1212	: 3HBAe \rightleftharpoons 3HBA				ANEW		
Alky/amines							
r1190	: BUTN \rightleftharpoons BUTNe				ANEW		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
Others							
r1223	: PENN \rightleftharpoons PENNe				ANEW		
r1095	: P1e \rightleftharpoons P1			Seshadri et al. (2004, Inferred)	ANIG, ANID		
r1087	: NH3e \rightleftharpoons NH3			David et al. (2003)	ANEW		
r1086	: HNO3e \rightleftharpoons HNO3			Seshadri et al. (2004, Inferred)	ANEW		
r1088	: H2SO3e \rightleftharpoons H2SO3				ANID		
r1089	: CHOSLFe \rightleftharpoons CHOSLF		Choline sulphate permease	Scott and Spencer (1968, A. nidulans)	ANEW		
r1090	: SLFe \rightleftharpoons SLF		Sulphate permease	Marzluf (1993); Borges-Walmsley et al. (1995, A. nidulans)	ANIG		
r1118	: DTBe \rightleftharpoons DTB			Parry and Naidu (1980, Inferred)	ANEW		
r1085	: UREAe \rightleftharpoons UREA			Ivanov (1925)	ANEW		
r1012	: OTA \rightleftharpoons OTAe		Ochratoxin A exporter		ANEW		
r1273	: GLYNe \rightleftharpoons GLYN			Witteveen et al. (1990, Inferred)	ANEW		
CARBOHYDRATES							
Dissacharides							
r1143	: TREe \rightleftharpoons TRE				ANID		
r1144	: LACTe \rightleftharpoons LACT				ANIG, ANID		
r1145	: MLTe \rightleftharpoons MLT			Pendl et al. (2004)	ANIG, ANID		
Monosacharides							
Hexoses							
r1037	: GLACe \rightleftharpoons GLAC			vanKuyk et al. (2004)	ANIG, ANID		
r1047	: GLCe \rightleftharpoons GLC			Karaffa et al. (2001)	ANIG, ANID		
r1048	: DGLCe \rightleftharpoons DGLC				ANIG		
r1046	: bDGLCe \rightleftharpoons bDGLC			David et al. (2003)	ANIG, ANID		
r1044	: FRUe \rightleftharpoons FRU			Karaffa et al. (2001); vanKuyk et al. (2004)	ANIG, ANID		
r1041	: MANe \rightleftharpoons MAN			vanKuyk et al. (2004)	ANIG, ANID		
r1039	: IDOLe \rightleftharpoons IDOL				ANIG, ANID		
r1040	: SORe \rightleftharpoons SOR			Seshadri et al. (2004, Inferred)	ANIG, ANID		
r1221	: RHAe \rightleftharpoons RHA			Fries and Kallstromer (1965, Inferred)	ANIG, ANEW		
Pentoses							
r1052	: ARABe \rightleftharpoons ARAB			David et al. (2003)	ANIG, ANID		
r1059	: LARABe \rightleftharpoons LARAB			de Groot et al. (2003)	ANIG, ANID		
r1049	: RIBe \rightleftharpoons RIB			David et al. (2003)	ANIG, ANID		
r1051	: RLe \rightleftharpoons RL				ANID		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1054	: XYL \Rightarrow XYL			Martinelli and Kinghorn (1994); Prathumpai et al. (2003); de Groot et al. (2003); vanKuyk et al. (2004)	ANIG, ANID		
r1055	: XUL \Rightarrow XUL				ANID		
r1056	: LXUL \Rightarrow LXUL				ANID		
Tetroses							
r1062	: Ee \Rightarrow E			Schuurink et al. (1990)	ANID		
r1060	: EUe \Rightarrow EU				ANID		
ALCOHOLS (polyols)							
r1064	: GLe \Rightarrow GL			Martinelli and Kinghorn (1994)	ANIG, ANID		
r1061	: EOLe \Rightarrow EOL			David et al. (2003)	ANIG, ANID		
r1053	: AOLe \Rightarrow AOL			Martinelli and Kinghorn (1994)	ANIG, ANID		
r1058	: LAOLe \Rightarrow LAOL			Martinelli and Kinghorn (1994)	ANIG, ANID		
r1050	: RIBOLe \Rightarrow RIBOL			David et al. (2003)	ANIG, ANID		
r1057	: XOLe \Rightarrow XOL			Prathumpai et al. (2003)	ANIG, ANID		
r1038	: GALOLe \Rightarrow GALOL				ANID		
r1043	: MNTe \Rightarrow MNT			Martinelli and Kinghorn (1994)	ANIG, ANID		
r1042	: SOTe \Rightarrow SOT			Martinelli and Kinghorn (1994)	ANIG, ANID		
ACIDS							
TCA cycle related organic acids							
r1139	: MALe \Rightarrow MAL			Netik et al. (1997); Alvarez-Vasquez et al. (2000)	ANIG, ANID		
r1138	: AKGe \Rightarrow AKG			Netik et al. (1997)	ANIG, ANID		
r1137	: ACOe \Rightarrow ACO				ANID		
r1134	: CITe \Rightarrow CIT			Burgstaller (2006); Netik et al. (1997)	ANIG, ANID		
r1136	: FUMe \Rightarrow FUM			David et al. (2003)	ANIG, ANID		
r1135	: ICITe \Rightarrow ICIT			Netik et al. (1997)	ANID		
r1140	: OXALe \Rightarrow OXAL			David et al. (2003)	ANIG, ANID		
r1132	: OAe \Rightarrow OA				ANID		
r1131	: PYRe \Rightarrow PYR			Netik et al. (1997); Alvarez-Vasquez et al. (2000)	ANIG, ANID		
r1130	: SUCCe \Rightarrow SUCC			Netik et al. (1997)	ANIG, ANID		
Other acids							
r1036	: GALNTe \Rightarrow GALNT				ANID		
r1035	: GALUNTe \Rightarrow GALUNT			Martinelli and Kinghorn (1994)	ANIG, ANID		
r1045	: GLCNTe \Rightarrow GLCNT			Muller (1986, Inferred)	ANIG, ANID		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1179	: GLCUNT \rightleftharpoons GLCUNT			David et al. (2003)	ANIG, ANID		
r1178	: KOJAe \rightleftharpoons KOJA				ANID		
r1063	: TARE \rightleftharpoons TAR			Patil and Ramakrishnan (1966)	ANIG, ANID		
r1067	: PROPe \rightleftharpoons PROP			Sealy-Lewis and Fairhurst (1998, Inferred)	ANIG, ANID		
r1096	: QTe \rightleftharpoons QT			Cain (1972a, Inferred)	ANEW		
r1097	: SMEe \rightleftharpoons SME			Cain (1972a, Inferred)	ANEW		
r1185	: GABAE \rightleftharpoons GABA			Kumar and Punekar (1998, Inferred)	ANEW	An16g02000	210724
AMINO ACIDS							
r1098	: GLXe \rightleftharpoons GLY			Oganesyan et al. (1998, Inferred)	ANID		
r1099	: ALAe \rightleftharpoons ALA			Sarma et al. (1961, Inferred)	ANID		
r1100	: bALAE \rightleftharpoons bALA				ANID		
r1101	: ARGe \rightleftharpoons ARG				ANID		
r1102	: ASNe \rightleftharpoons ASN			Sarma et al. (1961, Inferred)	ANID		
r1103	: ASPe \rightleftharpoons ASP				ANID		
r1104	: CYSe \rightleftharpoons CYS				ANID		
r1105	: GLUe \rightleftharpoons GLU				ANID		
r1106	: GLNe \rightleftharpoons GLN			Ram et al. (2004, Inferred)	ANID		
r1107	: HISE \rightleftharpoons HIS				ANID		
r1108	: ILEe \rightleftharpoons ILE				ANID		
r1109	: LEUe \rightleftharpoons LEU				ANID		
r1110	: LYSe \rightleftharpoons LYS				ANID		
r1111	: METe \rightleftharpoons MET				ANID		
r1112	: PHEe \rightleftharpoons PHE			Jones et al. (1981, A. nidulans)	ANID		
r1113	: PROe \rightleftharpoons PRO				ANID		
r1114	: SERe \rightleftharpoons SER				ANID		
r1115	: THRe \rightleftharpoons THR				ANID		
r1080	: TRPe \rightleftharpoons TRP			Sarma et al. (1961, Inferred)	ANID		
r1116	: TYRe \rightleftharpoons TYR				ANID		
r1117	: VALe \rightleftharpoons VAL				ANID		
r1184	: CITRe \rightleftharpoons CITR			Lenouvel et al. (2002, Inferred)	ANEW		
r1187	: ORNe \rightleftharpoons ORN			Lenouvel et al. (2002, Inferred)	ANEW		
ALDEHYDES							
r1068	: PROPALe \rightleftharpoons PROPAL			Kazimirova and Novotel'nov (1956, Inferred)	ANEW		
r1070	: ACALe \rightleftharpoons ACAL			Rippel and Wiangke (1941, Inferred)	ANEW		
Across the mitochondrial membrane							
OTHERS							
r1154	: PIm \rightleftharpoons PI		Phosphate carrier		ANIG, ANID		
r1181	: UREA \rightleftharpoons UREA _m				ANEW		
r1146	: PYR \rightleftharpoons PYR _m			Karaffa et al. (2001); Karaffa and Kubicek (2003)	ANIG, ANID		
r1169	: CIT _m + MAL \rightleftharpoons CIT + MAL _m			Karaffa et al. (2001); Karaffa and Kubicek (2003); Pel et al. (2007)	ANIG, ANID	An11g11230; An18g00070	136079; 42578
r1170	: ACO _m + MAL \rightleftharpoons ACO + MAL _m				ANID		

Continues on next page

Continued from last page

ID	Reaction	EC no	Enzyme	Source	Model	CBS	ATCC
r1171	: ICITm + MAL \Rightarrow ICIT ⁺ + MALm			David et al. (2003)	ANIG, ANID		
r1172	: AKG \rightleftharpoons AKGm				ANID		
r1173	: OA \rightleftharpoons OAm			Karaffa et al. (2001); Pel et al. (2007)	ANID	An14g06860	41991
r1174	: SUCC \rightleftharpoons SUCCm			David et al. (2003)	ANIG, ANID		
r1175	: FUM \rightleftharpoons FUMm				ANID		
r1176	: ICIT \rightleftharpoons ICITm				ANIG, ANID		
r1168	: FOR \rightleftharpoons FORm				ANID		
r1166	: THF \rightleftharpoons THFm			Cossins and Chen (1997, Inferred)	ANEW		
r1167	: METTHF \rightleftharpoons METTHFm			Cossins and Chen (1997, Inferred)	ANEW		
r1177	: CAP \rightleftharpoons CAPm			Cossins and Chen (1997, Inferred)	ANEW		
r1155	: 3OA \rightleftharpoons 3OAm				ANEW		
r1186	: GABA \rightleftharpoons GABAm			Kumar and Puneekar (1998, Inferred)	ANEW		
r1133	: GLX \rightleftharpoons GLXm				ANEW		
r1191	: PROPM \rightleftharpoons PROP				ANEW		
AMINO ACIDS							
r1158	: THRm \rightleftharpoons THR				ANEW		
r1159	: ARGm \rightleftharpoons ARG				ANEW		
r1160	: ASPm \rightleftharpoons ASP				ANEW		
r1161	: LEUm \rightleftharpoons LEU				ANEW		
r1162	: ILEm \rightleftharpoons ILE				ANEW		
r1163	: ORNm \rightleftharpoons ORN				ANEW		
r1164	: VALm \rightleftharpoons VAL				ANEW		
r1165	: LYSm \rightleftharpoons LYS				ANEW		
r1183	: CITR \rightleftharpoons CITRm			Lenouvel et al. (2002, Inferred)	ANEW		
Shuttles							
Malate-Aspartate shuttle							
r1157	: ASPm + GLU \rightleftharpoons ASP + GLUm			David et al. (2003)	ANIG, ANID		
r1156	: MAL + AKGm \rightleftharpoons MALm + AKG				ANID		

Suppl. Table II: List of the abbreviations for metabolite-names used in the reaction list of *A. niger* iMA871 (Suppl. Table I) and their full name. An "m" denotes that the metabolite is found in the mitochondrion, whereas an "e" is used to mark an extracellular metabolite.

Abbreviation	Full name
13GLUCAN	1,3-beta-D-Glucan
13GLUCANe	1,3-beta-D-Glucan (extracellular)
13PDG	1,3-Bisphospho-D-glycerate
14GLUCAN	1,4-alpha-glucan
2D3DGALT	2-Dehydro-3-deoxy-D-galactonate
2HPAC	2-hydroxyphenylacetic acid
2MAC	2-maleyl acetate
2MACOm	2-methyl aconitate
2MCITm	2-methyl citrate
2MICITm	2-methyl isocitrate
2PG	2-Phospho-D-glycerate
345THBe	Gallic acid
3CMUCO	3-Carboxymuconate
3CPYRD	3-cyanopyridine
3CPYRDe	3-cyanopyridine (extracellular)
3DDAH7P	2-Dehydro-3-deoxy-D-arabino-heptonate 7-phosphate
3FPYR	3-fumarylpyruvate
3HBA	3-hydroxybenzoate; m-hydroxybenzoate
3HBANe	3-hydroxybenzoate; m-hydroxybenzoate (extracellular)
3HIND	3-hydroxyindoxyle
3HPYR	3-hydroxypyruvate
3MPYR	3-maleylpyruvate
3OA	3-oxoadipate
3OACOA _m	3-oxoadipyl-CoA
3OAm	3-oxoadipate
3PG	3-Phospho-D-glycerate
3PSER	3-Phosphoserine
3PSME	5-O-(1-Carboxyvinyl)-3-phosphoshikimate
4CMUCL	4-Carboxymuconolactone
4HBA	4-hydroxybenzoic acid
4HBAL	4-hydroxybenzaldehyde
4HBFOR	4-hydroxybenzoylformic acid
4HMAND	4-hydroxymandelate

Continues on next page

Continued from last page

Abbreviation	Full name
4HPAC	4-hydroxyphenylacetic acid
4HPP	3-(4-Hydroxyphenyl)pyruvate
4PPNCYS	(R)-4'-Phosphopantothienoyl-L-cysteine
4PPNTE	Pantetheine 4'-phosphate
4PPNTO	D-4'-Phosphopantothenate
AACACP	Acetoacetyl [acyl-carrier protein]
AACCOA	Acetoacetyl coenzyme A
AACCOAm	Acetoacetyl coenzyme A (mitochondrial)
AAMYLe	Alpha-amylase (secreted to the medium)
ABUTm	2-Aceto-2-hydroxy butyrate (mitochondrial)
AC	Acetate
ACACP	Acyl-[acyl-carrier protein]
ACAL	Acetaldehyde
ACALe	Acetaldehyde, extracellular
ACALm	Acetaldehyde (mitochondrial)
ACCOA	Acetyl coenzyme A
ACCOAm	Acetyl coenzyme A (mitochondrial)
ACe	Acetate (extracellular)
ACLACm	2-Acetolactate (mitochondrial)
ACm	Acetate (mitochondrial)
ACNL	3-Indoleacetonitrile
ACO	cis-Aconitate
ACOE	cis-Aconitate (extracellular)
ACOm	cis-Aconitate (mitochondrial)
ACP	Acyl-carrier protein
ACTAC	Acetoacetate
ACTP	Acetyl phosphate
ACYBUT	gamma-Amino-gamma-cyanobutanoate
AD	Adenine
ADCHOR	4-Amino-4-deoxychorismate
ADe	Adenine (extracellular)
ADHLIPOm	S-Acetyldihydrolipoamide (mitochondrial)
ADN	Adenosine
ADP	ADP
ADPm	ADP (mitochondrial)
ADPR	ADP-Ribose
AHHMD	2-Amino-7,8-dihydro-4-hydroxy-6-(diphosphoxymethyl)pteridine

Continues on next page

Continued from last page

Abbreviation	Full name
AHHMP	2-Amino-4-hydroxy-6-hydroxymethyl-7,8-dihydropteridine
AHTD	2-Amino-4-hydroxy-6-(erythro-1,2,3-trihydroxypropyl)-dihydropteridine triphosphate
AICAR	AICAR
AIR	Aminoimidazole ribotide
AKAm	2-Oxoadipate (mitochondrial)
AKG	2-Oxoglutarate
AKGe	2-Oxoglutarate (extracellular)
AKGE1m	Alpha-ketoglutarate bound to alpha-ketoglutarate dehydrogenase
AKGE2m	Alpha-ketoglutarate bound to dihydrolipoyl transsuccinylase
AKGm	2-Oxoglutarate (mitochondrial)
AKP	2-Dehydropantoate
ALA	L-Alanine
ALAE	L-Alanine (extracellular)
ALAm	L-Alanine (mitochondrial)
AMAm	2-aminoadipate (mitochondrial)
AMASAm	2-aminoadipate-semialdehyde (mitochondrial)
AMP	AMP
AMPe	AMP, extracellular
AMPm	AMP (mitochondrial)
AMYLPe	Amylopectin (extracellular)
AMYLSe	Amylose (extracellular)
AN	Anthranilate
ANe	Anthranilate (extracellular)
AOL	D-Arabitol
AOLe	D-Arabitol (extracellular)
AONA	8-Amino-7-oxononanoate
APROP	alpha-Aminopropionitrile
APS	Adenylylsulfate
ARAB	D-Arabinose
ARABe	D-Arabinose (extracellular)
ARABINe	Arabinan (extracellular)
ARABLAC	D-Arabinono-1,4-lactone
ARG	L-Arginine
ARGe	L-Arginine (extracellular)
ARGm	L-Arginine (mitochondrial)

Continues on next page

Continued from last page

Abbreviation	Full name
ARGSUCCm	Argininosuccinate (mitochondrial)
ASER	O-Acetyl-L-serine
ASN	L-Asparagine
ASNe	L-Asparagine (extracellular)
ASP	L-Aspartate
ASPe	L-Aspartate (extracellular)
ASpm	L-Aspartate (mitochondrial)
ASPSA	L-Aspartate 4-semialdehyde
ASUC	N6-(1,2-Dicarboxyethyl)-AMP
ATN	Allantoin
ATNe	Allantoin (extracellular)
ATP	ATP
ATPe	ATP (extracellular)
ATPm	ATP (mitochondrial)
ATT	Allantoate
BA	Benzoic acid
BAe	Benzoic acid (extracellular)
BAL	Benzaldehyde
bALA	beta-Alanine
bAL Ae	beta-Alanine (extracellular)
BAMN	Benzoylamine
BAMNe	Benzoylamine (extracellular)
BASP	4-Phospho-L-aspartate
BCCP	Biotin-carboxyl-carrier protein
bDG6P	beta-D-Glucose 6-phosphate
bDGLC	beta-D-Glucose
bDGLCe	beta-D-Glucose (extracellular)
BFOR	Benzoylformate
bFRU	beta-D-fructose
bGLAC	beta-D-galactose
bLARAB	beta-L-arabinose
BN	Benzonitrile
BNe	Benzonitrile (extracellular)
BT	Biotin
BTe	Biotin (extracellular)
BTOL	benzene-1,2,4-triol
BUTAL	Butanal
BUTN	n-butylamine
BUTNe	n-butylamine (extracellular)

Continues on next page

Continued from last page

Abbreviation	Full name
C100	Decanoate
C100ACP	Decanoyl-[acyl-carrier protein]
C100COA	Decanoyl-CoA
C100COAm	Decanoyl-CoA (mitochondrial)
C100e	Decanoate (extracellular)
C10DACP	Dec-2-enoyl-[acyl-carrier protein]
C10DCOAm	Dec-2-enoyl-CoA (mitochondrial)
C10HACP	3-hydroxydecanoyl-[acyl-carrier protein]
C10HCOAm	3-hydroxydecanoyl-CoA (mitochondrial)
C10OACP	3-oxodecanoyl-[acyl-carrier protein]
C10OCOAm	3-oxodecanoyl-CoA (mitochondrial)
C110ACP	Undecanoyl-[acyl-carrier protein]
C110COAm	Undecanoyl-CoA (mitochondrial)
C11DACP	Undec-2-enoyl-[acyl-carrier protein]
C11DCOAm	Undec-2-enoyl-CoA (mitochondrial)
C11HACP	3-hydroxyundecanoyl-[acyl-carrier protein]
C11HCOAm	3-hydroxyundecanoyl-CoA (mitochondrial)
C11OACP	3-oxoundecanoyl-[acyl-carrier protein]
C11OCOAm	3-oxoundecanoyl-CoA (mitochondrial)
C120	Dodecanoate
C120ACP	Dodecanoyl-[acyl-carrier protein]
C120CAR	Dodecanoyl-carnitine
C120CARm	Dodecanoyl-carnitine (mitochondrial)
C120COA	Dodecanoyl-CoA
C120COAm	Dodecanoyl-CoA (mitochondrial)
C120e	Dodecanoate (extracellular)
C12DACP	Dodec-2-enoyl-[acyl-carrier protein]
C12DCOAm	Dodec-2-enoyl-CoA (mitochondrial)
C12HACP	3-hydroxydodecanoyl-[acyl-carrier protein]
C12HCOAm	3-hydroxydodecanoyl-CoA (mitochondrial)
C12OACP	3-oxododecanoyl-[acyl-carrier protein]
C12OCOAm	3-oxododecanoyl-CoA (mitochondrial)
C130ACP	Tridecanoyl-[acyl-carrier protein]
C130COAm	Tridecanoyl-CoA (mitochondrial)
C13DACP	Tridec-2-enoyl-[acyl-carrier protein]
C13DCOAm	Tridec-2-enoyl-CoA (mitochondrial)
C13HACP	3-hydroxytridecanoyl-[acyl-carrier protein]
C13HCOAm	3-hydroxytridecanoyl-CoA (mitochondrial)
C13OACP	3-oxotridecanoyl-[acyl-carrier protein]

Continues on next page

Continued from last page

Abbreviation	Full name
C13OCOAm	3-oxotridecanoyl-CoA (mitochondrial)
C140	Tetradecanoate
C140ACP	Tetradecanoyl-[acyl-carrier protein]
C140CAR	Tetradecanoyl-carnitine
C140CARm	Tetradecanoyl-carnitine (mitochondrial)
C140COA	Tetradecanoyl-CoA
C140COAm	Tetradecanoyl-CoA (mitochondrial)
C140e	Tetradecanoate (extracellular)
C141	Tetradecenoate
C141ACP	Tetradecenoyl-[acyl-carrier protein]
C141CAR	Tetradecenoyl-carnitine
C141CARm	Tetradecenoyl-carnitine (mitochondrial)
C141COA	Tetradecenoyl-CoA
C141COAm	Tetradecenoyl-CoA (mitochondrial)
C141e	Tetradecenoate (extracellular)
C14DACP	Tetradec-2-enoyl-[acyl-carrier protein]
C14DCOAm	Tetradec-2-enoyl-CoA (mitochondrial)
C14HACP	3-hydroxytetradecanoyl-[acyl-carrier protein]
C14HCOAm	3-hydroxytetradecanoyl-CoA (mitochondrial)
C14OACP	3-oxotetradecanoyl-[acyl-carrier protein]
C14OCOAm	3-oxotetradecanoyl-CoA (mitochondrial)
C150	Pentadecanoate
C150ACP	Pentadecanoyl-[acyl-carrier protein]
C150CAR	Pentadecanoyl-carnitine
C150CARm	Pentadecanoyl-carnitine (mitochondrial)
C150COA	Pentadecanoyl-CoA
C150COAm	Pentadecanoyl-CoA (mitochondrial)
C150e	Pentadecanoate (extracellular)
C15DACP	Pentadec-2-enoyl-[acyl-carrier protein]
C15DCOAm	Pentadec-2-enoyl-CoA (mitochondrial)
C15HACP	3-hydroxypentadecanoyl-[acyl-carrier protein]
C15HCOAm	3-hydroxypentadecanoyl-CoA (mitochondrial)
C15OACP	3-oxopentadecanoyl-[acyl-carrier protein]
C15OCOAm	3-oxopentadecanoyl-CoA (mitochondrial)
C160	Hexadecanoate
C160ACP	Hexadecanoyl-[acyl-carrier protein]
C160CAR	Hexadecanoyl-carnitine
C160CARm	Hexadecanoyl-carnitine (mitochondrial)
C160COA	Hexadecanoyl-CoA

Continues on next page

Continued from last page

Abbreviation	Full name
C160COAm	Hexadecanoyl-CoA (mitochondrial)
C160e	Hexadecanoate (extracellular)
C161	Hexadecenoate
C161ACP	Hexadecenoyl-[acyl-carrier protein]
C161CAR	Hexadecenoyl-carnitine
C161CARm	Hexadecenoyl-carnitine (mitochondrial)
C161COA	Hexadecenoyl-CoA
C161COAm	Hexadecenoyl-CoA (mitochondrial)
C161e	Hexadecenoate (extracellular)
C162	Hexadecadienoate
C162ACP	Hexadecadienoyl-[acyl-carrier protein]
C162CAR	Hexadecadienoyl-carnitine
C162CARm	Hexadecadienoyl-carnitine (mitochondrial)
C162COA	Hexadecadienoyl-CoA
C162COAm	Hexadecadienoyl-CoA (mitochondrial)
C162e	Hexadecadienoate (extracellular)
C16DACP	Hexadec-2-enoyl-[acyl-carrier protein]
C16DCOAm	Hexadec-2-enoyl-CoA (mitochondrial)
C16HACP	3-hydroxyhexadecanoyl-[acyl-carrier protein]
C16HCOAm	3-hydroxyhexadecanoyl-CoA (mitochondrial)
C16OACP	3-oxohexadecanoyl-[acyl-carrier protein]
C16OCOAm	3-oxohexadecanoyl-CoA (mitochondrial)
C170	Heptadecanoate
C170ACP	Heptadecanoyl-[acyl-carrier protein]
C170CAR	Heptadecanoyl-carnitine
C170CARm	Heptadecanoyl-carnitine (mitochondrial)
C170COA	Heptadecanoyl-CoA
C170COAm	Heptadecanoyl-CoA (mitochondrial)
C170e	Heptadecanoate (extracellular)
C171	Heptadecenoate
C171ACP	Heptadecenoyl-[acyl-carrier protein]
C171CAR	Heptadecenoyl-carnitine
C171CARm	Heptadecenoyl-carnitine (mitochondrial)
C171COA	Heptadecenoyl-CoA
C171COAm	Heptadecenoyl-CoA (mitochondrial)
C171e	Heptadecenoate (extracellular)
C17DACP	Heptadec-2-enoyl-[acyl-carrier protein]
C17DCOAm	Heptadec-2-enoyl-CoA (mitochondrial)
C17HACP	3-hydroxyheptadecanoyl-[acyl-carrier protein]

Continues on next page

Continued from last page

Abbreviation	Full name
C17HCOAm	3-hydroxyheptadecanoyl-CoA (mitochondrial)
C17OACP	3-oxoheptadecanoyl-[acyl-carrier protein]
C17OCOAm	3-oxoheptadecanoyl-CoA (mitochondrial)
C180	Octadecanoate
C180ACP	Octadecanoyl-[acyl-carrier protein]
C180CAR	Octadecanoyl-carnitine
C180CARm	Octadecanoyl-carnitine (mitochondrial)
C180COA	Octadecanoyl-CoA
C180COAm	Octadecanoyl-CoA (mitochondrial)
C180e	Octadecanoate (extracellular)
C181	Octadecenoate
C181ACP	Octadecenoyl-[acyl-carrier protein]
C181CAR	Octadecenoyl-carnitine
C181CARm	Octadecenoyl-carnitine (mitochondrial)
C181COA	Octadecenoyl-CoA
C181COAm	Octadecenoyl-CoA (mitochondrial)
C181e	Octadecenoate (extracellular)
C182	Octadecadienoate
C182ACP	Octadecadienoyl-[acyl-carrier protein]
C182CAR	Octadecadienoyl-carnitine
C182CARm	Octadecadienoyl-carnitine (mitochondrial)
C182COA	Octadecadienoyl-CoA
C182COAm	Octadecadienoyl-CoA (mitochondrial)
C182e	Octadecadienoate (extracellular)
C183	Octadecatrienoate
C183ACP	Octadecatrienoyl-[acyl-carrier protein]
C183CAR	Octadecatrienoyl-carnitine
C183CARm	Octadecatrienoyl-carnitine (mitochondrial)
C183COA	Octadecatrienoyl-CoA
C183COAm	Octadecatrienoyl-CoA (mitochondrial)
C183e	Octadecatrienoate (extracellular)
C18DACP	Octadec-2-enoyl-[acyl-carrier protein]
C18DCOAm	Octadec-2-enoyl-CoA (mitochondrial)
C18DHSPH	3-dehydrosphinganine(C18)
C18HACP	3-hydroxyoctadecanoyl-[acyl-carrier protein]
C18HCOAm	3-hydroxyoctadecanoyl-CoA (mitochondrial)
C18OACP	3-oxooctadecanoyl-[acyl-carrier protein]
C18OCOAm	3-oxooctadecanoyl-CoA (mitochondrial)
C18PSPH	Phytosphingosine(C18)

Continues on next page

Continued from last page

Abbreviation	Full name
C18SPH	Sphinganine(C18)
C190	Nonadecanoate
C190ACP	Nonadecanoyl-[acyl-carrier protein]
C190CAR	Nonadecanoyl-carnitine
C190CARm	Nonadecanoyl-carnitine (mitochondrial)
C190COA	Nonadecanoyl-CoA
C190COAm	Nonadecanoyl-CoA (mitochondrial)
C190e	Nonadecanoate (extracellular)
C191	Nonadecenoate
C191ACP	Nonadecenoyl-[acyl-carrier protein]
C191CAR	Nonadecenoyl-carnitine
C191CARm	Nonadecenoyl-carnitine (mitochondrial)
C191COA	Nonadecenoyl-CoA
C191COAm	Nonadecenoyl-CoA (mitochondrial)
C191DHSPH	3-dehydrosphinganine(C19:1)
C191e	Nonadecenoate (extracellular)
C191SPH	Sphinganine(C19:1)
C192	Nonadecadienoate
C192ACP	Nonadecadienoyl-[acyl-carrier protein]
C192CAR	Nonadecadienoyl-carnitine
C192CARm	Nonadecadienoyl-carnitine (mitochondrial)
C192COA	Nonadecadienoyl-CoA
C192COAm	Nonadecadienoyl-CoA (mitochondrial)
C192e	Nonadecadienoate (extracellular)
C19DACP	Nonadec-2-enoyl-[acyl-carrier protein]
C19DCOAm	Nonadec-2-enoyl-CoA (mitochondrial)
C19HACP	3-hydroxynonadecanoyl-[acyl-carrier protein]
C19HCOAm	3-hydroxynonadecanoyl-CoA (mitochondrial)
C19OACP	3-oxononadecanoyl-[acyl-carrier protein]
C19OCOAm	3-oxononadecanoyl-CoA (mitochondrial)
C200	Eicosanoate
C200ACP	Eicosanoyl-[acyl-carrier protein]
C200CAR	Eicosanoyl-carnitine
C200CARm	Eicosanoyl-carnitine (mitochondrial)
C200COA	Eicosanoyl-CoA
C200COAm	Eicosanoyl-CoA (mitochondrial)
C200e	Eicosanoate (extracellular)
C20DACP	Eicos-2-enoyl-[acyl-carrier protein]
C20DCOAm	Eicos-2-enoyl-CoA (mitochondrial)

Continues on next page

Continued from last page

Abbreviation	Full name
C20DHSPH	3-dehydrosphinganine(C20)
C20HACP	3-hydroxyeicosanoyl-[acyl-carrier protein]
C20HCOAm	3-hydroxyeicosanoyl-CoA (mitochondrial)
C20OACP	3-oxoeicosanoyl-[acyl-carrier protein]
C20OCOAm	3-oxoeicosanoyl-CoA (mitochondrial)
C20PSPH	Phytosphingosine(C20)
C20SPH	Sphinganine(C20)
C40	Butanoate
C40ACP	Butanoyl-[acyl-carrier protein]
C40COA	Butanoyl-CoA
C40COAm	Butanoyl-CoA (mitochondrial)
C40e	Butanoate (extracellular)
C4DACP	But-2-enoyl-[acyl-carrier protein]
C4DCOAm	But-2-enoyl-CoA (mitochondrial)
C4HACP	3-hydroxybutanoyl-[acyl-carrier protein]
C4HCOAm	3-hydroxybutanoyl-CoA (mitochondrial)
C50ACP	Pentanoyl-[acyl-carrier protein]
C50COA	Pentanoyl-CoA
C50COAm	Pentanoyl-CoA (mitochondrial)
C5DACP	Pent-2-enoyl-[acyl-carrier protein]
C5DCOAm	Pent-2-enoyl-CoA (mitochondrial)
C5HACP	3-hydroxypentanoyl-[acyl-carrier protein]
C5HCOAm	3-hydroxypentanoyl-CoA (mitochondrial)
C5OACP	3-oxopentanoyl-[acyl-carrier protein]
C5OCOAm	3-oxopentanoyl-CoA (mitochondrial)
C60	Hexanoate
C60ACP	Hexanoyl-[acyl-carrier protein]
C60COA	Hexanoyl-CoA
C60COAm	Hexanoyl-CoA (mitochondrial)
C60e	Hexanoate (extracellular)
C6DACP	Hex-2-enoyl-[acyl-carrier protein]
C6DCOAm	Hex-2-enoyl-CoA (mitochondrial)
C6HACP	3-hydroxyhexanoyl-[acyl-carrier protein]
C6HCOAm	3-hydroxyhexanoyl-CoA (mitochondrial)
C6OACP	3-oxohexanoyl-[acyl-carrier protein]
C6OCOAm	3-oxohexanoyl-CoA (mitochondrial)
C70ACP	Heptanoyl-[acyl-carrier protein]
C70COAm	Heptanoyl-CoA (mitochondrial)
C7DACP	Hept-2-enoyl-[acyl-carrier protein]

Continues on next page

Continued from last page

Abbreviation	Full name
C7DCOAm	Hept-2-enoyl-CoA (mitochondrial)
C7HACP	3-hydroxyheptanoyl-[acyl-carrier protein]
C7HCOAm	3-hydroxyheptanoyl-CoA (mitochondrial)
C7OACP	3-oxoheptanoyl-[acyl-carrier protein]
C7OCOAm	3-oxoheptanoyl-CoA (mitochondrial)
C80	Octanoate
C80ACP	Octanoyl-[acyl-carrier protein]
C80COA	Octanoyl-CoA
C80COAm	Octanoyl-CoA (mitochondrial)
C80e	Octanoate (extracellular)
C8DACP	Oct-2-enoyl-[acyl-carrier protein]
C8DCOAm	Oct-2-enoyl-CoA (mitochondrial)
C8HACP	3-hydroxyoctanoyl-[acyl-carrier protein]
C8HCOAm	3-hydroxyoctanoyl-CoA (mitochondrial)
C8OACP	3-oxooctanoyl-[acyl-carrier protein]
C8OCOAm	3-oxooctanoyl-CoA (mitochondrial)
C90ACP	Nonanoyl-[acyl-carrier protein]
C90COAm	Nonanoyl-CoA (mitochondrial)
C9DACP	Non-2-enoyl-[acyl-carrier protein]
C9DCOAm	Non-2-enoyl-CoA (mitochondrial)
C9HACP	3-hydroxynonanoyl-[acyl-carrier protein]
C9HCOAm	3-hydroxynonanoyl-CoA (mitochondrial)
C9OACP	3-oxononanoyl-[acyl-carrier protein]
C9OCOAm	3-oxononanoyl-CoA (mitochondrial)
CAASP	N-Carbamoyl-L-aspartate
CAIR	1-(5-Phospho-D-ribosyl)-5-amino-4-imidazolecarboxylate
CALH	2-(3-Carboxy-3-aminopropyl)-L-histidine
cAMP	3',5'-Cyclic AMP
cAMPe	3',5'-Cyclic AMP (extracellular)
CAP	Carbamoyl phosphate
CAPm	Carbamoyl phosphate (Mitochondrial)
CAR	Carnitine
CARm	Carnitine (mitochondrial)
CBCCP	Carboxybiotin-carboxyl-carrier protein
CCL	Catechol
cCMP	3',5'-Cyclic CMP
CDA	Cholesta-8,24-dien-3-ol-4-carboxylate
cdAMP	3',5'-Cyclic dAMP

Continues on next page

Continued from last page

Abbreviation	Full name
CDOL	4-methylcholesta-8,24-diene-3-ol
CDP	CDP
CDPDG	CDPdiacylglycerol
CELLOBe	Cellobiose (extracellular)
CELLOTe	Cellotriose (extracellular)
CELLUe	Cellulose (extracellular)
CELLWALL	Cellwall (1 g dry cellwall)
CERB1	Cerebrin 1
CERB1A	Cerebrin 1(comp. A)
CERB1B	Cerebrin 1(comp. B)
CERB1C	Cerebrin 1(comp. C)
CERB1D	Cerebrin 1(comp. D)
CERB2	Cerebrin 2
CERB2A	Cerebrin 2(comp. A)
CERB2B	Cerebrin 2(comp. B)
CERB2C	Cerebrin 2(comp. C)
CERB2D	Cerebrin 2(comp. D)
CEREB1	Cerebroside 1
CEREB2	Cerebroside 2
cGMP	3',5'-Cyclic GMP
CHCOA	6-Carboxyhexanoyl-CoA
CHIT	Chitin
CHITO	Chitosan
CHO	Choline
CHOR	Chorismate
CHOSLF	Choline sulphate
CHOSLFe	Choline sulphate (extracellular)
cIMP	3',5'-Cyclic IMP
CIT	Citrate
CITe	Citrate (extracellular)
CITm	Citrate (mitochondrial)
CITR	L-Citrulline
CITRe	L-Citrulline (extracellular)
CITRm	L-Citrulline (mitochondrial)
CL	Cardiolipin
CLAGL3P	1-acyl-sn-glycerol-3-phosphate used for cardiolipin
CLCDPDG	Cdp-diacylglycerol used for cardiolipin
CLPA	Phosphatidate used for cardiolipin

Continues on next page

Continued from last page

Abbreviation	Full name
CLPIGP	3(3-sn-phosphatidyl)-sn-glycerol 1-phosphate used for cardiolipin biosynthesis
CMP	CMP
CO ₂	Carbon dioxide
CO _{2e}	Carbon dioxide (extracellular)
CO _{2m}	Carbon dioxide (mitochondrial)
COA	Coenzyme A
COAm	Coenzyme A (mitochondrial)
COUM	Coumarate
COUMe	Coumarate (extracellular)
CPAD5P	1-(2-Carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate
CTP	CTP
CYS	L-Cysteine
CYSe	L-Cysteine (extracellular)
CYST	Cystine
CYTD	Cytidine
CYTS	Cytosine
D6PDGC	6-phospho-2-dehydro-D-gluconate
D6PGC	6-Phospho-D-gluconate
D6PGL	d-Glucono-1,5-lactone 6-phosphate
DA	Deoxyadenosine
DADP	dADP
DAGLY	Diacylglycerol
DAGLYP	Diacylglycerol-3-Phosphate
DAMP	dAMP
DAONA	7,8-diaminononanoate
DATP	dATP
DC	Deoxycytidine
DCDA	4-methylcholesta-8,24-diene-3-ol-4-carboxylate
DCDOL	4,4-Dimethylcholesta-8,24-diene-3-ol
DCDP	dCDP
DCMP	dCMP
DCTOL	4,4-Dimethylcholesta-8,14,24-triene-3-ol
DCTP	dCTP
DG	Deoxyguanosine
DGDG	Digalactosyl diglyceride
DGDMIPC	Digalactosyl-dimannosyl-inositol-P-ceramide
DGDP	dGDP

Continues on next page

Continued from last page

Abbreviation	Full name
DGLC	D-Glucose
DGLCe	D-Glucose (extracellular)
DGMP	dGMP
DGTP	dGTP
DHBA	2,3-dihydroxybenzoate
DHCHDDC	(1R,6S)-dihydroxycyclohexa-2,4-diene-1,4-dicarboxylate
DHF	7,8-Dihydrofolate
DHMVAm	(R)-2,3-dihydroxy-3-methylbutanoate (mitochondrial)
DHP	2-Amino-4-hydroxy-6-(D-erythro-1,2,3-trihydroxypropyl)-7,8-dihydropteridine
DHPLYSm	protein-dihydrolipoyllysine
DHPT	Dihydropteroate
DHSK	3-Dehydroshikimate
DHSKe	3-Dehydroshikimate (extracellular)
DHVALm	(R)-2,3-dihydroxy-3-methylbutanoate (mitochondrial)
DIMGP	D-erythro-1-(Imidazol-4-yl)glycerol 3-phosphate
DIN	Deoxyinosine
DMAND	D-mandelate
DMANDe	D-mandelate (extracellular)
DMIPC	Di-mannosyl-inositol-P-ceramide
DMNAD	Deamido-NAD
DMPP	Dimethylallyl diphosphate
DMT	Dimethylterephthalate
DMTe	Dimethylterephthalate (extracellular)
DNA	Deoxyribonucleic acid
DOROA	(S)-Dihydroorotate
DPCOA	Dephospho-CoA
DPTH	2-[3-Carboxy-3-(methylammonio)propyl]-L-histidine
DQT	3-Dehydroquinone
DR1P	Deoxy-ribose 1-phosphate
DSAM	S-Adenosylmethioninamine
DT	Thymidine
DTB	Dethiobiotin
DTBe	dethiobiotin (extracellular)
DTDP	dTDP
DTMP	dTMP

Continues on next page

Continued from last page

Abbreviation	Full name
DTTP	dTTP
DU	Deoxyuridine
DUDP	dUDP
DUMP	dUMP
DUTP	dUTP
E	D-Erythrose
E4P	D-Erythrose 4-phosphate
Ee	D-Erythrose (extracellular)
EOL	Erythritol
EOLe	Erythritol (extracellular)
EPST	Episterol
ERGOD	Ergosta-5,7-dienol
ERGOSE	Ergosterolester
ERGOST	Ergosterol
ERGOT	Ergosta-5,7,22,24-tetraenol
ETH	Ethanol
ETHe	Ethanol (extracellular)
ETHm	Ethanol (mitochondrial)
EU	L-Erythrulose
EU1P	L-Erythrulose 1-phosphate
EUe	L-Erythrulose (extracellular)
F26P	D-Fructose 2,6-bisphosphate
F6P	beta-D-Fructose 6-phosphate
FADH2m	FADH2 (mitochondrial)
FADm	FAD (mitochondrial)
FALD	Formaldehyde
FDP	beta-D-Fructose 1,6-bisphosphate
FER	Ferulic acid
FERCOA	trans-feruloyl-CoA
FERe	Ferulic acid (extracellular)
FERHCOA	4-hydroxy-3-methoxyphenyl-beta-hydroxypropionyl-CoA
FERIm	Ferricytochrome c (mitochondrial)
FEROm	Ferrocycytochrome c (mitochondrial)
FEST	Fecosterol
FGAM	2-(Formamido)-N1-(5'-phosphoribosyl)acetamidine
FGAR	5'-Phosphoribosyl-N-formylglycinamide
FGT	S-Formylglutathione
FKYN	L-Formylkynurenine

Continues on next page

Continued from last page

Abbreviation	Full name
FOR	Formate
FORe	Formate (extracellular)
FORm	Formate (mitochondrial)
FPP	trans,trans-Farnesyl diphosphate
FRU	D-Fructose
FRUe	D-Fructose (extracellular)
FTHF	10'-Formyltetrahydrofolate
FTHFm	10-Formyltetrahydrofolate (mitochondrial)
FUACAC	4-Fumarylacetoacetate
FUM	Fumarate
FUMe	Fumarate (extracellular)
FUMm	Fumarate (mitochondrial)
G	D-Glycerate
G1P	alpha-D-Glucose 1-phosphate
G6P	alpha-D-Glucose 6-phosphate
GA6P	D-Glucosamine 6-phosphate
GABA	4-Aminobutanoate
GABAE	4-Aminobutanoate (extracellular)
GABAm	4-Aminobutanoate (mitochondrial)
GAG	Galactosaminogalactan
GAL1P	alpha-D-Galactose 1-phosphate
GALCER	Galactosylceramide
GALCERA	Galactosylceramide(Comp. A)
GALCERB	Galactosylceramide(Comp. B)
GALN14LAC	D-Galactono-1,4-lactone
GALNT	D-Galactonate
GALNTE	D-Galactonate (extracellular)
GALOL	Galactitol
GALOLe	Galactitol (extracellular)
GALUNT	D-Galacturonate
GALUNTE	D-Galacturonate (extracellular)
GALUNTP	1-phospho-alpha-D-glucuronate
GAMYLE	Glucoamylase (secreted to the medium)
GAR	5'-Phosphoribosylglycinamide
GBAD	4-Guanidino-butanamide
GBAT	4-Guanidino-butanoate
GC	gamma-L-Glutamyl-L-cysteine
GDMIPC	Galactosyl-Dimannosyl-inositol-P-ceramide
GDP	GDP

Continues on next page

Continued from last page

Abbreviation	Full name
GDPm	GDP (mitochondrial)
GDPMAN	GDPmannose
GEN	Gentisate
GGM	Galactoglucomannan
GL	Glycerol
GL3P	Glycerol 3-phosphate
GLAC	D-Galactose
GLACe	D-Galactose (extracellular)
GLAL	Glycolaldehyde
GLC	alpha-D-Glucose
GLCe	alpha-D-Glucose (extracellular)
GLCN	D-Glucosamine
GLCN15LAC	d-Glucono-1,5-lactone
GLCN15LACe	d-Glucono-1,5-lactone (extracellular)
GLCNT	D-Gluconate
GLCNTe	D-Gluconate (extracellular)
GLCUNT	D-Glucuronate
GLCUNTe	D-Glucuronate (extracellular)
GLe	Glycerol (extracellular)
GLN	L-Glutamine
GLNe	L-Glutamine (extracellular)
GLU	L-Glutamate
GLUCER1	Glucocerebroside 1
GLUCER2	Glucocerebroside 2
GLUe	L-Glutamate (extracellular)
GLUGSAL	L-Glutamate 5-semialdehyde
GLUGSALm	L-Glutamate 5-semialdehyde (mitochondrial)
GLUm	L-Glutamate (mitochondrial)
GLUP	alpha-D-Glutamyl phosphate
GLX	Glyoxylate
GLY	Glycine
GLYA	Glycolate
GLYAL	D-Glyceraldehyde
GLYCOGEN	Glycogen
GLYCOGENe	Glycogen (extracellular)
GLYe	Glycine (extracellular)
GLYm	Glycine (mitochondrial)
GLYN	Glycerone (DHA/dihydroxyacetone)
GLYNe	Glycerone (DHA/dihydroxyacetone) (extracellular)

Continues on next page

Continued from last page

Abbreviation	Full name
GMP	GMP
GN	Guanine
GNTAL	Gentisate aldehyde
GPP	Geranyl diphosphate
GSN	Guanosine
GTP	GTP
GTPm	GTP (mitochondrial)
GUA	Guaiacol
H+	Intracellular protons
H+ _P O	Proton (energy metabolism)
H+ _P Om	Proton (mitochondrial) (energy metabolism)
H+e	Protons (extracellular)
H ₂ O	Water
H ₂ O ₂	Hydrogen peroxide
H ₂ O ₂ e	Hydrogen peroxide (extracellular)
H ₂ Oe	Water (extracellular)
H ₂ Om	Water (mitochondria)
H ₂ S	Hydrogen sulfide
H ₂ SO ₃	Sulfite
H ₂ SO ₃ e	Sulfite (extracellular)
H ₃ MCOA	(S)-3-Hydroxy-3-methylglutaryl-CoA
HACNm	But-1-ene-1,2,4-tricarboxylate (mitochondrial)
HAN	3-Hydroxyanthranilate
HCITm	2-Hydroxybutane-1,2,4-tricarboxylate (mitochondrial)
HCYS	L-Homocysteine
HICITm	Homoisocitrate (mitochondrial)
HIS	L-Histidine
HISe	L-Histidine (extracellular)
HISN	Histamine
HISOL	L-Histidinol
HISOLP	L-Histidinol phosphate
HIUR	5-hydroxyisourate
HKYN	3-Hydroxykynurenine
HNO ₂	Nitrite
HNO ₃	Nitrate
HNO ₃ e	Nitrate (extracellular)
HOMOGEN	Homogentisate
HPLYSm	H-protein-lipoyllysine

Continues on next page

Continued from last page

Abbreviation	Full name
HPSAMLYSm	H-protein-S-aminomethyldihydrolipoyllysine
HSER	L-Homoserine
HYXN	Hypoxanthine
HYXNe	Hypoxanthine (extracellular)
ICIT	Isocitrate
ICITe	Isocitrate (extracellular)
ICITm	Isocitrate (mitochondrial)
IDOL	L-Iditol
IDOLe	L-Iditol (extracellular)
IDP	IDP
IDPm	IDP (mitochondrial)
IGP	Indoleglycerol phosphate
ILE	L-Isoleucine
ILEe	L-Isoleucine (extracellular)
ILEm	L-Isoleucine (mitochondrial)
IMACP	3-(Imidazol-4-yl)-2-oxopropyl phosphate
IMASP	Iminoaspartate
IMP	IMP
INAC	Indoleacetate
IND	Indole
INDe	Indole (extracellular)
INS	Inosine
IPC	Inositol phosphorylceramide
IPPMALm	2-Isopropylmalate (mitochondrial)
IPPP	Isopentenyl diphosphate
ITP	ITP
ITPm	ITP (mitochondrial)
KDDGC	2-dehydro-3-deoxy-D-gluconate
KOJA	Kojic acid
KOJAe	Kojic acid (extracellular)
KYN	L-Kynurenine
KYNe	L-Kynurenine (extracellular)
LAC	D-Lactate
LACAL	D-Lactaldehyde
LACe	D-Lactate (extracellular)
LACm	(R)-Lactate (mitochondrial)
LACT	Lactose
LACTe	Lactose (extracellular)
LAOL	L-Arabitol

Continues on next page

Continued from last page

Abbreviation	Full name
LAOLe	L-Arabitol (extracellular)
LARAB	L-Arabinose
LARABe	L-Arabinose (extracellular)
LEU	L-Leucine
LEUe	L-Leucine (extracellular)
LEUm	L-Leucine (mitochondrial)
LGT	S-D-Lactoylglutathione
LIPIDS	Artificial metabolite. The metabolites found in the biomass. Measured in grams
LIPOm	Lipoamide (mitochondrial)
LLAC	L-Lactate
LLACe	L-Lactate (extracellular)
LLACm	(S)-Lactate (mitochondrial)
LLCT	L-Cystathionine
LMAND	L-mandelate
LMANDe	L-mandelate (extracellular)
LNST	Lanosterol
LPC	Lysophosphatidylcholine
LPE	Lysophosphatidylethanolamine
LPSE2m	(LipS2)-dihydrolipoyl transsuccinylase
LXUL	L-Xylulose
LXULe	L-Xylulose (extracellular)
LYS	L-Lysine
LYSe	L-Lysine (extracellular)
LYSm	L-Lysine (mitochondrial)
MACAC	maleylacetoacetate
MAGLY	Monoacylglycerol
MAGLYP	Monoacylglycerol-3-Phosphate
MAL	(S)-Malate
MALACP	Malonyl-[acyl-carrier protein]
MALCOA	Malonyl coenzyme A
MALe	(S)-Malate (extracellular)
MALm	(S)-Malate (mitochondrial)
MAN	D-Mannose
MAN1P	alpha-D-Mannose 1-phosphate
MAN6P	D-Mannose 6-phosphate
MANe	D-Mannose (extracellular)
MANNANe	Mannan (extracellular)
MELIe	Melibiose (extracellular)

Continues on next page

Continued from last page

Abbreviation	Full name
MET	L-Methionine
ME _{Te}	L-Methionine (extracellular)
METH	Methanethiol
METHF	5,10-Methenyltetrahydrofolate
METHF _m	5,10-Methenyltetrahydrofolate (mitochondrial)
METHOL	Methanol
METHOL _e	Methanol (extracellular)
METT _H F	5,10-Methylenetetrahydrofolate
METT _H F _m	5,10-Methylenetetrahydrofolate (mitochondrial)
MGC181	Monoglucosyloxyoctadecenoic acid
MGDG	Monogalactosyl diglyceride
MI1P	1L-myo-Inositol 1-phosphate
MIPC	Mannose-inositol-P-ceramide
MLT	Maltose
ML _{Te}	Maltose (extracellular)
MNT	D-Mannitol
MNT1P	D-Mannitol 1-phosphate
MN _{Te}	D-Mannitol (extracellular)
MTHF	5-Methyltetrahydrofolate
MTHF _m	5-Methyltetrahydrofolate (mitochondrial)
MTHGXL	Methylglyoxal
MTPHTH	Monomethylterephthalate
MUCL	Muconolactone
MUCO	cis,cis-muconate
MVL	(R)-Mevalonate
MYOI	myo-Inositol
NAD	NAD ⁺
NADH	NADH
NADH _m	NADH (mitochondrial)
NAD _m	NAD ⁺ (mitochondrial)
NADP	NADP ⁺
NADPH	NADPH
NADPH _m	NADPH (mitochondrial)
NADP _m	NADP ⁺ (mitochondrial)
NAG	N-Acetyl-D-glucosamine
NAGA1P	N-Acetyl-D-glucosamine 1-phosphate
NAGA6P	N-Acetyl-D-glucosamine 6-phosphate
NAGL _U m	N-Acetyl-L-glutamate (mitochondrial)
NAGL _U P _m	N-Acetyl-L-glutamate 5-phosphate (mitochondrial)

Continues on next page

Continued from last page

Abbreviation	Full name
NAGLUSm	N-Acetyl-L-glutamate 5-semialdehyde (mitochondrial)
NAHISN	N-acetylhistamine
NAMN	Nicotinate D-ribonucleotide
NAMR	Nicotinamide D-ribonucleoside
NAORNm	N2-Acetyl-L-ornithine (mitochondrial)
NAR	Nicotinate D-ribonucleoside
NFAN	N-formylanthranilate
NH3	Ammonia
NH3e	Ammonia (extracellular)
NH3m	Ammonia (mitochondrial)
NH4OH	Ammonium hydroxide
NICA	Nicotinate
NICAe	Nicotinate (extracellular)
NICD	Nicotinamide
NICDe	Nicotinamide (extracellular)
NIG	Nigeran (alpha-1,3-Glucose-alpha-1,4-Glucose)
NMN	Nicotinamide D-ribonucleotide
NPRAN	N-(5-Phospho-D-ribosyl)anthranilate
O2	Oxygen
O2e	Oxygen (extracellular)
O2m	Oxygen (mitochondrial)
OA	Oxaloacetate
OAe	Oxaloacetate (extracellular)
OAEL	3-Oxoadipate enol-lactone
OAHSER	O-Acetyl-L-homoserine
OAm	Oxaloacetate (mitochondrial)
OBUT	2-Oxobutanoate
OBUTm	2-Oxobutanoate (mitochondrial)
OGT	Oxidized glutathione
OICAP	3-Carboxy-4-methyl-2-oxopentanoate
OICAPm	3-Carboxy-4-methyl-2-oxopentanoate (mitochondrial)
OIVALm	(R)-2-Oxoisovalerate (mitochondrial)
OMP	Orotidine 5'-phosphate
OMVAL	3-Methyl-2-oxobutanoate
OMVALm	3-Methyl-2-oxobutanoate (mitochondrial)
ORN	L-Ornithine
ORNe	L-Ornithine (extracellular)

Continues on next page

Continued from last page

Abbreviation	Full name
ORNm	L-Ornithine (mitochondrial)
OROA	Orotate
OTA	Ochratoxin A
OTAE	Ochratoxin A (extracellular)
OTHIO	Oxidized thioredoxin
OTHIOm	Oxidized thioredoxin (mitochondrial)
OXAL	Oxalate
OXALe	Oxalate (extracellular)
OXAm	Oxaloglutamate (mitochondrial)
OXGLY	Oxaloglycolate
P5C	(S)-1-Pyrroline-5-carboxylate
P5Cm	(S)-1-Pyrroline-5-carboxylate (mitochondrial)
PABA	4-Aminobenzoate
PANT	(R)-Pantoate
PAP	Adenosine 3',5'-bisphosphate
PAPS	3'-Phosphoadenylylsulfate
PC	Phosphatidylcholine
PCAGL3P	1-acyl-sn-glycerol-3-phosphate used for phosphatidylcholine
PCAT3P2	1-acyl-sn-glycerone phosphate used for phosphatidylcholine
PCC	Protocatechuate
PCCDPDG	Cdp-diacylglycerol used for phosphatidylcholine
PCCe	Protocatechuate (extracellular)
PCPA	Phosphatidate used for phosphatidylcholine
PCPDME	Phosphatidyl-N-dimethylethanolamine
PCPE	Phosphatidylethanolamine used for phosphatidylcholine
PCPMME	Phosphatidyl-N-methylethanolamine
PCPS	Phosphatidylserine used for phosphatidylcholine
PE	Phosphatidylethanolamine
PEAGL3P	1-acyl-sn-glycerol-3-phosphate used for phosphatidylethanolamine
PEAT3P2	1-acyl-sn-glycerone phosphate used for phosphatidylethanolamine
PECDPDG	Cdp-diacylglycerol used for phosphatidylethanolamine
PECTATEe	Pectate (extracellular)
PENAL	Pentanal

Continues on next page

Continued from last page

Abbreviation	Full name
PENN	Pentylamine
PENNe	Pentylamine (extracellular)
PEP	Phosphoenolpyruvate
PEPA	Phosphatidate used for phosphatidylethanolamine
PEPS	Phosphatidylserine used for phosphatidylethanolamine
PG	Phosphatidylglycerol
PHAC	Phenylacetate
PHACe	Phenylacetate (extracellular)
PHAL	Phenylacetaldehyde
PHALe	Phenylacetaldehyde (extracellular)
PHE	L-Phenylalanine
PHEe	L-Phenylalanine (extracellular)
PHEN	Prephenate
PHP	3-Phosphonooxypyruvate
PHPYR	Phenylpyruvate
PHPYRe	Phenylpyruvate (extracellular)
PHSER	O-Phospho-L-homoserine
PI	Orthophosphate
PIe	Orthophosphate (extracellular)
PIm	Orthophosphate (mitochondrial)
PINS	1-Phosphatidyl-D-myo-inositol
PINSP	1-Phosphatidyl-1D-myo-inositol 3-phosphate
PMVL	(R)-5-Phosphomevalonate
PNT0	(R)-Pantothenate
POOL	Artificial metabolite. A group of small molecules found in the biomass
PPI	Pyrophosphate
PPIIm	Pyrophosphate (mitochondrial)
PPMVL	(R)-5-Diphosphomevalonate
PRAM	5-Phosphoribosylamine
PRBAMP	N1-(5-Phospho-D-ribosyl)-AMP
PRBATP	N1-(5-Phospho-D-ribosyl)-ATP
PRCP	5-Phosphoribosyl monophosphate
PRFICA	1-(5'-Phosphoribosyl)-5-formamido-4-imidazolecarboxamide
PRFP	5-(5-Phospho-D-ribosylaminoformimino)-1-(5-phosphoribosyl)-imidazole-4-carboxamide

Continues on next page

Continued from last page

Abbreviation	Full name
PRLP	N-(5'-Phospho-D-1'-ribulosylformimino)-5-amino-1-(5''-phospho-D-ribosyl)-4-imidazolecarboxamide
PRO	L-Proline
PROe	L-Proline (extracellular)
PROm	L-Proline (mitochondrial)
PROP	Propanoate
PROPACP	Propanoyl-[acyl-carrier protein]
PROPAL	Propionaldehyde
PROPALe	Propionaldehyde (extracellular)
PROPCOA	Propanoyl-CoA
PROPCOAm	Propanoyl-CoA (mitochondrial)
PROPe	Propanoate (extracellular)
PROPm	Propanoate (mitochondrial)
Protein	Protein
PRPP	5-Phospho-alpha-D-ribose 1-diphosphate
PS	Phosphatidylserine
PSAGL3P	1-acyl-sn-glycerol-3-phosphate used for phosphatidylserine
PSAT3P2	1-acyl-sn-glycerone phosphate used for phosphatidylserine
PSCDPDG	Cdp-diacylglycerol used for phosphatidylserine
PSNIG	Pseudonigeran (1,3-alpha-glucan)
PSPA	Phosphatidate used for phosphatidylserine
PYR	Pyruvate
PYRe	Pyruvate (extracellular)
PYRm	Pyruvate (mitochondrial)
QH2m	Ubiquinol (mitochondrial)
Qm	Ubiquinone (mitochondrial)
QT	Quinate
QTe	Quinate (extracellular)
QUIN	Quinolate
QUINe	Quinolate (extracellular)
R1P	D-Ribose 1-phosphate
R5P	D-Ribose 5-phosphate
RAFFe	Raffinose (extracellular)
RES	Resocinol
RESe	Resocinol (extracellular)
RGT	Glutathione
RHA	L-Rhamnose

Continues on next page

Continued from last page

Abbreviation	Full name
RHAe	Extracellular rhamnose
RHAMN	L-rhamnulose
RHAMNP	L-rhamnulose 1-phosphate
RIB	D-Ribose
RIBe	D-Ribose (extracellular)
RIBOL	Ribitol
RIBOLe	Ribitol (extracellular)
RL	D-Ribulose
RL5P	D-Ribulose 5-phosphate
RLe	D-Ribulose (extracellular)
RNA	Ribonucleic acid
RTHIO	Reduced thioredoxin
RTHIOm	Reduced thioredoxin (mitochondrial)
S	Sulfur
S23E	(S)-2,3-Epoxy-squalene
S7P	Sedoheptulose 7-phosphate
SACPm	Saccharopine (mitochondrial)
SAH	S-Adenosyl-L-homocysteine
SAICAR	1-(5'-Phosphoribosyl)-5-amino-4-(N-succinocarboxamide)-imidazole
SALI	Salicylate
SALIE	Salicylate (extracellular)
SAM	S-Adenosyl-L-methionine, S-Adenosyl-L-methionine; Acylcarnitine
SAMOB	S-adenosyl-4-methylthio-2-oxobutanoate
SEDAG	1,2-diacyl-sn-glycerol (for Sterolesters)
SEDAGP	1,2-diacyl-sn-glycerol 3-phosphate (for Sterolesters)
SEMAG	Monoacylglycerol (for Sterolesters)
SEMAGP	Monoacylglycerol-3-phosphate (for Sterolesters)
SER	L-Serine
SERe	L-Serine (extracellular)
SLF	Sulfate
SLFe	Sulphate (extracellular)
SME	Shikimate
SME3P	Shikimate 3-phosphate
SMEe	Shikimate (extracellular)
SOR	L-Sorbose
SORe	L-Sorbose (extracellular)
SOT	D-Sorbitol

Continues on next page

Continued from last page

Abbreviation	Full name
SOTe	D-Sorbitol (extracellular)
SQL	Squalene
STACe	Stachyose
STARe	Starch (extracellular)
SUCC	Succinate
SUCCe	Succinate (extracellular)
SUCCm	Succinate (mitochondrial)
SUCCOAm	Succinyl coenzyme A (mitochondrial)
SUCCSALm	Succinate-semialdehyde (mitochondrial)
SUCe	Sucrose (extracellular)
T3P1	D-Glyceraldehyde 3-phosphate
T3P2	Glycerone phosphate (DHAP)
TAGLY	Triacylglycerol
TANAE	Tannic acid (extracellular)
TAR	Tartrate
TARe	Tartrate (extracellular)
TDPE1m	(thiamine diphosphate)-alpha-ketoglutarate dehydrogenase
TGDMIPC	Trigalactosyldimannosylinositol-P-ceramide
THF	Tetrahydrofolate
THFG	Tetrahydrofolyl-[Glu](n)
THFm	Tetrahydrofolate (mitochondrial)
THR	L-Threonine
THRe	L-Threonine (extracellular)
THRm	L-Threonine (mitochondrial)
THY	Thymine
TPHTH	Terephthalate
TPHTHe	Terephthalate (extracellular)
TRE	alpha,alpha-Trehalose
TRE6P	alpha,alpha-Trehalose 6-phosphate
TREe	alpha,alpha-Trehalose (extracellular)
TRP	L-Tryptophan
TRPe	L-Tryptophan (extracellular)
TYR	L-Tyrosine
TYRe	L-Tyrosine (extracellular)
UDP	UDP
UDPG	UDPglucose
UDPGAL	UDPgalactose
UDPGALU	UDP-galacturonate

Continues on next page

Continued from last page

Abbreviation	Full name
UDPNAG	UDP-N-acetyl-D-glucosamine
UDPNAGAL	UDP-N-acetyl-D-galactosamine
UGC	(-)-Ureidoglycolate
UMP	UMP
URA	Uracil
URAc	Uracil (extracellular)
UREA	Urea
UREAC	Urea-1-carboxylate
UREAc	Urea (extracellular)
UREAm	Urea (mitochondrial)
URI	Uridine
URIC	Ureate
URi	Uridine (extracellular)
UTP	UTP
VAL	L-Valine
VALe	L-Valine (extracellular)
VALm	L-Valine (mitochondrial)
VAN	Vanillate
VANe	Vanillate (extracellular)
VANIN	Vanillin
XAN	Xanthine
XANe	Xanthine (extracellular)
XMP	Xanthosine 5'-phosphate
XOL	Xylitol
XOLe	Xylitol (extracellular)
XTSINE	Xanthosine
XUL	D-Xylulose
XUL5P	D-Xylulose 5-phosphate
XULe	D-Xylulose (extracellular)
XYL	D-Xylose
XYLANe	Xylan (extracellular)
XYLe	D-Xylose (extracellular)
ZYMST	Zymosterol

Suppl. Table III: Protein composition of *A. niger*. The measured values are from Christias et al. (1975). It is assumed that the ASP/ASN and GLU/GLN ratios are 3:1 as in Oura (1972). Polymerization cost is calculated from (Ingraham et al., 1983). A large proportion of the weight of a glucoprotein can be sugar (Leskovac et al. (2005) reports as much as 10-16% of the weight of glucose oxidase) but data on an average ratio of sugar/protein is neither available nor easily estimated.

Amino acid	Amount [mmole/g protein]
ALA	1.048
ARG	0.419
ASN	0.213
ASP	0.638
CYS	0.080
GLU	0.913
GLN	0.304
GLY	0.875
HIS	0.208
ILE	0.402
LEU	0.715
LYS	0.660
MET	0.107
PHE	0.317
PRO	0.448
SER	0.638
THR	0.510
TRP	0.128
TYR	0.208
VAL	0.544
Polymerization cost:	
ATP	39.729

Suppl. Table IV: RNA composition of *A. niger*. The measured values are from Uryson and Belozerskii (1960). Polymerization cost is calculated from (Ingraham et al., 1983).

Ribonucleotide	Amount mmole/g RNA
AMP	0.773
GMP	0.931
CMP	0.773
UMP	0.615
Polymerization cost:	
ATP	7.424

Suppl. Table V: DNA composition of *A. niger*. The measured values are from Uryson and Belozerskii (1960) and in accordance with the ratio of the genome sequence of CBS 513.88 (Pel et al., 2007). Polymerization cost is calculated from Ingraham et al. (1983).

Deoxyribonucleotides	Amount mmol/g DNA
dAMP	0.782
dCMP	0.814
dTMP	0.782
dGMP	0.814
Polymerization cost:	
ATP	10.849

Suppl. Table VI: Small molecules in the biomass of *A. niger*. The references from which the values are calculated, are found next to each component.

Component	Reference	Amount mmol/g DW
Isocitrate	Promper et al. (1993)	0.075
Citrate	Promper et al. (1993)	2.498
Succinate	Promper et al. (1993)	0.107
Fumarate	Promper et al. (1993)	0.008
Malate	Promper et al. (1993)	0.087
NAD	Fuhrer et al. (1980)	1.128
NADH	Fuhrer et al. (1980)	0.120
NADP	Fuhrer et al. (1980)	0.104
NADPH	Fuhrer et al. (1980)	0.060
Trehalose	Witteveen and Visser (1995)	13.692
Mannitol	Witteveen and Visser (1995)	32.791
Glycerol	Witteveen and Visser (1995)	42.363
Erythritol	Witteveen and Visser (1995)	36.636
Arabitol	Witteveen and Visser (1995)	1.521

Suppl. Table VII: Cell wall composition of *A. niger*. The references from which the values are calculated, are found next to each component.

Cell wall component	Reference	Amount mmol/g cell wall
Galactosaminogalactan	Bardalaye and Nordin (1976)	0.04
Nigeran	(Johnston, 1965; Damveld et al., 2005)	0.25
Pseudonigeran (α -1,3-glucan)	Horisberger et al. (1972)	0.33
Galactoglucomannan	Bardalaye and Nordin (1977); Horisberger et al. (1972)	0.37
1,4- α -glucan	Stagg and Feather (1973)	0.38
Chitin	Ram et al. (2004); Stagg and Feather (1973); Blumenthal and Roseman (1957)	1.57
1,3- β -glucan	Stagg and Feather (1973); Ram et al. (2004)	2.64

Suppl. Table VIII: Lipid composition of *A. niger*. The amounts are sorted into categories of neutral lipids, sphingolipids and phospholipids. The references from which the values are calculated, are found next to each component.

Lipids	Reference	Amount mmol/g DW
Neutral lipids		
Triacylglycerols	Morozova et al. (2002)	0.010083
Diacylglycerols	Morozova et al. (2002)	0.001009
Monoacylglycerols	Morozova et al. (2002)	0.008912
C14:0 acyl	Morozova et al. (2002)	0.000223
C16:0 acyl	Morozova et al. (2002)	0.001480
C18:0 acyl	Morozova et al. (2002)	0.000245
C18:1 acyl	Morozova et al. (2002)	0.001678
C18:2 acyl	Morozova et al. (2002)	0.001664
C18:3 acyl	Morozova et al. (2002)	0.000047
Ergosterol	Nemec and Jernejc (2002)	0.034062
Ergosterol esters	Nemec and Jernejc (2002)	0.010038
Glucolipids		
Monogalactosyldiglyceride	Chattopadhyay et al. (1985a)	0.030053
Monoglucosyloxyoctadecenoic acid	Brennan et al. (1974)	0.012374
Digalactosyldiglyceride	Chattopadhyay et al. (1985a)	0.007859
Sphingolipids		
Trigalactosyldimannosylinositolphosphorylceramide (GPSL G)	Byrne and Brennan (1976)	0.000005
Cerebrin 1 (with C18 or C20 Phytosphingosin)	Byrne and Brennan (1976)	0.000030
Cerebrin 2 (with C18 or C20 sphingosin)	Byrne and Brennan (1976)	0.000031
Cerebroside (Galactosylceramide)	Byrne and Brennan (1976)	0.000025
Glucocerebroside 1	Byrne and Brennan (1976)	0.000024
Glucocerebroside 2	Byrne and Brennan (1976)	0.000024
Phospholipids		
Cardiolipin	Chattopadhyay et al. (1985a)	0.001746
Phosphatidylcholine	Chattopadhyay et al. (1985a)	0.015312
Phosphatidylserine	Chattopadhyay et al. (1985a)	0.000359
Phosphatidylethanolamine	Chattopadhyay et al. (1985a)	0.034807

Suppl. Table IX: Carbon sources found in literature available to the model. Substrates that are only found as carbon sources together with glucose are indicated by *.

C-source		Reference
Acetate		Ruijter et al. (1999)
Alanine	*	Nomachi and Komano (1980)
Anthranilic acid	*	Reddy and Vaidyanathan (1975)
Arabinose		vanKuyk et al. (2001); de Groot et al. (2003); de Vries et al. (2002b); Witteveen et al. (1994)
Arabitol		vd Veen et al. (1993)
Aspartic acid	*	Nomachi and Komano (1980)
Benzoate	*	Reddy and Vaidyanathan (1975)
Benzyl-vanillic acid	*	Milstein et al. (1988)
Citrate		Muller (1975a)
Coumaric acid	*	Milstein et al. (1988)
Dethiobiotin	*	Tepper et al. (1966); Li et al. (1968)
D-galacturonic acid		de Vries et al. (2002b); de Vries et al. (2002)
D-glucuronic acid		de Vries et al. (2002b); de Vries et al. (2002)
Dihydroxyacetone		Witteveen et al. (1990)
Dimethylterephthalate		Ganji et al. (1995)
DL-mandelic acid	*	Jamaluddin et al. (1970)
D-xylose		Ngiam et al. (2000)
Ferulic acid		Milstein et al. (1988)
Fructose		Ruijter et al. (1999); de Vries et al. (2002b)
Fumarate		Muller (1975a)
Galactose		Ademark et al. (2001); Basten et al. (2005); de Vries et al. (2002b)
Gluconate		Elzainy et al. (1973); Ruijter et al. (1999)
Gluconic acid lactone		Lakshminarayana et al. (1969a)
Glucose		Numerous
Glutamate	*	Nomachi and Komano (1980)
Glycerol		Tereshina et al. (2004)
Indole	*	Kamath and Vaidyanathan (1990)
Lactose		Arisan-Atac et al. (1996)
L-rhamnose		Fries and Kallstromer (1965)

Continues on next page

Continued from last page

C-source		Reference
Maltose		Pedersen et al. (2000b)
Mannitol		Tereshina et al. (2004)
Mannose		Adya and Elbein (1977); de Vries et al. (2002b)
Methanol		Kirimura et al. (1999)
m-hydroxybenzoic acid	*	Premkumar et al. (1969); Kumar et al. (1973)
Phenylacetic acid	*	Sugumaran et al. (1973)
Phenylalanine	*	Kishore et al. (1974, 1976)
Resorcinol		Shailubhai et al. (1983)
Rhamnose		de Vries et al. (2002b)
Salicylate		Shailubhai et al. (1983)
Sorbitol		Desai et al. (1967, 1969a); vd Veen et al. (1991)
Succinate		Muller (1975a)
Sucrose		Arisan-Atac et al. (1996); de Graaff et al. (1992)
Tannic acid		Bhardwaj et al. (2003)
Tartrate		Patil and Ramakrishnan (1966)
Trehalose		Tereshina et al. (2004)
Tryptophan	*	Sreeleela et al. (1969); Subramanian and Vaidyanathan (1984)
Vanillic acid	*	Milstein et al. (1988)
Xylitol		vd Veen et al. (1993)
Xylose		Ngiam et al. (2000)

Suppl. Table X: Sole carbon sources that are utilizable by *A. niger* iMA871, but with no available reference.

Carbon source
3-hydroxybenzoate
Arginine
Asparagine
Benzonitrile
Benzoylamine
Butanoate
Citrulline
Decanoate
D-Erythrose
D-Lactate
D-mandelate
Dodecanoate
D-Ribose
D-Ribulose
D-Xylulose
Eicosanoate
Ethanol
GABA
Galactitol
Galactonate
Galacturonate
Glutamine
Glycine
Heptadecanoate
Heptadecenoate
Hexadecadienoate
Hexadecanoate
Hexadecenoate
Hexanoate
Isocitrate
L-Arabinose
L-Arabitol
L-Erythrulose
L-Iditol
L-Lactate
L-mandelate
L-Sorbose
Continues on next page

Continued from last page

Carbon source

L-Xylulose

Malate

Melibiose

Nonadecadienoate

Nonadecanoate

Nonadecenoate

Octadecadienoate

Octadecanoate

Octadecatrienoate

Octadecenoate

Octanoate

Ornithine

Oxalate

Oxaloacetate

Pentadecanoate

Phenylpyruvate

Proline

Propanoate

Protocatechuate

Pyruvate

Raffinose

Ribitol

Serine

Stachyose

Terephthalate

Tetradecanoate

Tetradecenoate

Threonine

Tyrosine

Suppl. Table XI: Compounds utilizable by *A. niger* iMA871 as sole nitrogen source. Compounds, where the use as sole nitrogen source has found described in literature, are followed by one or more references.

Nitrogen source	Reference
Alanine	Lenouvel et al. (2001)
Ammonia	Basten et al. (2001)
Anthranilate	Kamath et al. (1987)
Arginine	Lenouvel et al. (2001)
Asparagine	Lenouvel et al. (2001); Laine et al. (1972)
Aspartate	
Butylamine	Schilling and Lerch (1995a)
Citrulline	Lenouvel et al. (2002)
GABA	Kumar and Puneekar (1998)
Glutamate	Lenouvel et al. (2001)
Glutamine	
Glycine	Morton and Broadbent (1955)
Nitrate	Pedersen and Nielsen (2000)
Ornithine	Lenouvel et al. (2002)
Pentylamine	Schilling and Lerch (1995a)
Phenylalanine	
Proline	Lenouvel et al. (2001)
Serine	
Threonine	
Tryptophan	
Tyrosine	
Urea	Smith et al. (1993)
Xanthin	Taha and Sharabash (1956)

Suppl. Table XII: Enzymatic activities that were found in the literature, but not added to the reaction list of *A. niger* iMA871. References, EC-number and enzyme name is added to the reactions where possible.

Reaction	EC-no	Enzyme	Source
Degradation of biopolymers			
RNA + H ₂ O ⇌ 3'-phosphomononucleotides	3'- 3.1.27.1	RNase I	Nomachi and Komano (1980)
RNA-bound phospho-guanine + H ₂ O ⇌ RNA + 3'-phospho-guanine	3.1.27.3	RNase II	Nomachi and Komano (1980)
Extracellular RNA + H ₂ O ⇌ ribonucleotides	3.1.27.1	ribonuclease	Xiong et al. (2005)
Dinucleoside monophosphates + H ₂ O ⇌ Nucleotide 5'-phosphate + Nucleoside	3.1.4.1	Cyclic-ribonucleotide phosphomutase-5'-phosphodiesterase (phosphodiesterase I/5'-exonuclease activity)	Chohnan et al. (1994)
DNA + H ₂ O ⇌ Nucleotide monophosphates	3.1.4.1	Phosphodiesterase I (5'-exonuclease)	Chohnan et al. (1994)
Extracellular proteins + H ₂ O ⇌ Amino acid components	3.4.11.5	prolyl aminopeptidase (papA)	Basten et al. (2005)
Extracellular proteins + H ₂ O ⇌ Amino acid components	3.4.14.5	dipeptidyl-peptidase IV (dapB)	Javing et al. (2005)

Continues on next page

Continued from last page

Reaction	EC- no	Enzyme	Source
Extracellular proteins + H ₂ O ⇌ Amino acid components	3.4.16.5	Carboxypeptidase I	dal Degan et al. (1992)
Extracellular proteins + H ₂ O ⇌ Amino acid components	3.4.16.5	Carboxypeptidase II	dal Degan et al. (1992)
Extracellular proteins + H ₂ O ⇌ Amino acid components	3.4.16.5	Serine-type carboxypeptidase (pepF)	Krishnan and Vijayalakshmi (1985); van den Hombergh et al. (1994)
Extracellular proteins + H ₂ O ⇌ Amino acid components	PEPC	carboxypeptidase C (pepC)	Frederick et al. (1993)
Extracellular proteins + H ₂ O ⇌ Amino acid components	3.4.21.61	Kexin	Jalving et al. (2000)
Extracellular proteins + H ₂ O ⇌ Amino acid components	3.4.23.18	Aspergillopepsin A (I) (pepA)	Mattern et al. (1992)
Extracellular proteins + H ₂ O ⇌ Amino acid components	3.4.23.19	Aspergillopepsin B (II) (pepB)	Mattern et al. (1992); Huang et al. (2000)
removes AAs from peptide end	3.4.11.2	lysine aminopeptidase	Basten et al. (2001)
Peptide with N-terminal aromatic amino acid + H ₂ O ⇒ Peptide + aromatic AA	No EC	phenylalanine peptidase	Basten et al. (2003)
Extracellular tri-acyl glycerol + H ₂ O ⇌ Di-acyl glycerol + Fatty acid	3.1.1.3	Lipase (extracellular)	Namoodiri and Chatopadhyaya (2000)
Extracellular diacyl glycerol + H ₂ O ⇌ Mono-acyl glycerol + Fatty acid	3.1.1.3	Lipase (extracellular)	Namoodiri and Chatopadhyaya (2000)

Continues on next page

Continued from last page

Reaction	EC- no	Enzyme	Source
Degradation of complex carbon sources			
Glycyrrhizinate + H ₂ O ⇌ 1,2-beta-D-glucuronosyl-D-glucuronate + Glycyrrhetinate	3.2.1.128	glycyrrhizinate glucuronidase	Sasaki et al. (1988)
1,2-beta-D-glucuronosyl-D-glucuronate + H ₂ O ⇌ 2 D-Glucuronate	3.2.1.15	Polygalacturonase	Behere et al. (1993); Acuña-Argüelles et al. (1995); de Vries and Visser (2001); de Vries et al. (2002a)
Extracellular phytate + 4 H ₂ O ⇌ myo-inositol-di-phosphate + 4 Phosphate	3.1.3.8	3-phytase	Skowronski (1978); van Hartingsveldt et al. (1993); Martinelli and Kinghorn (1994); Wyss et al. (1998, 1999); Nagashima et al. (1999); Dvorakova et al. (2000); Vohra and Satyanarayana (2003); Vats and Banerjee (2005)
Extracellular phytate + 5 H ₂ O ⇌ Inositol-monophosphate + 5 Phosphate	3.1.3.26	6-phytase	Wyss et al. (1999); Vohra and Satyanarayana (2003); Casey and Walsh (2003)
Aromatic degradations			

Continues on next page

Continued from last page

Reaction	EC- no	Enzyme	Source
2-chlorobenzoate + NADPH + O ₂ ⇌	1.14.13.1	benzoate	4- Sahasrabudhe and Modi (1985)
2-chloro-4-hydroxybenzoate + NADP + H ₂ O		monooxygenase (benzoate-para-hydroxylase A, bphA)	
3-chlorobenzoate + NADPH + O ₂ ⇌	1.14.13.1	benzoate	4- Sahasrabudhe and Modi (1985)
3-chloro-4-hydroxybenzoate + NADP + H ₂ O		monooxygenase (benzoate-para-hydroxylase A, bphA)	
2-hydroxybenzoate + NADPH + O ₂ ⇌	1.14.13.1	benzoate	4- Faber et al. (2001); Malonek et al. (2004)
⇌ 2,4-dihydroxybenzoate + NADP + H ₂ O		monooxygenase	
3-Hydroxyanthranilate + Dihydrobiopterin + H ₂ O ⇌ Anthranilate + Tetrahydrobiopterin + O ₂	1.14.16.5	anthranilate monooxygenase	3- Subba Rao et al. (1971)
Phenylacetate + O ₂ + NADPH ⇌	No EC	Phenylacetate hydroxylase	Sugumaran and Vaidyanathan (1978)
3-hydroxy-phenylacetate + H ₂ O + NADP			
3-hydroxybenzylalcohol + NADP ⇌ 3-hydroxybenzaldehyde + NADPH	No EC	3-hydroxy benzylalcohol dehydrogenase	Sugumaran et al. (1973)
3-hydroxybenzaldehyde + NAD ⇌	No EC	3-hydroxy benzylaldehyde dehydrogenase	Sugumaran et al. (1973)
3HBA + NADH			
Orcinol + NADH + O ₂ ⇌ 2,3,5-trihydroxytoluene + NAD + H ₂ O	1.14.13.6	orcinol monooxygenase	2- Sahasrabudhe et al. (1986)

Continues on next page

Continued from last page

Reaction	EC- no	Enzyme	Source
4-nitrophenyl phosphate + H ₂ O ⇌ 4-nitrophenol + Phosphate	3.1.3.41	4-nitrophenylphosphatase	Versaw et al. (1991)
2-hydroxymuconate semialdehyde ⇌ Catechol + O ₂	1.13.11.2	catechol dioxygenase	2,3-Sahasrabudhe et al. (1986)
Miscellaneous			
Sulcaton + NADH ⇌ sulcatol + NAD	1.1.1.260	sulcatone reductase	Belan et al. (1987)
Propanol + NADPH ⇌ Propanol + NADP	1.1.1.78	Methylglyoxal reductase II	Inoue et al. (1988)
Butanal + NAD + H ₂ O ⇌ Butanate + NADH	1.2.1.3	Aldehyde dehydrogenase (NAD+)	Kazimirova and Novotel'nov (1956)
Heptanal + NAD + H ₂ O ⇌ Heptanate + NADH	1.2.1.3	Aldehyde dehydrogenase (NAD+)	Kazimirova and Novotel'nov (1956)
Quercetin + O ₂ ⇒ 2-protocatechuoylphloroglucinol carboxylic acid + CO	1.13.11.2	Flavonol 2,4 dioxynase	Hund et al. (1999)
Phloretin + H ₂ O ⇌ Phloretate + 1,3,5-Trihydroxybenzene	3.7.1.4	phloretin hydrolase	Minamikawa et al. (1970)
2',3'-Cyclic AMP ⇌ cyclic AMP	3.1.4.16	Cyclic-ribonucleotide phosphomutase-5'-phosphodiesterase	Chohan et al. (1994)
2',3'-Cyclic CMP ⇌ cyclic CMP	3.1.4.16	Cyclic-ribonucleotide phosphomutase-5'-phosphodiesterase	Chohan et al. (1994)

Continues on next page

Continued from last page

Reaction	EC- no	Enzyme	Source
2',3'-Cyclic GMP \rightleftharpoons cyclic GMP	3.1.4.16	Cyclic-ribonucleotide phosphomutase-5'-phosphodiesterase	Chohan et al. (1994)
2',3'-Cyclic IMP \rightleftharpoons cyclic IMP	3.1.4.16	Cyclic-ribonucleotide phosphomutase-5'-phosphodiesterase	Chohan et al. (1994)
Carbaryl \rightleftharpoons 1-hydroxynaphthalene + N-methylcarbamate	No EC	Carbaryl hydrolase	Qing et al. (2003)
Methionine + Glyoxalate \rightleftharpoons 4-methylthio-2-oxobutanoate + Glycine	2.6.1.73	L-methionine-glyoxylate transaminase	Oganesyan et al. (2004)
Diacetyl + NADPH \rightleftharpoons Acetoin + NADP	1.1.1.72	Glycerol dehydrogenase (NADP+)	Schuurink et al. (1990)
Methylglyoxal + NADPH \rightleftharpoons 1-Hydroxy-2-propanone + NADP	1.1.1.72	Glycerol dehydrogenase (NADP+)	Schuurink et al. (1990)
4-hydroxyphenylacetaldehyde + NADPH + O ₂ \rightleftharpoons 4-hydroxymandelonitrile + NADP + 2 H ₂	1.13.14.6	NADPH-cytochrome P450 reductase (cprA)	van den Brink et al. (1996); Malonek et al. (2004)
2 Superoxide + 2 H ⁺ \Rightarrow O ₂ + H ₂ O ₂	1.15.1.1	Cu,Zn superoxide dismutase	Sugumaran and Vaidyanathan (1978); Holdom et al. (1996)
R-CH ₂ -NH ₂ + H ₂ O + O ₂ \rightleftharpoons R-CHO + H ₂ O ₂ + NH ₃	1.4.3.4	amine oxidase (flavin-containing)	Schilling and Lerch (1995a)

Continues on next page

Continued from last page

Reaction	EC- no	Enzyme	Source
R-CH ₂ -NH ₂ + H ₂ O + O ₂ ⇌ R-CHO + H ₂ O ₂ + NH ₃	1.4.3.6	amine oxidase (copper-containing)	Schilling and Lerch (1995a)
Glycerol triacetate + H ₂ O ⇌ Glycerol + 3 Acetate	3.1.1.3	triacylglycerol lipase	Hannan (1959)
Chlorogenate + H ₂ O ⇒ Caffate + Quinate	3.1.1.42	chlorogenic acid hydrolase	Schobel and Pollmann (1980); Asther et al. (2005)
Several epoxides to their di-ols	3.3.2.3	epoxide hydrolase	Morisseau et al. (1999); Arand et al. (1999)
Serine + Glyoxylate ⇌ hydroxypyruvate + Glycine	3-2.6.1.45	L-serine-glyoxylate transaminase	Oganesyan et al. (2004)
Serine + Pyruvate ⇌ Hydroxypyruvate + Alanine	3-2.6.1.51	L-serine-pyruvate transaminase	Oganesyan et al. (2004)
Methionine + Pyruvate ⇌ methylthio-2-oxobutanoate + Alanine	4-2.6.1.41	L-methionine-pyruvate transaminase	Oganesyan et al. (2004)
Valine + Glyoxylate ⇌ Oxoisovalerate + Glycine	(R)-2-No EC	L-valine-glyoxylate transaminase	Oganesyan et al. (2004)
Leucine + Glyoxylate ⇌ oxopentanoate + Glycine	4-Methyl-2-No EC	L-leucine-glyoxylate transaminase	Oganesyan et al. (2004)
Methylamine + H ₂ O + O ₂ ⇒ Methanal + H ₂ O ₂	NH ₃ + 1.4.3.4	amine oxidase (flavin-containing)	Schilling and Lerch (1995b)
2-Phenylethylamine + H ₂ O + O ₂ ⇒ 2-phenylethanal + NH ₃ + H ₂ O ₂	1.4.3.4	amine oxidase (flavin-containing)	Schilling and Lerch (1995a)

Continues on next page

Continued from last page

Reaction	EC- no	Enzyme	Source
Dopamine + H ₂ O + O ₂ ⇒ (3,4-dihydroxyphenyl)acetaldehyde + NH ₃ + H ₂ O ₂	1.4.3.4	amine oxidase (flavin-containing)	Schilling and Lerch (1995a)
Ethylamine + H ₂ O + O ₂ ⇒ Acetaldehyde + NH ₃ + H ₂ O ₂	1.4.3.4	amine oxidase (flavin-containing)	Schilling and Lerch (1995a)
Simigrin + H ₂ O ⇒ D-Glucose + isothiocyanate	3.2.1.147	Myrosinase	Ohtsuru et al. (1973)
UDP-N-acetyl-D-glucosamine + Dolichyl phosphate ⇌ UMP + N-acetyl-D-glucosaminyl-diphosphodolichol	2.7.8.15	UDP-N-acetylglucosamine: dolichyl-phosphate N-acetylglucosaminephosph	Sorensen et al. (2003)
Nitrophenylsulphate + H ₂ O ⇌ Nitrophenol + Sulphate	3.1.6.1	arylsulfatase	Sakurai et al. (1980)

Suppl. Table XIII: Pathways that were reported in literature to be present, but not included in the reaction list of *A. niger* MA871.

Compound	Source
Degradation	
2-heptanone	(Baltazar et al., 1999)
2-nonanone	(Baltazar et al., 1999)
Anthracene	Yogambal and Karegoudar (1997)
Caproic acid	Lewis (1970)
Carbaryl	Qing et al. (2003)
Ceramide-phosphoinositol	Hackett and Brennan (1977)
Cerebrosine	Wagner and Fiebert (1969)
Dolichol	Sorensen et al. (2003)
Naphthalene	Yogambal and Karegoudar (1997)
Orcinol	Sahasrabudhe et al. (1986)
PAH	Sack et al. (1997)
Phenanthrene	Yogambal and Karegoudar (1997); Sack et al. (1997)
Pyrene	Wunder et al. (1994)
Secondary metabolites	
1,1-heptanediol diacetate	Abo-Dahab (2002)
1,4-diaza-2,5-dioxo-3-isobutylbicyclo (4.3.0) nonane	Abo-Dahab (2002)
4,9-dimethyl-furano(2,3h) coumarin	Abo-Dahab (2002)
Amphetamine	Abo-Dahab (2002)
Asperazine	Varoglu et al. (1997); Varoglu and Crews (2000)
Aspergillin	Rawat (1968); Ray and Eakin (1975)
Asperic acid	Varoglu and Crews (2000)
Aspernigrin A	Hiort et al. (2004)
Aspernigrin B	Hiort et al. (2004)
Aurasperone B	Bouras et al. (2005)
Aurasperone C	Bouras et al. (2005)
Aurasperone D	Blumenthal (2004); Samson et al. (2004)
Aurasperone E	Bouras et al. (2005)
Aurasperone F	Bouras et al. (2005)
Bicoumanigrin	Hiort et al. (2004)
Butanoic acid 2-[(difluoroacetyl)amino]-butyl ester	Abo-Dahab (2002)
Cycloleucomelone	Hiort et al. (2004)
Dihydroergotamine	Abo-Dahab (2002)

Continues on next page

Continued from last page

Compound	Source
Flavasperone (Asperxanthone)	Bycroft et al. (1962)
Fonsecin	Bouras et al. (2005)
hexylitaconic acid	Varoglu and Crews (2000)
Kotanin	Samson et al. (2004)
Malformin A1 (Formerly known as A)	Yukioka and Winnick (1966); Schuster et al. (2002); Blumenthal (2004); Kobbe et al. (1977); Yukioka and Winnick (1966)
Malformin A2	Schuster et al. (2002); Blumenthal (2004); Kobbe et al. (1977); Yukioka and Winnick (1966)
Malformin B	Schuster et al. (2002); Blumenthal (2004); Kobbe et al. (1977); Yukioka and Winnick (1966)
Malformin C	Kobbe et al. (1977); Varoglu and Crews (2000)
Melanin	McGovern and Bentley (1975)
Mlaviolin	McGovern and Bentley (1975)
Nerolidol-epoxyacetate	Abo-Dahab (2002)
n-heptanal	Abo-Dahab (2002)
Nigerazine B	Blumenthal (2004)
Nigragillin	Blumenthal (2004)
N-methylmorpholine	Abo-Dahab (2002)
Ochratoxin A	Abarca et al. (1994); Varga et al. (2003); O'Callaghan et al. (2003); Samson et al. (2004); Blumenthal (2004)
Orobol	Nishioka et al. (1989)
Phatalimide	Abo-Dahab (2002)
Phenol-3,5-dimethoxyphenyl acetate	Abo-Dahab (2002)
Pyranonigrin A	Samson et al. (2004); Hiort et al. (2004)
Pyranonigrin B	Samson et al. (2004); Hiort et al. (2004)
Pyranonigrin C	Samson et al. (2004); Hiort et al. (2004)
Pyranonigrin D	Samson et al. (2004); Hiort et al. (2004)
Pyrophen	Varoglu and Crews (2000)
Roridine E	Abo-Dahab (2002)

Bibliography

- M. L. Abarca, M. R. Bragulat, G. Castella, and F. J. Cabanes. Ochratoxin A production by strains of *Aspergillus niger* var. *niger*. *Appl. Environ. Microbiol.*, 60(7):2650–2652, 1994.
- N.F. Abo-Dahab. Volatilizable secondary metabolites in the phylogeny of certain Aspergilli. *African Journal of Mycology and Biotechnology*, 10(3): 29–47, 2002.
- M.R. Abu-Shady, A.M. Elshafei, F.M. El-Beih, and L.A. Mohamed. Properties of adenosine deaminase in extracts of *Aspergillus terricola*. *Acta Microbiologica Polonica*, 43(3/4):305–311, 1994.
- M. E. Acuña-Argüelles, M. Gutiérrez-Rojas, G. Viniegra-González, and E. Favela-Torres. Production and properties of three pectinolytic activities produced by *Aspergillus niger* in submerged and solid-state fermentation. *Appl. Microbiol. Biotechnol.*, 43(5):808–814, 1995.
- R.R. Adams and R. Royer. Complete genomic sequence encoding *trpC* from *Aspergillus niger* var. *awamori*. *Nucleic Acids Research*, 18(16):4931, 1990.
- P. Ademark, R. P. de Vries, P. Hagglund, H. Stalbrand, and J. Visser. Cloning and characterization of *Aspergillus niger* genes encoding an α -galactosidase and a β -mannosidase involved in galactomannan degradation. *Eur. J. Biochem.*, 268(10):2982–2990, 2001.
- S. Adya and A. D. Elbein. Glucoprotein enzymes secreted by *Aspergillus niger*: Purification and properties of α -galactosidase. *Journal of Bacteriology*, 129(2):850–856, 1977.
- A. Aleksenko, W. Liu, Z. Gojkovic, J. Nielsen, and J. Piskur. Structural and transcriptional analysis of the *pyrABCN*, *pyrD* and *pyrF* genes in *Aspergillus nidulans* and the evolutionary origin of fungal dihydroorotases. *Mol. Microbiol.*, 33(3):599–611, 1999.
- T. H. Ali. Some kinetic studies on cytidine aminohydrolase activity from *Aspergillus niger* NRRL3. *Acta Microbiol. Pol.*, 47(4):365–372, 1998.

- T. H. Ali and T. A. Elzainy. Hydrolysis of RNA monomers by extracts of *Aspergillus niger* NRRL3. *Antonie Van Leeuwenhoek*, 77(3):229–234, 2000.
- A. M. Allam, M. M. Hassan, and T. A. Elzainy. Formation and cleavage of 2-keto-3-deoxygluconate by 2-keto-3-deoxygluconate aldolase of *Aspergillus niger*. *J. Bacteriol.*, 124(3):1128–1131, 1975.
- F. Alvarez-Vasquez, C. González-Alcon, and N. V. Torres. Metabolism of citric acid production by *Aspergillus niger*: model definition, steady-state analysis and constrained optimization of citric acid production rate. *Biotechnology and Bioengineering*, 70(1):82–108, 2000.
- M. Arand, H. Hemmer, H. Durk, J. Baratti, A. Archelas, R. Furstoss, and F. Oesch. Cloning and molecular characterization of a soluble epoxide hydrolase from *Aspergillus niger* that is related to mammalian microsomal epoxide hydrolase. *Biochem. J.*, 344 Pt 1:273–280, 1999.
- I. Arisan-Atac, M. F. Wolschek, and C. P. Kubicek. Trehalose-6-phosphate synthase A affects citrate accumulation by *Aspergillus niger* under conditions of high glycolytic flux. *FEMS Microbiology Letters*, 140:77–83, 1996.
- H.N. Arst and D.J. Cove. Methylammonium resistance in *Aspergillus nidulans*. *Journal of Bacteriology*, 98(3):1284–1293, 1969.
- M. Asther, M. I. Estrada Alvarado, M. Haon, D. Navarro, M. Asther, L. Lesage-Meessen, and E. Record. Purification and characterization of a chlorogenic acid hydrolase from *Aspergillus niger* catalysing the hydrolysis of chlorogenic acid. *J. Biotechnol.*, 115(1):47–56, 2005.
- B. S. Baliga, G. M. Bhatnagar, and V. Jagannathan. Nicotinamide adenine dinucleotide phosphate-specific glycerol dehydrogenase of *Aspergillus niger*. *Indian J. Biochem.*, 1(2):86–92, 1964.
- M. Balinska and A. Paszewski. Betaine-homocysteine methyltransferase in the fungus *Aspergillus nidulans*. *Biochemical and Biophysical Research Communications*, 91(3):1095–1100, 1979.
- M. F. Baltazar, F. M. Dickinson, and C. Ratledge. Oxidation of medium-chain acyl-CoA esters by extracts of *Aspergillus niger*: enzymology and characterization of intermediates by HPLC. *Microbiology*, 145:271–278, 1999.
- P. C. Bardalaye and J. H. Nordin. Galactosaminogalactan from cell walls of *Aspergillus niger*. *J. Bacteriol.*, 125(2):655–669, 1976.

- P. C. Bardalaye and J. H. Nordin. Chemical structure of the galactomannan from the cell wall of *Aspergillus niger*. *J. Biol. Chem.*, 252(8):2584–2591, 1977.
- D. E. Basten, J. Visser, and P. J. Schaap. Lysine aminopeptidase of *Aspergillus niger*. *Microbiology*, 147(Pt 8):2045–2050, 2001.
- D. E. J. W. Basten, P. J. T. Dekker, and P. J. Schaap. Aminopeptidase C of *Aspergillus niger* is a novel phenylalanine aminopeptidase. *Applied and Environmental Microbiology*, 69(2):1246–1250, 2003.
- D.E.J.W. Basten, A.P.H.A. Moers, A.J.J. van Ooyen, and P.J. Schaap. Characterisation of *Aspergillus niger* prolyl aminopeptidase. *Molecular Genetics and Genomics*, 272(6):673–679, 2005.
- F. J. Behal and R. D. Hamilton. Hydroxypyruvic acid metabolism in *Aspergillus niger*. I. Isolation and properties of hydroxypyruvic acid reductase. *Arch. Biochem. Biophys.*, 96:530–533, 1962.
- F.J. Behal. Possible role of hydroxypyruvic acid reductase in growth of *Aspergillus niger*. *Proceedings for the Society for Experimental Biology and Medicine*, 126(1):190–193, 1967.
- A. Behere, V. Satyananarayan, and S. R. Padwal-Desai. Separation and limited characterization of three polygalacturonases of *Aspergillus niger*. *Enzyme Microb. Technology*, 15:158–161, 1993.
- A. Belan, J. Bolte, A. Fauve, J. G. Gourcy, and H. Veschambre. Use of biological systems for the preparation of chiral molecules. 3. An application in pheromone synthesis: Preparation of sulcatol enantiomers. *J. Org. Chem*, 52:256–260, 1987.
- A. Bercovitz, Y. Peleg, E. Battat, J. S. Rokem, and I. Roldberg. Localization of pyruvate carboxylase in organic acid-producing *Aspergillus* strains. *Applied and Environmental Microbiology*, 56(6):1594–1597, 1990.
- T. Berges, C. Barreau, J. F. Peberdy, and L. M. Boddy. Cloning of an *Aspergillus niger* invertase gene by expression in *Trichoderma reesei*. *Current Genetics*, 24:53–59, 1993.
- Mary B. Berlyn. GENE-enzyme relationships in histidine biosynthesis in *Aspergillus nidulans*. *Genetics*, 57(3):561–570, 1967.
- R. Bhardwaj, B. Singh, and T. K. Bhat. Purification and characterization of tannin acyl hydrolase from *Aspergillus niger* MTCC 2425. *J. Basic Microbiol.*, 43(6):449–461, 2003.

- H.N. Bhatti, M. Madeeha, M. Asgher, and N. Batool. Purification and thermodynamic characterization of glucose oxidase from a newly isolated strain of *Aspergillus niger*. *Can. J. Microbiol.*, 52:519–524, 2006.
- A. Blair, L. Ngo, J. Park, I. T. Paulsen, and M. H. Saier, Jr. Phylogenetic analyses of the homologous transmembrane channel-forming proteins of the F_0F_1 -ATPases of bacteria, chloroplasts and mitochondria. *Microbiology*, 142:17–32, 1996.
- C. Z. Blumenthal. Production of toxic metabolites in *Aspergillus niger*, *Aspergillus oryzae*, and *Trichoderma reesei*: justification of mycotoxin testing in food grade enzyme preparations derived from the three fungi. *Regul. Toxicol. Pharmacol.*, 39(2):214–228, 2004.
- H. J. Blumenthal and S. Roseman. Quantitative estimation of chitin in fungi. *J. Bacteriol.*, 74(2):222–224, 1957.
- T. F. Bobbitt, J. H. Nordin, M. Roux, J. F. Revol, and R. H. Marchessault. Distribution and conformation of crystalline nigeran in hyphal walls of *Aspergillus niger* and *Aspergillus awamori*. *J. Bacteriol.*, 132(2):691–703, 1977.
- L. M. Boddy, T. Berges, C. Barreau, M. H. Vainstein, M. J. Dobson, D. J. Ballance, and J. F. Peberdy. Purification and characterisation of an *Aspergillus niger* invertase and its DNA sequence. *Curr. Genet.*, 24(1-2):60–66, 1993.
- M.I. Borges-Walmsley, G. Turner, A. M. Bailey, J. Brown, J. Lehmbeck, and I. G. Clausen. Isolation and characterization of genes for sulfate activation and reduction in *Aspergillus nidulans*: implications for evolution of an allosteric control region by gene duplication. *Molecular and General Genetics*, 247(4):423–429, 1995.
- J. G. Boschloo, E. Moonen, R. F. van Gorcom, H. F. Hermes, and C. J. Bos. Genetic analysis of *Aspergillus niger* mutants defective in benzoate-4-hydroxylase function. *Curr. Genet.*, 19(4):261–264, 1991.
- J.G. Boschloo, A. Paffen, T. Koot, W.J.J. van den Tweel, R.F.M. van Gorcom, J.H.G. Cordewener, and C.J. Bos. Genetic analysis of benzoate metabolism in *Aspergillus niger*. *Applied Microbiology and Biotechnology*, 34(2):225–228, 1990.
- N. Bouras, F. Mathieu, Y. Coppel, and A. Lebrihi. Aurasperone F - a new member of the naphtho-gamma-pyrone class isolated from a cultured microfungus, *Aspergillus niger* C-433. *Nat. Prod. Res.*, 19(7):653–659, 2005.

- P.J. Brennan, P.F.S. Griffin, D.M. Lösel, and D. Tyrrell. The lipids of fungi. *Progress in the Chemistry of Fats and Other Lipids*, 14(Pt. 2):49–89, 1974.
- W. Burgstaller. Thermodynamic boundary conditions suggest that a passive transport step suffices for citrate excretion in *Aspergillus* and *Penicillium*. *Microbiology*, 152:887–893, 2006.
- S. Busch, B. Hoffmann, O. Valerius, K. Starke, K. Düvel, and G. H. Braus. Regulation of the *Aspergillus nidulans hisB* gene by histidine starvation. *Curr. Genet.*, 38:314–322, 2001.
- F. P. Buxton, D. I. Gwynne, S. Garven, S. Sibley, and R. W. Davies. Cloning and molecular analysis of the ornithine carbamoyl transferase gene of *Aspergillus niger*. *Gene*, 60(2-3):255–265, 1987.
- F. P. Buxton, D. I. Gwynne, and R. W. Davies. Cloning of a new bidirectionally selectable marker for *Aspergillus* strains. *Gene*, 84(2):329–334, 1989.
- B.W. Bycroft, T.A. Dobson, and J.C. Roberts. Mycological chemistry. VIII. Structure of flavasperone (“asperxanthone”), a metabolite of *Aspergillus niger*. *Journal of the Chemical Society, Abstracts*, pages 40–44, 1962.
- P. F. Byrne and P. J. Brennan. Isolation and characterization of inositol-containing glycosphingolipids from *Aspergillus niger*. *Biochem. Soc. Trans.*, 4(5):893–895, 1976.
- R. B. Cain. The identity of shikimate dehydrogenase and quinate dehydrogenase in *Aspergillus niger*. *Biochem. J.*, 127(2):15P, 1972a.
- R. B. Cain. Metabolism of shikimate and quinate by *Aspergillus niger* and its regulation. *Biochem. J.*, 127(2):15P–16P, 1972b.
- A. Casey and G. Walsh. Purification and characterization of extracellular phytase from *Aspergillus niger* ATCC 9142. *Bioresour. Technol.*, 86(2):183–188, 2003.
- P. Chattopadhyay, S. K. Banerjee, K. Sen, and P. Chakrabarti. Lipid profiles of *Aspergillus niger* and its unsaturated fatty acid auxotroph, *UFA2*. *Can. J. Microbiol.*, 31(4):352–355, 1985a.
- P. Chattopadhyay, S.K. Banerjee, K. Sen, and P. Chakrabarti. An unsaturated fatty acid mutant of *Aspergillus niger* with partially defective $\Delta 9$ -desaturase. *Canadian Journal of Microbiology*, 31(4):346–351, 1985b.

- JM Cherry, C Adler, C Ball, SA Chervitz, SS Dwight, ET Hester, Y Jia, G Juvik, T Roe, M Schroeder, S Weng, and D Botstein. SGD: *Saccharomyces* Genome Database. *Nucl. Acids Res.*, 26(1):73–79, 1998.
- S. Chohnan, T. Nagata, and Y. Midorikawa. Purification of a novel bifunctional enzyme, cyclic-ribonucleotide phosphomutase-5'-phosphodiesterase, from *Aspergillus niger*. *Biosci. Biotech. Biochem.*, 58(2):250–255, 1994.
- A. Chopra and G.K. Khuller. Lipid metabolism in fungi. *CRC Critical reviews in microbiology*, 11(3):209–271, 1984.
- B. Chowdhury, S. K. Bose, S. Bhaduri, and S. K. Bose. Isolation and properties of an ATP transporter from a strain of *Aspergillus niger*. *Eur. J. Biochem.*, 247(2):673–680, 1997.
- C. Christias, C. Couvaraki, S. G. Georgopoulos, and V. Vomvoyanni. Protein content and amino acid composition of certain fungi evaluated for microbial protein production. *Applied Microbiology*, 29(2):250–254, 1975.
- D. L. Clarke, R. W. Newbert, and G. Turner. Cloning and characterisation of the adenosyl phosphosulphate kinase gene from *Aspergillus nidulans*. *Curr. Genet.*, 32(6):408–412, 1997.
- K. A. Cook and R. B. Cain. Enzymes of the 3-oxoadipate pathway in fungi: A serological study of 3-carboxymuconate cyclase (lactonizing enzyme) in fungi and its possible taxonomic significance. *Journal of General Microbiology*, 102:81–94, 1977.
- E.A. Cossins and L. Chen. Folates and one-carbon metabolism in plants and fungi. *Phytochemistry*, 45(3):437–452, 1997.
- E.H. Creaser and R. Varela-Torres. Immunological comparisons of histidinol dehydrogenases. *Journal of General Microbiology*, 67(Pt. 1):85–90, 1971.
- F. dal Degan, B. Ribadeau-Dumas, and K. Breddam. Purification and characterization of two serine carboxypeptidases from *Aspergillus niger* and their use in C-terminal sequencing of proteins and peptide synthesis. *Appl. Environ. Microbiol.*, 58(7):2144–2152, 1992.
- R. A. Damveld, P. A. vanKuyk, M. Arentshorst, F. M. Klis, C. A. van den Hondel, and A. F. Ram. Expression of *agsA*, one of five 1,3- α -D-glucan synthase-encoding genes in *Aspergillus niger*, is induced in response to cell wall stress. *Fungal. Genet. Biol.*, 42(2):165–177, 2005.
- A.J. Darlington, C. Scazzocchio, and J.A. Pateman. Biochemical and genetic studies of purine breakdown in *Aspergillus*. *Nature*, 206(4984):599–600, 1965.

- H. David, M. Åkesson, and J. Nielsen. Reconstruction of the central carbon metabolism of *Aspergillus niger*. *European Journal of Biochemistry*, 270: 4243–4253, 2003.
- L. de Graaff, H. van den Broeck, and J. Visser. Isolation and characterization of the *Aspergillus niger* pyruvate kinase gene. *Curr. Genet.*, 22(1):21–27, 1992.
- M. J. L. de Groot, P. J. I. van de Vondervoort, R. P. de Vries, G. J. Ruijter P. A. vanKuyk, and J. Visser. Isolation and characterization of two specific regulatory *Aspergillus niger* mutants shows antagonistic regulation of arabinan and xylan metabolism. *Microbiology*, 149:1183–1191, 2003.
- M.J. de Groot, W. Prathumpai, J. Visser, and G.J. Ruijter. Metabolic control analysis of *Aspergillus niger* L-arabinose catabolism. *Biotechnol Prog*, 21(6):1610–1616, 2005.
- R. P. de Vries and J. Visser. *Aspergillus* enzymes involved in degradation of plant cell wall polysaccharides. *Microbiology and Molecular Biology Reviews*, 65(4):497–522, 2001.
- R. P. de Vries, H. C. van den Broeck, E. Dekkers, P. Manzanares, L. H. de Graaff, and J. Visser. Differential expression of three α -galactosidase genes and a single β -galactosidase gene from *Aspergillus niger*. *Appl. Environ. Microbiol.*, 65(6):2453–2460, 1999.
- R. P. de Vries, J. Jansen, G. Aguilar, L. Parenicova, V. Joosten, F. Wulfert, J. A. Benen, and J. Visser. Expression profiling of pectinolytic genes from *Aspergillus niger*. *FEBS Lett.*, 530(1-3):41–47, 2002.
- R. P. de Vries, L. Parenicova, S. W. Hinz, H. C. Kester, G. Beldman, J. A. Benen, and J. Visser. The β -1,4-endogalactanase A gene from *Aspergillus niger* is specifically induced on arabinose and galacturonic acid and plays an important role in the degradation of pectic hairy regions. *Eur. J. Biochem.*, 269(20):4985–4993, 2002a.
- R. P. de Vries, P. van de Vondervoort, L. Hendriks, M. van de Belt, and J. Visser. Regulation of the α -glucuronidase-encoding gene (*aguA*) from *Aspergillus niger*. *Mol. Genet. Genomics*, 268(1):96–102, 2002b.
- I. den Herder, A. M. Rosell, C. M. van Zuilen, P. J. Punt, and C. A. van den Hondel. Cloning and expression of a member of the *Aspergillus niger* gene family encoding α -galactosidase. *Mol. Gen. Genet.*, 233(3):404–410, 1992.
- C. d’Enfert and T. Fontaine. Molecular characterization of the *Aspergillus nidulans treA* gene encoding an acid trehalase required for growth on trehalose. *Molecular Microbiology*, 24(1):203–216, 1997.

- B. M. Desai, V. V. Modi, and V. K. Shah. Studies on polyol metabolism in *Aspergillus niger*. I. Nutritional requirements of a strain of *Aspergillus niger* cultivated on sorbitol as sole source of carbon. *Arch. Mikrobiol.*, 67(1):6–11, 1969a.
- B. M. Desai, V. V. Modi, and V. K. Shah. Studies on polyol metabolism in *Aspergillus niger*. II. Comparative studies on the enzyme make-up of the adapted strain and parent strain. *Arch. Mikrobiol.*, 67(1):12–15, 1969b.
- B. M. Desai, V. V. Modi, and V. K. Shah. Studies on polyol metabolism in *Aspergillus niger*. 3. Purification and properties of sorbitol dehydrogenase. *Arch. Mikrobiol.*, 67(1):16–20, 1969c.
- B.M. Desai, V.V. Modi, and V.K. Shah. Induction of sorbitol dehydrogenase by sorbitol in *Aspergillus niger*. *Acta Microbiologica Polonica*, 56:300–304, 1967.
- J. Dvorakova, J. Kopecky, V. Havlicek, and V. Kren. Formation of myo-inositol phosphates by *Aspergillus niger* 3-phytase. *Folia Microbiol. (Praha)*, 45(2):128–132, 2000.
- A.M. Elshafei, S.M. Mohawed, M.S. Ammar, and O.M. Abdel-Fatah. Properties of enzymes involved in d-galactonate catabolism in fungi. *Antonie Van Leeuwenhoek*, 67(2):211–216, 1995.
- T. A. Elzainy, M. M. Hassan, and A. M. Allam. New pathway for nonphosphorylated degradation of gluconate by *Aspergillus niger*. *J. Bacteriol.*, 114(1):457–459, 1973.
- T.A. Elzainy and T.H. Ali. Pathways of NADP⁺ and NAD⁺ degradation by *Aspergillus niger* extracts. *Annals of Microbiology*, 50(1):65–75, 2000.
- T.A. Elzainy, M.M. Hassan, and A.M. Allam. Hydrolytic cleavage of purine nucleotides in *Aspergillus niger*. *Egyptian Journal of Botany*, 21(1):53–60, 1978.
- T.A. Elzainy, Z.A. Elawamry, M.M. Hassan, and T.H. Aly. Nucleotide catabolism in *Aspergillus niger*. *Acta Microbiologica Polonica*, 38(1):27–36, 1989.
- E. Emiliani and B. Riera. Enzymatic oxalate decarboxylation in *Aspergillus niger*. II. Hydrogen peroxide formation and other characteristics of the oxalate decarboxylase. *Biochim. Biophys. Acta*, 167(2):414–421, 1968.
- F. Ertan and E. Aksoz. Purification of uricase enzyme from *Aspergillus niger* and determination of some factors affecting the activity. *Turkish Journal of Biology*, 24(Turk. Suppl.):11–23, 2000.

- D. R. Evans and H. I. Guy. Mammalian pyrimidine biosynthesis: fresh insights into an ancient pathway. *J. Biol. Chem.*, 279(32):33035–33038, 2004.
- J.L. Evans and M.A. Gealt. The 3-hydroxy-3-methylglutaryl-coenzyme A reductase of *Aspergillus nidulans*. *Experimental Mycology*, 12(2):132–140, 1988.
- B. W. Faber, R. F. van Gorcom, and J. A. Duine. Purification and characterization of benzoate-para-hydroxylase, a cytochrome P450 (CYP53A1), from *Aspergillus niger*. *Arch. Biochem. Biophys.*, 394(2):245–254, 2001.
- M.E. Ferreira, A.L. Colombo, I. Paulsen, Q. Ren, J. Wortman, J. Huang, M.H. Goldman, and G.H. Goldman. The ergosterol biosynthesis pathway, transporter genes, and azole resistance in *Aspergillus fumigatus*. *Med Mycol*, 43 Suppl 1:S313–S319, 2005.
- J. Fiedurek. Production of *Aspergillus niger* catalase under various stress conditions. *Acta Microbiol. Pol.*, 49(1):43–49, 2000.
- J.M. Foley, N.H. Giles, C.F. Roberts, and J.W. Gibbs. Complementation at the adenylosuccinase locus in *Aspergillus nidulans*. *Genetics*, 52(6):1247–1263, 1965.
- T. Fowler, M.W. Rey, P. Vähä-Vahe, S.D. Power, and R.M. Berka. The *catR* gene encoding a catalase from *Aspergillus niger* primary structure and elevated expression through increased gene copy number and use of a strong promoter. *Mol. Microbiol.*, 9(5):989–998, 1993.
- I. Frebort, H. Tamaki, H. Ishida, P. Pec, L. Luhova, H. Tsuno, M. Halata, Y. Asano, Y. Kato, K. Matsushita, H. Toyama, H. Kumagai, and O. Adachi. Two distinct quinoprotein amine oxidases are induced by n-butylamine in the mycelia of *Aspergillus niger* AKU 3302. Purification, characterization, cDNA cloning and sequencing. *Eur. J. Biochem.*, 237(1):255–265, 1996.
- I. Frebort, K. Matsushita, H. Toyama, K. Lemr, M. Yamada, and O. Adachi. Purification and characterization of methylamine oxidase induced in *Aspergillus niger* AKU 3302. *Biosci. Biotechnol. Biochem.*, 63(1):125–134, 1999.
- G. D. Frederick, P. Rombouts, and F. P. Buxton. Cloning and characterisation of *pepC*, a gene encoding a serine protease from *Aspergillus niger*. *Gene*, 125(1):57–64, 1993.
- K. R. Frederick, J. tung, R. S. Emerick, F. R. Masiarz, S. H. Chamberlain, A. Vasavada, and S. Rosenberg. Glucose oxidase from *Aspergillus niger*. *Journal of Biological Chemistry*, 265(7):3793–3802, 1990.

- N. Fries and L. Kallstromer. Requirement for biotin in *Aspergillus niger* when grown on a rhamnose medium at high temperature. *Physiologia Plantarum*, 18(1):191–200, 1965.
- L. Fuhrer, C. P. Kubicek, and M. Rohr. Pyridine nucleotide levels and ratios in *Aspergillus niger*. *Can. J. Microbiol.*, 26(3):405–408, 1980.
- T. Fukami. Pyrimidine metabolism of a pyrimidine requiring mutant, *Aspergillus nidulans*. *Nippon Nogei Kagaku Kaishi*, 35:1049–1057, 1961.
- T. Fukazawa, K. Tanaka, and M. Mizuno. Preparation of *Aspergillus niger* chitinase and use of the enzyme for food product processing. Patent: JP 2004357620, 2004.
- S. H. Ganji, C. S. Karigar, and B. G. Pujar. Metabolism of dimethylterephthalate by *Aspergillus niger*. *Biodegradation.*, 6(1):61–66, 1995.
- R.C. Garrad and J.K. Bhattacharjee. Lysine biosynthesis in selected pathogenic fungi: Characterization of lysine auxotrophs and the cloned *LYS1* gene of *Candida albicans*. *Journal of Bacteriology*, 174(22):7379–7384, 1992.
- P. Gomez, F. Reyes, and R. Lahoz. Effect of the level of the carbon source on the activity of some lytic enzymes released during autolysis of *Aspergillus niger*. *Mycopathologia*, 62(1):23–25, 1977.
- T. Goosen, G. Bloemheuvel, C. Gysler, D. A. de Bie, H. W. van den Broek, and K. Swart. Transformation of *Aspergillus niger* using the homologous orotidine-5'-phosphate-decarboxylase gene. *Curr. Genet.*, 11(6-7):499–503, 1987.
- J. Grosshans and R. Wolfenden. Transition-state discrimination by adenosine deaminase from *Aspergillus oryzae*. *Biochim. Biophys. Acta*, 1161(1):28–32, 1993.
- H. Gruft, R. Ruck, and J. Traynor. Properties of a unique catalase isolated from *Aspergillus niger*. *Can. J. Biochem.*, 56(9):916–919, 1978.
- M. Grynberg, M. Piotrowska, E. Pizzini, G. Turner, and A. Paszewski. The *Aspergillus nidulans metE* gene is regulated by a second system independent from sulphur metabolite repression. *Biochimica et Biophysica Acta*, 1519:78–84, 2001.
- G.D. Gustafson and C. Waldron. Cloning of wild-type and mutant *Aspergillus nidulans* dihydro-orotate dehydrogenase genes and use of the mutant genes as selectable markers for fungi. Patent: EP 471466, 1992.

- A. Habison, C. P. Kubicek, and M. Rohr. Partial purification and regulatory properties of phosphofructokinase from *Aspergillus niger*. *Biochem. J.*, 209 (3):669–676, 1983.
- J. A. Hackett and P. J. Brennan. The isolation and biosynthesis of the ceramide-phosphoinositol of *Aspergillus niger*. *FEBS Lett.*, 74(2):259–263, 1977.
- B.E. Halsall, J.A. Darrah, and R.B. Cain. Regulation of enzymes of aromatic-ring fission in fungi: Organisms using both catechol and protocatechuate pathways. *Biochemical Journal*, 114(4):75P–76P, 1969.
- P. J. Hannan. Location of an esterase in *Aspergillus niger*. *Appl. Microbiol.*, 7(2):115–117, 1959.
- H. J. M. Harmsen, E. M. Kubicek-Pranz, M. Röhr, J. Visser, and C. P. Kubicek. Regulation of 6-phosphofructo-2-kinase from the citric-acid-accumulating fungus *Aspergillus niger*. *Appl. Microbiol. Biotechnol.*, 37: 784–788, 1992.
- M. Hartmann, G. Heinrich, and G.H. Braus. Relative fine-tuning of the two novel DAHP isoenzymes aroFp and aroGp of the filamentous fungus *Aspergillus nidulans*. *Archives of Microbiology*, 175(2):112–121, 2001.
- A. A. Hasper, E. Dekkers, M. van Mil, P. J. I. van de Vondervoort, and L. H. de Graaf. EglC, a new endoglucanase from *Aspergillus niger* with major activity towards xyloglucan. *Applied and Environmental Microbiology*, 68 (4):1556–1560, 2002.
- J.G. Hauge. Formic acid oxidation in *Aspergillus niger*. *Biochimica et Biophysica Acta*, 25:148–155, 1957.
- A. R. Hawkins. The complex *Arom* locus of *Aspergillus nidulans*. Evidence for multiple gene fusions and convergent evolution. *Curr. Genet.*, 11(6-7): 491–498, 1987.
- J. Hiort, K. Maksimenka, M. Reichert, S. Perovic-Ottstadt, W. H. Lin, V. Wray, K. Steube, K. Schaumann, H. Weber, P. Proksch, R. Ebel, W. E. Muller, and G. Bringmann. New natural products from the sponge-derived fungus *Aspergillus niger*. *J. Nat. Prod.*, 67(9):1532–1543, 2004.
- C. Hjort and H. Pedersen. Oxaloacetate hydrolase deficient fungal host cells. Patent WO 00/50576, 2000.
- S. Hockertz, J. Ploenzig, and G. Auling. Impairment of DNA formation is an early event in *Aspergillus niger* under manganese starvation. *Applied Microbiology and Biotechnology*, 25(6):590–593, 1987.

- M. D. Holdom, R. J. Hay, and A. J. Hamilton. The Cu,Zn Superoxide dismutases of *Aspergillus flavus*, *Aspergillus niger*, *Aspergillus nidulans*, and *Aspergillus terreus*: Purification and biochemical comparison with the *Aspergillus fumigatus* Cu,Zn superoxide dismutase. *Infection and Immunity*, 64(8):3326–3332, 1996.
- D. Hondmann. *Regulation of polyol metabolism in Aspergillus nidulans*. PhD thesis, Rijksuniversiteit Groningen, 1994.
- S. Horie, T. Watanabe, and S. Nakamura. Isolation, properties, and crystallization of an iron-chlorin protein from *Aspergillus niger*. *J. Biochem. (Tokyo)*, 80(3):579–593, 1976.
- M. Horisberger, B. A. Lewis, and F. Smith. Structure of a (1 leads to 3)-D-glucan (pseudonigeran) of *Aspergillus niger* NNRL 326 cell wall. *Carbohydr. Res.*, 23(2):183–188, 1972.
- J. S. Horng, J. E. Linz, and J. J. Pestka. Cloning and characterization of the trpC gene from an aflatoxigenic strain of *Aspergillus parasiticus*. *Appl. Environ. Microbiol.*, 55(10):2561–2568, 1989.
- J. Hoshino, A. Nishi, and T. Yanagita. Alanine metabolism in conidiospores of *Aspergillus niger* in the early phase of germination. *Journal of General and Applied Microbiology*, 8(4):233–245, 1962.
- X-P. Huang, N. Kagami, H. Inoue, M. Kojima, T. Kimura, O. Makabe, K. Suzuki, and K. Takahashi. Identification of a glutamic acid and an aspartic acid residue essential for catalytic activity of aspergillopepsin II, a non-pepsin type acid proteinase. *Journal of Biological Chemistry*, 275(34):26607–26614, 2000.
- E.P. Hull, P.M. Green, H.N. Arst Jr, and C. Scazzocchio. Cloning and physical characterization of the L-proline catabolism gene cluster of *Aspergillus nidulans*. *Molecular Microbiology*, 3(4):553–559, 1989.
- K. Hult, A. Veide, and S. Gatenbeck. The distribution of the NADPH regenerating mannitol cycle among fungal species. *Archives of Microbiology*, 128(2):253–255, 1980.
- H. K. Hund, J. Breuer, F. Lingens, J. Huttermann, R. Kappl, and S. Fetzner. Flavonol 2,4-dioxygenase from *Aspergillus niger* DSM 821, a type 2 CuII-containing glycoprotein. *Eur. J. Biochem.*, 263(3):871–878, 1999.
- C. Hussey and B. Spencer. Regulation of choline sulfotransferase in *Aspergillus nidulans*. *Biochemical Journal*, 100(3):60P–61P, 1966.

- O. Ibrahim-Granet, B. Philippe, H. Boleti, E. Boisvieux-Ulrich, D. Grenet, M. Stern, and J.P. Latge. Phagocytosis and intracellular fate of *Aspergillus fumigatus* conidia in alveolar macrophages. *Infect. Immun.*, 71(2):891–903, 2003.
- J.L. Ingraham, O. Maaløe, and F.C. Neidhardt. *Growth of the bacterial cell*. Sinauer Associates, Sunderland, 1983.
- Y. Inoue, H. Rhee, K. Watanabe, K. Murata, and A. Kimura. Metabolism of 2-ketoaldehydes in mold: purification and characterization of glyoxalase I from *Aspergillus niger*. *J. Biochem. (Tokyo)*, 102(3):583–589, 1987.
- Y. Inoue, H. Rhee, K. Watanabe, K. Murata, and A. Kimura. Metabolism of 2-oxoaldehyde in mold. Purification and characterization of two methylglyoxal reductases from *Aspergillus niger*. *Eur. J. Biochem.*, 171(1-2):213–218, 1988.
- N.N. Ivanov. Excretion of urea by fungi. *Biochemische Zeitschrift*, 157:228–242, 1925.
- K. Iwai, M. Ikeda, and S. Fujino. Studies on the biosynthesis of folic acid compounds. XI. Nutritional requirements for folate compounds and some enzyme activities involved in the folate biosynthesis. *Journal of Nutritional Science and Vitaminology*, 23(2):95–100, 1977.
- V. Jagannathan and K. Singh. Carbohydrate metabolism in citric acid fermentation. II. The glycolytic enzymes of *Aspergillus niger*. *Enzymologia.*, 16(3):150–160, 1953.
- V. Jagannathan, K. Singh, and M. Modaran. Carbohydrate metabolism in citric acid fermentation. 4. Purification and properties of aldolase from *Aspergillus niger*. *Biochem. J.*, 63(1):94–105, 1956.
- W. M. Jaklitsch, C. P. Kubicek, and M. C. Scrutton. Intracellular location of enzymes involved in citrate production by *Aspergillus niger*. *Canadian Journal of Microbiology*, 37:823–827, 1991.
- R. Jalving, P.J. van de Vondervoort, J. Visser, and P. J. Schaap. Characterization of the kexin-like maturase of *Aspergillus niger*. *Appl. Environ. Microbiol.*, 66(1):363–368, 2000.
- M. Jamaluddin, P. V. Subba Rao, and C. S. Vaidyanathan. Involvement of the protocatechuate pathway in the metabolism of mandelic acid by *Aspergillus niger*. *Journal of Bacteriology*, 101(3):786–793, 1970.

- R. Javing, J. Godefrooij, W.J. ter Veen, A.J.J. van Opyen, and P.J. Schaap. Characterisation of the *Aspergillus niger* *dapB* gene, which encodes a novel fungal type IV dipeptyl aminopeptidase. *Molecular Genetics and Genomics*, 273(4):319–325, 2005.
- D. H. Jennings. Polyol metabolism in fungi. *Adv. Microb. Physiol*, 25:149–193, 1984.
- S. Jerebzoﬀ and S. Jerebzoﬀ-Quintin. Metabolism of sodium β -methylvalerate-114C by *Aspergillus niger*. *Physiologie Vegetale*, 9(3):337–52, 1971.
- K. Jernejc and M. Legisa. Activation of plasma membrane H⁺-ATPase by ammonium ions in *Aspergillus niger*. *Appl. Microbiol. Biotechnol.*, 57(3):368–373, 2001.
- K. Jernejc and M. Legisa. The influence of metal ions on malic enzyme activity and lipid synthesis in *Aspergillus niger*. *FEMS Microbiol. Lett.*, 217(2):185–190, 2002.
- K. Jernejc and M. Legisa. Purification and properties of carnitine acetyltransferase from citric acid producing *Aspergillus niger*. *Appl. Biochem. Biotechnol.*, 60(2):151–158, 1996.
- F. J. Jin, J. Maruyama, P. R. Juvvadi, M. Arioka, and K. Kitamoto. Adenine auxotrophic mutants of *Aspergillus oryzae*: development of a novel transformation system with triple auxotrophic hosts. *Biosci. Biotechnol. Biochem.*, 68(3):656–662, 2004.
- I. R. Johnston. The composition of the cell wall of *Aspergillus niger*. *Biochem. J.*, 96(3):651–658, 1965.
- C. S. Jones and D. J. Kosman. Purification, properties, kinetics and mechanism of β – N-acetylglucosamidase from *A. niger*. *Journal of Biological Chemistry*, 255(24):11861–11869, 1980 1980.
- S.A. Jones, H.N. Arst Jr., and D.W. MacDonald. Gene roles in the *prn* cluster of *Aspergillus nidulans*. *Current Genetics*, 3(1):49–56, 1981.
- A. Juhász, M. Láday, A. Gácsér, J. Kucsera, I. Pfeiffer, F. Kevei, and Z. Hamari. Mitochondrial DNA organisation of the mtDNA type 2b of *A. tubingensis* compared to the *A. niger* mtDNA type 1a. *FEMS Microbiology Letters*, 241:119–126, 2004.
- A. V. Kamath and C. S. Vaidyanathan. New pathway for the biodegradation of indole in *Aspergillus niger*. *Appl. Environ. Microbiol.*, 56(1):275–280, 1990.

- A. V. Kamath, D. Dasgupta, and C. S. Vaidyanathan. Enzyme-catalysed non-oxidative decarboxylation of aromatic acids: I. Purification and spectroscopic properties of 2,3 dihydroxybenzoic acid decarboxylase from *Aspergillus niger*. *Biochem. Biophys. Res. Commun.*, 145(1):586–595, 1987.
- M. Kanehisa, S. Goto, S. Kawashima, and A. Nakaya. The KEGG databases at GenomeNet. *Nucleic Acids Research*, 30(1):42–46, 2002.
- L. Karaffa and C. P. Kubicek. *Aspergillus niger* citric acid accumulation: do we understand this well working black box? *Appl. Microbiol. Biotechnol.*, 61(3):189–196, 2003.
- L. Karaffa, E. Sándor, E. Fekete, and A. Szentirmai. The biochemistry of citric acid accumulation by *Aspergillus niger*. *Acta Microbiologica et Immunologica Hungarica*, 48(3–4):429–440, 2001.
- I.D. Kasatkina and E.T. Zheltova. Cystine reductase activity in *Aspergillus niger*. *Mikrobiologiya*, 32(6):973–980, 1963.
- V.F. Kazimirova and N.V. Novotel'nov. The oxidative conversion of aldehydes under biochemical conditions. *Kholodil. Prom.*, 14:194–199, 1956.
- K. Kersters and J. de Ley. D-gluconate dehydratase from *Alcaligenes*. *Methods Enzymol.*, 42:301–304, 1975.
- R. Khanna and K.K. Tewari. Phosphoglucomutase activity in *Aspergillus niger*. *Archiv fuer Mikrobiologie*, 45(4):398–406, 1963.
- A. Kiesel. The action of arginase upon agmatine and tetramethylenediguandine. *Z. physiol. Chem.*, 118:284–300, 1922.
- K. Kikuchi-Torii, S. Hayashi, H. Nakamoto, and S. Nakamura. Properties of *Aspergillus niger* catalase. *J. Biochem*, 92:1449–1456, 1982.
- J.H. Kim. Glutamine synthetase activity in *Aspergillus niger* during the differentiation. *Nonchong - Han'guk Saenghwal Kwahak Yonguwon*, 27:183–90, 1981.
- M. Y. Kim, H. J. Chung, S. Y. Hong, H. R. Kim, J. C. Lee, S. M. Park, J. H. Lee, M. S. Yang, and D. H. Kim. Characterization of a novel allele of glucose oxidase from a Korean wild type strain of *Aspergillus niger*. *Mol. Cells*, 11(3):281–286, 2001.
- S. Kinoshita, K. Kadota, and H. Taguchi. Purification and properties of aldose 1-epimerase from *Aspergillus niger*. *Biochim. Biophys. Acta*, 662(2):285–290, 1981.

- K. Kirimura, M. Yoda, and S. Usami. Cloning and expression of the cDNA encoding an alternative oxidase gene from *Aspergillus niger* WU-2223L. *Current Genetics*, 34:472–477, 1999.
- K. Kirimura, M. Yoda, H. Shimizu, S. Sugano, M. Mizuno, K. Kino, and S. Usami. Contribution of cyanide-insensitive respiratory pathway, catalyzed by the alternative oxidase, to citric acid production in *Aspergillus niger*. *Biosci. Biotechnol. Biochem.*, 64(10):2034–2039, 2000.
- K. Kirimura, S. Ogawa, T. Hattori, and K. Kino. Expression analysis of alternative oxidase gene (*aox1*) with enhanced green fluorescent protein as marker in citric acid-producing *Aspergillus niger*. *J. Biosci. Bioeng.*, 102(3):210–214, 2006.
- K.C. Kiser and W.G. Niehaus Jr. Purification and kinetic characterization of mannitol-1-phosphate dehydrogenase from *Aspergillus niger*. *Archives of biochemistry and biophysics*, 211(2):611–621, 1981.
- G. Kishore, M. Sugumaran, and C. S. Vaidyanathan. p-Hydroxymandelic acid—a key intermediate in the metabolism of DL (plus or minus)-phenylalanine by *Aspergillus niger*. *Biochem. Biophys. Res. Commun.*, 56(4):851–859, 1974.
- G. Kishore, M. Sugumaran, and C. S. Vaidyanathan. Metabolism of DL-(±)-phenylalanine by *Aspergillus niger*. *Journal of Bacteriology*, 128(1):182–191, 1976.
- I.H. Knap, C.M. Hjort, T. Halkier, and L.V. Kofod. An alpha-galactosidase enzyme. Patent WO 94/23022, 1994.
- B. Kobbe, M. Cushman, G. N. Wogan, and A. L. Demain. Production and antibacterial activity of malformin C, a toxic metabolite of *Aspergillus niger*. *Appl. Environ. Microbiol.*, 33(4):996–997, 1977.
- G.B. Kohlhaw. Leucine biosynthesis in fungi: Entering metabolism through the back door. *Microbiology and Molecular Biology Reviews*, 67(1):1–15, 2003.
- A. Kos, J. Kuijvenhoven, K. Wernars, C.J. Bos, H.W. van den Broek, P.H. Pouwels, and C.A. van den Hondel. Isolation and characterization of the *Aspergillus niger trpC* gene. *Gene*, 39(2–3):231–238, 1985.
- S. Krappmann, K. Helmstaedt, T. Gerstberger, S. Eckert, B. Hoffmann, M. Hoppert, G. Schnappaf, and G.H. Braus. The *aroC* gene of *Aspergillus nidulans* codes for a monofunctional, allosterically regulated chorismate mutase. *Journal of Biological Chemistry*, 274(32):2227–22282, 1999.

- S. Krishnan and M.A. Vijayalakshmi. Purification of an acid protease and a serine carboxypeptidase from *Aspergillus niger* using metal-chelate affinity chromatography. *Journal of Chromatography*, 329(1):165–170, 1985.
- L. R. Krupka, F. A. Racle, and Marderosian A. Der. Degradation of salicylate by *Aspergillus niger*. *Nature*, 216(114):486–487, 1967.
- C. P. Kubicek, G. Schreferl-Kunar, W. Wöhrer, and M. Röhr. Evidence for a cytoplasmic pathway of oxalate biosynthesis in *Aspergillus niger*. *Applied and Environmental Microbiology*, 54(3):633–637, 1988.
- E. M. Kubicek-Pranz, M. Mozelt, M. Rohr, and C. P. Kubicek. Changes in the concentration of fructose 2,6-bisphosphate in *Aspergillus niger* during stimulation of acidogenesis by elevated sucrose concentration. *Biochim. Biophys. Acta*, 1033(3):250–255, 1990.
- R. P. Kumar, P. V. Rao, and C. S. Vaidyanathan. m-Hydroxybenzoate 4-hydroxylase from *Aspergillus niger*: purification and properties. *Indian J. Biochem. Biophys.*, 10(3):184–190, 1973.
- S. Kumar and N. S. Punekar. Inhibition of succinic semialdehyde dehydrogenase by N-formylglycine. *J. Enzyme Inhib.*, 13(5):369–376, 1998.
- S. Kumar, N. S. Punekar, V. SatyaNarayan, and K. V. Venkatesh. Metabolic fate of glutamate and evaluation of flux through the 4-aminobutyrate (GABA) shunt in *Aspergillus niger*. *Biotechnology and Bioengineering*, 67(5):575–584, 2000.
- Kuswandi and C.F. Roberts. Genetic control of the protocatechuic acid pathway in *Aspergillus nidulans*. *Journal of General Microbiology*, 138:817–823, 1992.
- M. Kuwahara and T. Fujii. Purification and some properties of NAD-degrading purine nucleosidase from *Aspergillus niger*. *Can. J. Biochem.*, 56(5):345–348, 1978.
- M. Kuwahara, Y. Ishida, and Y. Miyagawa. Biosynthesis of pyridine coenzymes by *Aspergillus* fungi. *Journal of Fermentation Technology*, 60(5):399–404, 1982.
- M. Kuwahara, Y. Ishida, and M. Okatani. Nicotinamide nucleoside amidase activity, a novel deamidating reaction in NAD metabolism, in *Aspergillus* fungi. *J. Ferment. Technol.*, 61(1):61–66, 1983.

- E. Kuzniak, A. Wyrwicka, B. Gabara, A. Kozirog, and M. Sklodowska. Effects of N,N-Bis(3-aminopropyl)dodecylamine on antioxidant enzyme activities, mitochondrial morphology and metabolism in *Aspergillus niger*. *Folia Microbiol.*, 51(1):38–44, 2006.
- R.A. Laine, P.F.S. Griffin, C.C. Sweeley, and P.J. Brennan. Monoglucosyloxyoctadecenoic acid — a glycolipid from *Aspergillus niger*. *Biochemistry*, 11(12):2267–2271, 1972.
- K. Lakshminarayana, V. V. Modi, and V. K. Shah. Studies on gluconate metabolism in *Aspergillus niger*. II. Comparative studies on the enzyme make-up of the adapted and parent strains of *Aspergillus niger*. *Arch. Mikrobiol.*, 66(4):396–405, 1969a.
- K. Lakshminarayana, V. V. Modi, and V. K. Shah. Studies on gluconate metabolism in *Aspergillus niger*. I. Nutritional requirements of *Aspergillus niger* cultivated in gluconate medium. *Arch. Mikrobiol.*, 66(4):389–395, 1969b.
- K. Lakshminarayana, V. V. Modi, and V. K. Shah. Studies on gluconate metabolism in *Aspergillus niger*. 3. Purification and properties of phosphogluconate dehydrogenase. *Arch. Mikrobiol.*, 66(4):406–412, 1969c.
- F. Lenouvel, L. Fraissinet-Tachet, P.J.I. van de Vondervoort, and J. Visser. Isolation of UV-induced mutations in the *areA* nitrogen regulatory gene of *Aspergillus niger*, and construction of a disruption mutant. *Mol. Genet. Genomics*, 266:42–47, 2001.
- F. Lenouvel, P.J.I. van de Vondervoort, and J. Visser. Disruption of the *Aspergillus niger argB* gene: a tool for transformation. *Current Genetics*, 41(6):425–432, 2002.
- H. Lenz, P. Wunderwald, and H. Eggerer. Partial purification and some properties of oxalacetase from *Aspergillus niger*. *Eur. J. Biochem.*, 65(1):225–236, 1976.
- L. Lesage-Meessen, M. Delattre, M. Haon, J. F. Thibault, B. C. Ceccaldi, P. Brunerie, and M. Asther. A two-step bioconversion process for vanillin production from ferulic acid combining *Aspergillus niger* and *Pycnoporus cinnabarinus*. *J. Biotechnol.*, 50(2-3):107–113, 1996.
- V. Leskovac, S. Trivic, G. Wohlfahrt, J. Kandrak, and D. Pericin. Glucose oxidase from *Aspergillus niger*: the mechanism of action with molecular oxygen, quinones, and one-electron acceptors. *Int. J. Biochem. Cell Biol.*, 37(4):731–750, 2005.

- S.B. Levery, M.S. Toledo, R.L. Doong, A. H. Straus, and H.K. Takahashi. Comparative analysis of ceramide structural modification found in fungal cerebrosides by electrospray tandem mass spectrometry with low energy collision-induced dissociation of Li^+ adduct ions. *Rapid Communications in Mass Spectrometry*, 14:551–563, 2000.
- I. Lewandowska, M. Balinska, R. Natorff, and A. Paszewski. Regulation of folate-dependent enzyme levels in *Aspergillus nidulans*: studies with regulatory mutants. *Biochimica et Biophysica Acta*, 1290(1):89–94, 1996.
- H. L. Lewis. Caproic acid metabolism and the production of 2-pentanone and gluconic acid by *Aspergillus niger*. *J. Gen. Microbiol.*, 63(2):203–210, 1970.
- L. L’Hocine, Z. Wang, B. Jiang, and S. Xu. Purification and partial characterization of fructosyltransferase and invertase from *Aspergillus niger* AS0023. *J. Biotechnol.*, 81(1):73–84, 2000.
- H.-C. Li, D. B. McCormick, and L. D. Wright. Metabolism of dethiobiotin in *Aspergillus niger*. *Journal of Biological Chemistry*, 243(16):4391–4395, 1968.
- X. Lin, C. Momany, and M. Momany. SwoHp, a nucleoside diphosphate kinase, is essential in *Aspergillus nidulans*. *Eukaryotic Cell*, 2(6):1169–1177, 2003.
- K.A. Lusta, O.V. Sysoev, and A.A. Sharyshev. Cytochemical characterization of *Aspergillus terreus* 17P utilizing various carbon substrates. *Journal of Basic Microbiology*, 31(4):265–277, 1991.
- H. Ma, C.P. Kubicek, and M. Röhr. Malate dehydrogenase isoenzymes in *Aspergillus niger*. *FEMS Microbiology Letters*, 12:127–151, 1981.
- D.W. MacDonald, H.N. Arst Jr., and D.J. Cove. Threonine dehydratase structural gene in *Aspergillus nidulans*. *Biochimica et Biophysica Acta*, 362(1):60–65, 1974.
- S. Malonek, M.C. Rojas, P. Hedden, P. Gaskin, P. Hopkins, and B. Tudzynski. The NADPH-cytochrome P450 reductase gene from *Gibberella fujikuroi* is essential for gibberellin biosynthesis. *The Journal of Biological Chemistry*, 279(24):25075–25084, 2004.
- S. M. Mandala, B. R. Frommer, R. A. Thornton, M. B. Kurtz, N. M. Young, M. A. Cabello, O. Genilloud, J. M. Liesch, J. L. Smith, and W. S. Horn. Inhibition of serine palmitoyl-transferase activity by lipoxamycin. *J. Antibiot. (Tokyo)*, 47(3):376–379, 1994.

- P. Manzanares, L. H. de Graaff, and J. Visser. Characterization of galactosidases from *Aspergillus niger*: purification of a novel α -galactosidase activity. *Enzyme Microb. Technol.*, 22(5):383–390, 1998.
- S. D. Martinelli and J. R. Kinghorn. *Aspergillus: 50 years on*. Elsevier Science, 1994.
- G.A. Marzluf. Regulation of sulfur and nitrogen metabolism in filamentous fungi. *Annu. Rev. Microbiol.*, 47:31–55, 1993.
- I.E. Mattern, J.M. van Noort, P. van den Berg, D.B. Archer, I.N. Roberts, and C.A.M.J.J. van den Hondel. Isolation and characterization of mutants of *Aspergillus niger* deficient in extracellular proteases. *Molecular and General Genetics*, 234(2):332–336, 1992.
- P. Mazur, W. J. Henzel, S. Mattoo, and J. W. Kozarich. 3-Carboxy-cis,cis-muconate lactonizing enzyme from *Neurospora crassa*: an alternate cycloisomerase motif. *J. Bacteriol.*, 176(6):1718–1728, 1994.
- M. W. McDonough and S. M. Martin. The hexosemonophosphate pathway in *Aspergillus niger*. *Can. J. Microbiol.*, 4(4):329–333, 1958.
- E. P. McGovern and R. Bentley. Biosynthesis of flaviolin and 5,8-dihydroxy-2,7-dimethoxy-1,4-naphthoquinone. *Biochemistry*, 14(14):3138–3143, 1975.
- B. Meixner-Monori, C. P. Kubicek, and M. Rohr. Pyruvate kinase from *Aspergillus niger*: a regulatory enzyme in glycolysis? *Can. J. Microbiol.*, 30(1):16–22, 1984.
- B. Meixner-Monori, C. P. Kubicek, A. Habison, E. M. Kubicek-Pranz, and M. Rohr. Presence and regulation of the α -ketoglutarate dehydrogenase multienzyme complex in the filamentous fungus *Aspergillus niger*. *J. Bacteriol.*, 161(1):265–271, 1985.
- B. Meixner-Monori, C. P. Kubicek, W. Harrer, G. Schreferl, and M. Rohr. NADP-specific isocitrate dehydrogenase from the citric acid-accumulating fungus *Aspergillus niger*. *Biochem. J.*, 236(2):549–557, 1986.
- A. Memon, J.D.E. Patterson, C.E.L. Shaw, and J.A. Blain. Phospholipase B activity in mycelia of *Aspergillus niger*. *FEMS Microbiology Letters*, 18(1–2):15–18, 1983.
- O. Milstein, J. Trojanowski, A. Huttermann, and J. Gressel. Catabolism of single ring aromatic acids by four *Aspergillus* species. *Microbios*, 55(222):7–16, 1988.

- T. Minamikawa, N. P. Jayasankar, B. A. Bohm, I. E. Taylor, and G. H. Towers. An inducible hydrolase from *Aspergillus niger*, acting on carbon-carbon bonds, for phlorrhizin and other C-acylated phenols. *Biochem. J.*, 116(5):889–897, 1970.
- H.K. Mitschell and W.D. McElroy. Adenosine deaminase from *Aspergillus oryzae*. *Archives of Biochemistry*, 10:251–258, 1946.
- S. Miyakoshi, H. Uchiyama, T. Someya, T. Satoh, and T. Tabuchi. Distribution of the methylcitrate acid cycle and β -oxidation pathway for propionate catabolism in fungi. *Agric. Biol. Chem.*, 51(9):2381–2387, 1987.
- C. Morisseau, A. Archelas, C. Guitton, D. Faucher, R. Furstoss, and J. C. Baratti. Purification and characterization of a highly enantioselective epoxide hydrolase from *Aspergillus niger*. *European Journal of Biochemistry*, 263:386–395, 1999.
- E. V. Morozova, V. P. Kozlov, V. M. Tereshina, A. S. Memorskaya, and E. P. Feofilova. Changes in lipid composition and carbohydrate composition of *Aspergillus niger* conidia during germination. *Applied Biochemistry and Microbiology*, 38(2):129–133, 2002.
- A.G. Morton and D. Broadbent. Formation of extracellular nitrogen compounds by fungi. *Journal of General Microbiology*, 12:248–258, 1955.
- H. M. Muller. Oxalate accumulation from citrate by *Aspergillus niger*. I. Biosynthesis of oxalate from its ultimate precursor. *Arch. Microbiol.*, 103(2):185–189, 1975a.
- H. M. Muller. Oxalate accumulation from citrate by *Aspergillus niger*. II. Involvement of the tricarboxylic acid cycle. *Arch. Microbiol.*, 104:159–162, 1975b.
- H. M. Muller. [Gluconic acid forming enzymes in *Aspergillus niger* (author's transl)]. *Zentralbl. Bakteriol. Parasitenkd. Infektionskr. Hyg.*, 132(1):14–24, 1977.
- H. M. Muller. Utilization of gluconate by *Aspergillus niger*. I. Enzymes of phosphorylating and non-phosphorylating pathways. *Zentralbl. Mikrobiol.*, 140:475–484, 1985.
- H. M. Muller. Utilization of gluconate by *Aspergillus niger*. II. Enzymes of degradation pathways and main end products. *Zentralbl. Mikrobiol.*, 141(6):461–469, 1986.
- K. Murata, A. Kimura, and N. Yajima. Glutathione synthetase of *Aspergillus niger*. *Agricultural and Biological Chemistry*, 53(4):1145–1149, 1989.

- A. Mustranta, P. Forssell, and K. Poutanen. Comparison of lipases and phospholipases in the hydrolysis of phospholipids. *Process Biochemistry*, 30(5):393–401, 1995.
- T. Nagashima, T. Tange, and H. Anazawa. Dephosphorylation of phytate by using the *Aspergillus niger* phytase with a high affinity for phytate. *Appl. Environ. Microbiol.*, 65(10):4682–4684, 1999.
- V. M. Namboodiri and R. Chattopadhyaya. Purification and biochemical characterization of a novel thermostable lipase from *Aspergillus niger*. *Lipids*, 35(5):495–502, 2000.
- N. E. Neilson. The aconitase of *Aspergillus niger*. *Biochimie et Biophysica Acta*, 17(1):139–140, 1955.
- T. Nemec and K. Jernejc. Influence of Tween 80 on lipid metabolism of an *Aspergillus niger* strain. *Appl. Biochem. Biotechnol.*, 101(3):229–238, 2002.
- A. Netik, N. V. Torres, J-M. Riol, and C. P. Kubicek. Uptake and export of citric acid by *Aspergillus niger* is reciprocally regulated by manganese ions. *Biochimica et Biophysica Acta*, 1326(2):287–294, 1997.
- A.F. Neuwald, J.D. York, and P.W. Majerus. Diverse proteins homologous to inositol monophosphatase. *FEBS Letters*, 294(1–2):16–18, 1991.
- C. Ngiam, D. J. Jeenes, P. J. Punt, C. A. M. J. J. van den Hondel, and D. B. Archer. Characterization of a foldase, protein disulfide isomerase A in the protein secretory pathway of *Aspergillus niger*. *Applied and Environmental Microbiology*, 66(2):775–782, 2000.
- C.E. Nichols, A.R. Hawkins, and D.K. Stammers. Structure of the ‘open’ form of *Aspergillus nidulans* 3-dehydroquinate synthase at 1.7 Å resolution from crystals grown following enzyme turnover. *Acta Crystallographica, Section D*, D60(5):971–973, 2004.
- C.B. Nielsen, B. Friedman, B. Bruce, and C.B. Burge. Patterns of intron gain and loss in fungi. *PLoS Biology*, 2(12):2234–2242, 2004.
- H. Nishioka, M. Imoto, T. Sawa, M. Hamada, H. Naganawa and T. Takeuchi, and K. Umezawa. Screening of phosphatidylinositol kinase inhibitors from *Streptomyces*. *Journal of Antibiotics*, 42(5):823–825, 1989.
- Y. Nomachi and T. Komano. Purification and some properties of two acid ribonucleases from the mycelia of *Aspergillus niger*. *J. Gen. Appl. Microbiol.*, 26:375–385, 1980.

- S. Noor and N. S. Puneekar. Allosteric nadp-glutamate dehydrogenase from aspergilli: purification, characterization and implications for metabolic regulation at the carbon-nitrogen interface. *Microbiology*, 151(Pt 5):1409–1419, 2005.
- J. O’Callaghan, M. X. Caddick, and A. D. Dobson. A polyketide synthase gene required for ochratoxin A biosynthesis in *Aspergillus ochraceus*. *Microbiology*, 149:3485–3491, 2003.
- M. J. O’Connell and J. M. Kelly. Differences in the regulation of aldehyde dehydrogenase genes in *Aspergillus niger* and *Aspergillus nidulans*. *Curr. Genet.*, 14(2):95–103, 1988.
- M. J. O’Connell and J. M. Kelly. Physical characterization of the aldehyde-dehydrogenase-encoding gene of *Aspergillus niger*. *Gene*, 84(1):173–180, 1989.
- M. J. O’Connell and J. M. Kelly. Cis-acting control elements 5’ to *aldA*, the aldehyde dehydrogenase-encoding gene of *Aspergillus niger*. *Gene*, 117(1):151–156, 1992.
- S.P. Oganessian, A.R. Papoyan, and M.A. Davtyan. L-amino acid oxidase from *Aspergillus niger* R-3. *Biologicheskii Zhurnal Armenii*, 51(3):161–166, 1998.
- S.P. Oganessian, M. A. Davtyan, and A. E. Papoyan. Peroximal transaminases from *Aspergillus niger*. *Hayastani Kensabanakan Handesi*, 56(1-2):100–103, 2004.
- K. Ogawa, T. Nakajima-Kambe, T. Nakahara, and E. Kokufuta. Coimmobilization of gluconolactonase with glucose oxidase for improvement in kinetic property of enzymatically induced volume collapse in ionic gels. *Biomacromolecules.*, 3(3):625–631, 2002.
- M. Ohtsuru, I. Tsuruo, and T. Hata. The production and stability of intracellular myrosinase from *A. niger*. *Agr. Biol. Chem.*, 37(5):967–971, 1973.
- E. Oura. *The effect of aeration on the growth energetics and biochemical composition of baker’s yeast, with an appendix: Reactions leading to the formation of yeast cell material from glucose and ethanol*. PhD thesis, Helsinki university, 1972.
- A. Pain, J. Woodward, M.A. Quail, M.J. Anderson, R. Clark, M. Collins, N. Fosker, A. Fraser, D. Harris, N. Larke, L. Murphy, S. Humphray, S. O’Neil, M. Perteau, C. Price, E. Rabinowitsch, M.A. Rajandream,

- S. Salzberg, and D. Saunders. Insight into the genome of *Aspergillus fumigatus*: analysis of a 922 kb region encompassing the nitrate assimilation gene cluster. *Fungal Genet Biol*, 41(4):443–453, 2004.
- M.L. Pall. Adenosine 3',5'-phosphate in fungi. *Microbiological Reviews*, 45(3):462–480, 1981.
- L.M. Palmer, C. Scazzocchio, and D.J. Cove. Pyrimidine biosynthesis in *Aspergillus nidulans*. Isolation and characterization of mutants resistant to fluoropyrimidines. *Molecular and General Genetics*, 140(2):165–173, 1975.
- H. Panneman, G. J. Ruijter, H. C. van den Broeck, E. T. Driever, and J. Visser. Cloning and biochemical characterisation of an *Aspergillus niger* glucokinase. Evidence for the presence of separate glucokinase and hexokinase enzymes. *Eur. J. Biochem.*, 240(3):518–525, 1996.
- H. Panneman, G. J. Ruijter, H. C. van den Broeck, and J. Visser. Cloning and biochemical characterisation of *Aspergillus niger* hexokinase—the enzyme is strongly inhibited by physiological concentrations of trehalose 6-phosphate. *Eur. J. Biochem.*, 258(1):223–232, 1998.
- R. J. Parry and M. G. Kunitani. Synthesis and use of specifically tritiated dethiobiotin in the study of biotin biosynthesis by *Aspergillus niger*. *Methods Enzymol.*, 62:353–370, 1979.
- R.J. Parry and M. Naidu. Biotin biosynthesis. Incorporation of 5(RS)-3H-dethiobiotin into biotin. *Tetrahedron Letters*, 21(50):4783–4786, 1980.
- A. Paszewski and J. Grabski. Homolanthionine in fungi: accumulation in the methionine-requiring mutants of *Aspergillus nidulans*. *Acta Biochimica Polonica*, 22(3):263–268, 1975.
- M.A. Pathak and A. Sreenivasan. Phosphatase and pyrophosphatase activities of *Aspergilli*. *Archives of Biochemistry and Biophysics*, 59:366–372, 1955.
- K. C. Patil and C. V. Ramakrishnan. Comparison of chemical changes and enzyme make-up of wild strain and citrate- and tartrate-adapted strains of *A. niger*. *Indian Journal of Biochemistry*, 3(2):86–88, 1966.
- H. Pedersen and J. Nielsen. The influence of nitrogen sources on the α -amylase productivity of *Aspergillus oryzae* in continous sources. *Applied Microbiology and Biotechnology*, 53:278–281, 2000.
- H. Pedersen, C. Hjort, and J. Nielsen. Cloning and characterization of oah, the gene encoding oxaloacetate hydrolase in *Aspergillus niger*. *Mol. Gen. Genet.*, 263(2):281–286, 2000a.

- H. Pedersen, C. Hjort, and J. Nielsen. Cloning and characterization of oah, the gene encoding oxaloacetate hydrolase in *Aspergillus niger*. *Mol. Gen. Genet.*, 263(2):281–286, 2000b.
- Y. Pei, Y. Zhang, X. Zheng, and W. Fang. Ecdysone induced regulatory system for expression of transgene in fungus and method for improving the safety of the recombinant fungus. Patent: CN 1410526, 2003.
- H.J. Pel, J.H. de Winde, D.B. Archer, P.S. Dyer, G. Hofmann, P.J. Schaap, G. Turner, R.P. de Vries, R. Albang, K. Albermann, M.R. Andersen, J.D. Bendtsen, J.A. Benen, M. van den Berg, S. Breestraat, M.X. Cad-dick, R. Contreras, M. Cornell, P.M. Coutinho, E.G. Danchin, A.J. Debets, P. Dekker, P.W. van Dijck, A. van Dijk, L. Dijkhuizen, A.J. Driessen, C. d’Enfert, S. Geysens, C. Goosen, G.S. Groot, P.W. de Groot, T. Guillemette, B. Henrissat, M. Herweijer, J.P. van den Hombergh, C.A. van den Hondel, R.T. van der Heijden, R.M. van der Kaaij, F.M. Klis, H.J. Kools, C.P. Kubicek, P.A. van Kuyk, J. Lauber, X. Lu, M.J. van der Maarel, R. Meulenbergh, H. Menke, M.A. Mortimer, J. Nielsen, S.G. Oliver, M. Olsthoorn, K. Pal, N.N. van Peij, A.F. Ram, U. Rinas, J.A. Roubos, C.M. Sagt, M. Schmoll, J. Sun, D. Ussery, J. Varga, W. Vervecken, P.J. van de Vondervoort, H. Wedler, H. A. Wosten, A.P. Zeng, A.J. van Ooyen, J. Visser, and H. Stam. Genome sequencing and analysis of the versatile cell factory *Aspergillus niger* CBS 513.88. *Nature Biotechnology*, 25(2): 221–231, 2007.
- J. Pendl, F. Hotek, and V. Cerny. Production strain of *Aspergillus niger* microorganism for submersion fermentation of citric acid. Patent: CZ 292924, 2004.
- L. M. Pera, M. V. Infante Majolli, and M. D. Baigori. Purification and characterization of a thermostable and highly specific β -N-acetyl-D-glucosaminidase from *Aspergillus niger* 419. *Biotechnol. Appl. Biochem.*, 26 (Pt 3):183–187, 1997.
- M. Perl. Adenosine nucleotides and ATP synthesizing enzymes in conidia of *Aspergillus niger*. *Physiologia Plantarum*, 56(3):329–332, 1982.
- A. Pfitzner, C. P. Kubicek, and M. Rohr. Presence and regulation of atp:citrate lyase from the citric acid producing fungus *Aspergillus niger*. *Arch. Microbiol.*, 147(1):88–91, 1987.
- N.J. Pieniazek, P.P. Stepien, and A. Paszewski. *Aspergillus nidulans* mutant lacking cystathionine β -synthase. Identity of L-serine sulfhydrylase with cystathionine β -synthase and its distinctness from O-acetyl-L-serine sulfhydrylase. *Biochimica et Biophysica Acta*, 297(1):37–47, 1973.

- N.J. Pieniazek, J. Bal, E. Balbin, and P. P. Stepien. *Aspergillus nidulans* mutant lacking serine transacetylase. Evidence for two pathways of cysteine biosynthesis. *Molecular and General Genetics*, 132(4):363–366, 1974.
- W. Prathumpai, J. B. Gabelgaard, P. Wanchanthuek, V de van, M. J. de Groot, M. McIntyre, and J. Nielsen. Metabolic control analysis of xylose catabolism in *Aspergillus*. *Biotechnol. Prog.*, 19(4):1136–1141, 2003.
- R. Premkumar, P. V. Rao, N. S. Sreeleela, and C. S. Vaidyanathan. m-Hydroxybenzoic acid 4-hydroxylase from *Aspergillus niger*. *Can. J. Biochem.*, 47(8):825–827, 1969.
- C. Promper, R. Schneider, and H. Weiss. The role of the proton-pumping and alternative respiratory chain NADH:ubiquinone oxidoreductases in overflow catabolism of *Aspergillus niger*. *Eur. J. Biochem.*, 216(1):223–230, 1993.
- N.S. Puneekar, C.S. Vaidyanathan, N. Rao, and N. Appaji. Role of glutamine synthetase in citric acid fermentation by *Aspergillus niger*. *Journal of Biosciences*, 7(3–4):269–287, 1985.
- Z. Qing, L. Yang, and L. Yu-Huan. Purification and characterization of a novel carbaryl hydrolase from *Aspergillus niger* PY168. *FEMS Microbiology Letters*, 228(1):39–44, 2003.
- A. F. Ram, M. Arentshorst, R. A. Damveld, P. A. vanKuyk, F. M. Klis, and C. A. van den Hondel. The cell wall stress response in *Aspergillus niger* involves increased expression of the glutamine : fructose-6-phosphate amidotransferase-encoding gene (gfaA) and increased deposition of chitin in the cell wall. *Microbiology*, 150(Pt 10):3315–3326, 2004.
- A. Rama and E.R.B Shanmugasundaram. Membrane bound phosphatases of temperature sensitive mutants of *Aspergillus nidulans*. *Arogya*, 11(2): 130–142, 1985.
- A. Ramachandran, V. Subramanian, M. Sugumaran, and C.S. Vaidyanathan. Purification and properties of pyrocatechuate decarboxylase from *Aspergillus niger*. *FEMS Microbiology Letters*, 5:421–425, 1979.
- C.V. Ramakrishnan and P.N. Raina. Detection of acetyl coenzyme A deacylase in citric acid-producing strain of *Aspergillus niger*. *Current Science*, 27:487–488, 1958.
- C.V. Ramakrishnan, P.N. Raina, N.T. Patel, and A.P. Joshi. MEchanism of formation and accumulation of citric acid in *Aspergillus niger*. II. Citric acid formation and acetylcoenzyme A deacylase in citric acid-producing strain of *Aspergillus niger*. *Enzymologia*, 21:52–60, 1959.

- T. S. Raman and E. R. B. Shanmugasundaram. Metabolism of some aromatic acids by *Aspergillus niger*. *Journal of Bacteriology*, 84:1339–1340, 1962.
- M. Ramanarayanan and C. S. Vaidyanathan. Mandelate oxidase of *Aspergillus niger*. I. Properties of particulate D(-)-mandelate oxidase. *Indian J. Biochem. Biophys.*, 10(4):254–256, 1973.
- V. Ramaswamy and B. Bheemeswar. Repressible alkaline phosphatase in *Aspergillus niger*. *Experientia*, 32(7):852–853, 1976.
- M. A. Ramirez-Coronel, G. Viniegra-Gonzalez, A. Darvill, and C. Augur. A novel tannase from *Aspergillus niger* with β -glucosidase activity. *Microbiology*, 149(Pt 10):2941–2946, 2003.
- P.V. Subba Rao, K. Moore, and G.H.N. Towers. O-Pyrocatechuic acid carboxylase from *Aspergillus niger*. *Archives of Biochemistry and Biophysics*, 122(2):466–473, 1967.
- A. K. Rawat. Some observations on the aspergillin of *Aspergillus niger*. *Arch. Biochem. Biophys.*, 124(1):418–421, 1968.
- A. C. Ray and R. E. Eakin. Studies on the biosynthesis of aspergillin by *Aspergillus niger*. *Appl. Microbiol.*, 30(6):909–915, 1975.
- C. C. Reddy and C. S. Vaidyanathan. Purification, properties and induction of a specific benzoate-4-hydroxylase from *Aspergillus niger* (UBC 814). *Biochim. Biophys. Acta*, 384(1):46–57, 1975.
- C. Ribard, C. Scazzocchio, and N. Oestreicher. The *oxpA5* mutation of *Aspergillus nidulans* is an allele of *adB*, the gene encoding adenylosuccinate synthetase. *Mol. Genet. Genomics*, 266:701–710, 2001.
- C. Ribard, M. Rochet, B. Labedan, B. ignan Fournier, P. Alzari, C. Scazzocchio, and N. Oestreicher. Sub-families of α /beta barrel enzymes: a new adenine deaminase family. *J. Mol. Biol.*, 334(5):1117–1131, 2003.
- A. Rippel and H. Wiangke. Fixation of acetaldehyde in cultures of *Aspergillus niger*. *Archiv fuer Mikrobiologie*, 12:124–127, 1941.
- J. Rogalski, J. Fiedurek, and A. Gromada. Purification of extracellular catalase from *Aspergillus niger*. *Acta Microbiol. Pol.*, 47(1):31–43, 1998.
- A. A. Rokosu and O. Uadia. Isolation, purification and partial characterization of alkaline phosphatase from *Aspergillus niger*. *Int. J. Biochem.*, 11(6):541–544, 1980.

- M. J. Rudick, Z. E. Fitzgerald, and V. L. Rudick. Intra- and extracellular forms of α -glucosidase from *Aspergillus niger*. *Arch. Biochem. Biophys.*, 193(2):509–520, 1979.
- G. J. Ruijter and J. Visser. Characterization of *Aspergillus niger* phosphoglucose isomerase. Use for quantitative determination of erythrose 4-phosphate. *Biochimie*, 81(3):267–272, 1999.
- G. J. G. Ruijter, P. J. I. van de Vondervoort, and J. Visser. Oxalic acid production by *Aspergillus niger*: an oxalate-non-producing mutant produces citric acid at pH 5 and in the presence of manganese. *Microbiology*, 145: 2569–2576, 1999.
- W. Rymowicz and D. Lenart. Oxalic acid production from lipids by a mutant of *Aspergillus niger* at different pH. *Biotechnology Letters*, 25:955–958, 2003.
- U. Sack, T. M. Heinze, J. Deck, C. E. Cerniglia, M. C. Cazau, and W. Fritsche. Novel metabolites in phenanthrene and pyrene transformation by *Aspergillus niger*. *Appl. Environ. Microbiol.*, 63(7):2906–2909, 1997.
- S. R. Sahasrabudhe and V. V. Modi. Hydroxylation of benzoate and its chlorinated derivatives in *Aspergillus niger*. *Biochem. Int.*, 10(4):525–529, 1985.
- S. R. Sahasrabudhe, D. Lala, and V. V. Modi. Degradation of orcinol by *Aspergillus niger*. *Can. J. Microbiol.*, 32(7):535–538, 1986.
- Y. Sakurai, K. Isobe, and H. Shiota. Partial purification and some properties of an alkaline srylsulfatase produced by *Aspergillus* fungi. *Agric. Biol. Chem.*, 44(1):1–7, 1980.
- R. A. Samson, J. A. M. P. Houbraken, A. F. A. Kuijpers, J. M. Frank, and J. C. Frisvad. New ochratoxin A or sclerotium producing species in *Aspergillus* section *Nigri*. *Studies in Mycology*, 50:45–61, 2004.
- R. Santha, H. S. Savithri, N. A. Rao, and C. S. Vaidyanathan. 2,3-Dihydroxybenzoic acid decarboxylase from *Aspergillus niger*. A novel decarboxylase. *Eur. J. Biochem.*, 230(1):104–110, 1995.
- D. S. Sarma, S. Rajalakshmi, and P. S. Sarma. Pyridine nucleotide biosynthesis in *Aspergillus niger*. *J. Sci. Ind. Res. (C.)*, 20C:301–302, 1961.
- D. S. Sarma, S. Rajalakshmi, and P. S. Sarma. Metabolism of nicotinic acid and nicotinamide in *Aspergillus niger*. *Enzymologia.*, 24:148–154, 1962.

- D. S. Sarma, S. Rajalakshmi, and P. S. Sarma. Studies on the enzymes involved in nicotinamide adenine dinucleotide metabolism in *Aspergillus niger*. *Biochim. et Biophys. Acta*, 81:311–322, 1964.
- Y. Sasaki, T. Morita, T. Kuramoto, K. Mizutani, R. Ikeda, and O. Tanaka. Specificity of glycyrrhinic acid hydrolase. *Agric. Biol. Chem.*, 52(1):207–210, 1988.
- V.A. Savov, A. Kuyumdzieva, A.P. Atev, and H.A. Panaiotov. Influence of nitrogen limitation on the activity of certain nitrogen metabolic enzymes in the *Aspergillus niger* A₃ strain. *Doklady Bolgarsoi Akademii Nauk*, 39(8):101–3, 1986.
- C. Scazzocchio, N. Sdrin, and G. Ong. Positive regulation in a eukaryote, a study of the *uaY* gene of *Aspergillus nidulans*: I. characterization of alleles, dominance and complementation studies, and a fine structure map of the *uaY* - *oxpA* cluster. *Genetics*, 100(2):185–208, 1982.
- B. Schilling and K. Lerch. Amine oxidases from *Aspergillus niger*: identification of a novel flavin-dependent enzyme. *Biochim. Biophys. Acta*, 1243(3):529–537, 1995a.
- B. Schilling and K. Lerch. Cloning, sequencing and heterologous expression of the monoamine oxidase gene from *Aspergillus niger*. *Mol. Gen. Genet.*, 247(4):430–438, 1995b.
- B. Schobel and W. Pollmann. Isolation and characterization of a chlorogenic acid esterase from *Aspergillus niger*. *Z. Naturforsch. [C.]*, 35(3-4):209–212, 1980.
- G. Schreferl-Kunar, M. Grotz, M. Roehr, and C.P. Kubicek. Increased citric acid production by mutants of *Aspergillus niger* with increased glycolytic capability. *FEMS Microbiology Letters*, 59(3):297–300, 1989.
- E. Schuster, N. Dunn-Coleman, J. C. Frisvad, and P. W. N. van Dijck. On the safety of *Aspergillus niger* – a review. *Applied Microbiology and Biotechnology*, 59:426–435, 2002.
- R. Schuurink, R. Busink, D. H. Hondmann, C. F. Witteveen, and J. Visser. Purification and properties of NADP(+)-dependent glycerol dehydrogenases from *Aspergillus nidulans* and *A. niger*. *J. Gen. Microbiol.*, 136(6):1043–1050, 1990.
- K. Schwenk and A.S. Bennett. Effect of avidin on the biosynthesis of fatty acids in *Aspergillus niger* and *Aspergillus flavus*. *Proceedings of the Indiana Academy of Science*, 79:351–355, 1969.

- J.M. Scott and B. Spencer. Regulation of choline sulfatase synthesis and activity in *Aspergillus nidulans*. *Biochemical Journal*, 106(2):471–477, 1968.
- H. M. Sealy-Lewis and V. Fairhurst. Isolation of mutants deficient in acetyl-CoA synthetase and a possible regulator of acetate induction in *Aspergillus niger*. *Microbiology*, 144:1895–1900, 1998.
- M. Servouse and F. Karst. Regulation of early enzymes of ergosterol biosynthesis in *Saccharomyces cerevisiae*. *Biochem J*, 240(2):541–547, 1986.
- S. Seshadri, S. Ignacimuthu, and C. Lakshminarasimhan. Effect of nitrogen and carbon sources on the inorganic phosphate solubilization by different *Aspergillus niger* strains. *Chem. Eng. Comm.*, 191(8):1043–1052, 2004.
- V. K. Shah and C. V. Ramakrishnan. Studies on acid metabolism in *Aspergillus niger*. III. Isocitrate lyase in *Aspergillus niger*. *Enzymologia.*, 26: 44–52, 1963.
- K. Shailubhai, N. N. Rao, and V. V. Modi. Degradation of benzoate and salicylate by *Aspergillus niger*. *Indian J. Exp. Biol.*, 20(2):166–168, 1982.
- K. Shailubhai, R. Somayaji, N. N. Rao, and V. V. Modi. Metabolism of resorcinol and salicylate in *Aspergillus niger*. *Experientia*, 39(1):70–72, 1983.
- A. S. Shetty and F. H. Gaertner. Kynureninase-Type enzymes of *Penicillium roqueforti*, *Aspergillus niger*, *Rhizopus stolonifer*, and *Pseudomonas fluorescens*: further evidence for distinct kynureninase and hydroxykynureninase activities. *J. Bacteriol.*, 122(1):235–244, 1975.
- A. Shi, J. Gu, E. Zhang, and L. Wang. Immobilization and properties of glutaminase from *Aspergillus niger* strain APS-1. *Zhongguo Nianqiao*, 2: 31–33, 1996.
- S. Shimizu, K. Kubo, H. Morioka, Y. Tani, and K. Ogata. Metabolism of pantothenic acid in microorganisms. IX. Enzyme activities involved in coenzyme A biosynthesis in various microorganisms. *Agricultural and Biological Chemistry*, 38(5):1015–1021, 1974.
- M. Sieńko and A. Paszewski. The *metG* gene of *Aspergillus nidulans* encoding cystathionine β -lyase: cloning and analysis. *Current Genetics*, 35:638–646, 1999.
- T. Skowronski. Some properties of partially purified phytase from *Aspergillus niger*. *Acta Microbiol. Pol.*, 27(1):41–48, 1978.

- V.I. Smirnov and V.P. Chubova. Biochemical indexes of mycelium of *Aspergillus niger*. *Mikrobiologicheskie Protessy v Pochvakh Moldavii*, 2:88–91, 1965.
- P. T. Smith, Jr. A. D. King, and N. Goodman. Isolation and characterization of urease from *Aspergillus niger*. *J. Gen. Microbiol.*, 139(5):957–962, 1993.
- R. Snajdrova, V. Kristova-Mylerova, D. Crestia, K. Nikolaou, M. Kuzma, M. Lemaire, E. Gallienne, J. Bolte, K. Bezouska, V. Kren, and L. Martinkova. Nitrile biotransformation by *Aspergillus niger*. *Journal of Molecular Catalysis B: Enzymatic*, 29(1–6):227–232, 2004.
- T. K. Sorensen, P. S. Dyer, F. Fierro, U. Laube, and J. F. Peberdy. Characterisation of the gptA gene, encoding UDP N-acetylglucosamine: dolichol phosphate N-acetylglucosaminylphosphoryl transferase, from the filamentous fungus, *Aspergillus niger*. *Biochim. Biophys. Acta*, 1619(1):89–97, 2003.
- N. S. Sreeleela, P. V. SubbaRao, R. Premkumar, and C. S. Vaidyanathan. A new anthranilic acid hydroxylase from *Aspergillus niger*. Purification and properties. *J. Biol. Chem.*, 244(9):2293–2298, 1969.
- C. M. Stagg and M. S. Feather. The characterization of a chitin-associated D-glucan from the cell walls of *Aspergillus niger*. *Biochim. Biophys. Acta*, 320(1):64–72, 1973.
- P.P. Stepien, N.J. Pieniazek, and J. Bal. Cysteine biosynthesis in *Aspergillus nidulans*. *Acta Microbiologica Polonica, Series A*, 7(4):201–210, 1975.
- P. V. Subba Rao, N. S. Sreeleela, R. Premakumar, and C. S. Vaidyanathan. Regulation of the pathway of anthranilate in *Aspergillus niger*. *Journal of Bacteriology*, 107(1):100–105, 1971.
- V. Subramanian and C. S. Vaidyanathan. Anthranilate hydroxylase from *Aspergillus niger*: new type of NADPH-linked nonheme iron monooxygenase. *J. Bacteriol.*, 160(2):651–655, 1984.
- M. Sugumaran and C.S. Vaidyanathan. Affinity chromatography of homogentisate-1,2-dioxygenase from *Aspergillus niger*. *FEMS Microbiology Letters*, 4(6):343–347, 1978.
- M. Sugumaran, M. Ramanarayanan, and C. S. Vaidyanathan. Involvement of protocatechuic acid in the metabolism of phenylacetic acid by *Aspergillus niger*. *FEBS Lett.*, 29(1):69–72, 1973.
- F.T. Sukhenko and E.S. Podgainaya. The utilization of arginine by some fungi. *Akad. Nauk. S.S.S.R.*, 8:96–106, 1959.

- K. Swart, A. J. Debets, G. Kobus, and C. J. Bos. Arginine and proline genes of *Aspergillus niger*. *Antonie Van Leeuwenhoek*, 61(4):259–264, 1992.
- D. E. Sykes, S. A. Abbas, J. J. Barlow, and K. L. Matta. Substrate specificity and other properties of the β -D-galactosidase from *Aspergillus niger*. *Carbohydr. Res.*, 116(1):127–138, 1983.
- K. Tachibana. Assimilation of carbon dioxide by microorganisms. *Hakko Kyokaishi*, 22(5):210–217, 1964.
- E.E.M Taha and M.M. Sharabash. Utilization of xanthin by fungi. *Nature*, 177:622–623, 1956.
- T. Tanaka, M. Akutagawa, M. Makino, A. Kadota, and J. Ando. Formation of histamine and N-acetyl histamine by pathogenic fungi. *Shinkin to Shinkinsho*, 18(1):58–64, 1977.
- J. P. Tepper, D. B. McCormick, and L. D. Wright. Direct evidence for the conversion of dethiobiotin to biotin in *Aspergillus niger*. *J. Biol. Chem.*, 241(23):5734–5735, 1966.
- V.M. Tereshina, A.V. Kovtunencko, A.S. Memorskaya, and E.P. Feofilova. Effect of carbohydrate composition of the cytosol of *Aspergillus niger* conidia on their viability during storage. *Applied Biochemistry and Microbiology*, 40(5):454–459, 2004.
- D. R. Thatcher and R. B. Cain. The kinetic properties of 3-carboxy-cis-cis-muconate cycloisomerase. *Biochem J.*, 127(2):33P–34P, 1972.
- H. Tomoda, Y. Ohyama, T. Abe, N. Noriko, Y. Michio, Y. Yamaguchi, R. Masuma, and S. Omura. Roselipins, inhibitors of diacylglycerol acyltransferase, produced by *Gliocladium roseum* KF-1040. *Journal of Antibiotics*, 52(8):689–694, 1999.
- J. Topczewski, M. Sienko, and A. Paszewski. Cloning and characterization of the *Aspergillus nidulans* *cysB* gene encoding cysteine synthase. *Curr. Genet.*, 31(4):348–356, 1997.
- H. Trembacz and M. M. Jezewska. The route of non-enzymic and enzymic breakdown of 5-phosphoribosyl 1-pyrophosphate to ribose 1-phosphate. *Biochem. J.*, 271(3):621–625, 1990.
- S. E. Unkles, E. I. Campbell, P. J. Punt, K. L. Hawker, R. Contreras, A. R. Hawkins, C. A. van den Hondel, and J. R. Kinghorn. The *Aspergillus niger* *niaD* gene encoding nitrate reductase: upstream nucleotide and amino acid sequence comparisons. *Gene*, 111(2):149–155, 1992.

- S. O. Uryson and A. N. Belozerskii. Nucleotide composition of deoxyribonucleic and ribonucleic acids of some fungi. *Doklady Akademii Nauk SSSR*, 132:708–710, 1960.
- L.M. Utkin. Homogentisic acid in the metabolism of molds. *Biochimiya*, 15: 330–333, 1950.
- O. Valerius, O. Draht, E. Kubler, K. Adler, B. Hoffmann, and G.H. Braus. Regulation of *hisHF* transcription of *Aspergillus nidulans* by adenine and amino acid limitation. *Fungal Genetics and Biology*, 32(1):21–31, 2001.
- H.J.M. van den Brink, H.J.G.M. van Nistelrooy, M.A. de Waard, C.A.M.J.J. van den Hondel, and R.F.M. van Gorcom. Increased resistance to 14 α -demethylase inhibitors (DMIs) in *Aspergillus niger* by coexpression of the *Penicillium italicum* eburicol 14 α -demethylase (*cyp51*) and the *A. niger* cytochrome P450 reductase (*cprA*) genes. *J. Biotechnol.*, 49(1-3):13–18, 1996.
- P. van den Broek, T. Goosen, B. Wennekes, and H. van den Broek. Isolation and characterization of the glucose-6-phosphate dehydrogenase encoding gene (*gsdA*) from *Aspergillus niger*. *Mol. Gen. Genet.*, 247(2):229–239, 1995.
- J. P. van den Hombergh, G. Jarai, F. P. Buxton, and J. Visser. Cloning, characterization and expression of *pepF*, a gene encoding a serine carboxypeptidase from *Aspergillus niger*. *Gene*, 151(1-2):73–79, 1994.
- A.D. van Diepeningen, A.J.M. Debets, J. Varga, M. van der Gaag, K. Swart, and R.F. Hoekstra. Efficient degradation of tannic acid by black *Aspergillus* species. *Mycol. Res.*, 108(8):919–925, 2004.
- R. F. van Gorcom, J. G. Boschloo, A. Kuijvenhoven, J. Lange, A. J. van Vark, C. J. Bos, J. A. van Balken, P. H. Pouwels, and C. A. van den Hondel. Isolation and molecular characterisation of the benzoate-para-hydroxylase gene (*bphA*) of *Aspergillus niger*: a member of a new gene family of the cytochrome P450 superfamily. *Mol. Gen. Genet.*, 223(2):192–197, 1990.
- W. van Hartingsveldt, C. M. van Zeijl, G. M. Harteveld, R. J. Gouka, M. E. Suykerbuyk, R. G. Luiten, P. A. van Paridon, G. C. Selten, A. E. Veenstra, and R. F. van Gorcom. Cloning, characterization and overexpression of the phytase-encoding gene (*phyA*) of *Aspergillus niger*. *Gene*, 127(1):87–94, 1993.
- P. A. vanKuyk, M. J. L. de Groot, G. J. G. Ruijter, R. P. de Vries, and J. Visser. The *Aspergillus niger* D-xululose kinase gene is co-expressed with genes encoding arabinan degrading enzymes, and is essential for growth on

- D-xylose and L-arabinose. *European Journal of Biochemistry*, 268:5414–5423, 2001.
- P. A. vanKuyk, J. A. Diderich, A. P. MacCabe, O. Hererro, G. J. Ruijter, and J. Visser. *Aspergillus niger mstA* encodes a high-affinity sugar/H⁺ symporter which is regulated in response to extracellular pH. *Biochem. J.*, 379(Pt 2):375–383, 2004.
- J. Varga, K. Rigo, S. Kocsube, B. Farkas, and K. Pal. Diversity of polyketide synthase gene sequences in *Aspergillus* species. *Res. Microbiol.*, 154(8):593–600, 2003.
- M. Varoglu and P. Crews. Biosynthetically diverse compounds from a salt-water culture of sponge-derived *Aspergillus niger*. *J. Nat. Prod.*, 63(1):41–43, 2000.
- M. Varoglu, T. H. Corbett, F. A. Valeriote, and P. Crews. Asperazine, a Selective Cytotoxic Alkaloid from a Sponge-Derived Culture of *Aspergillus niger*. *J. Org. Chem.*, 62(21):7078–7079, 1997.
- P. Vats and U. C. Banerjee. Biochemical characterisation of extracellular phytase (myo-inositol hexakisphosphate phosphohydrolase) from a hyper-producing strain of *Aspergillus niger* van Teighem. *J. Ind. Microbiol. Biotechnol.*, 32(4):141–147, 2005.
- P. vd Veen, M. J. Flipphi, A. G. Voragen, and J. Visser. Induction, purification and characterisation of arabinases produced by *Aspergillus niger*. *Arch. Microbiol.*, 157(1):23–28, 1991.
- P. vd Veen, M. J. Flipphi, A. G. Voragen, and J. Visser. Induction of extracellular arabinases on monomeric substrates in *Aspergillus niger*. *Arch. Microbiol.*, 159(1):66–71, 1993.
- W. K. Versaw, M. A. Bevins, and J. Markwell. Purification and properties of a 4-nitrophenylphosphatase from *Aspergillus niger*. *Arch. Biochem. Biophys.*, 287(1):85–90, 1991.
- C. Vignaud, N. Kaid, L. Rakotozafy, S. Davidou, and J. Nicolas. Partial purification and characterization of sulfhydryl oxidase from *Aspergillus niger*. *Journal of Food Science*, 67(6):2016–2022, 2002.
- A. Vohra and T. Satyanarayana. Phytases: microbial sources, production, purification, and potential biotechnological applications. *Crit Rev. Biotechnol.*, 23(1):29–60, 2003.

- H. Wagner and E. Fiebert. Sphingolipids and glycolipids of fungi and higher plants. III. isolation of a cerebroside from *Aspergillus niger*. *Zeitschrift fuer Naturforschung, Teil B.*, 24(3):359, 1969.
- G. L. Wallis, R. L. Easton, K. Jolly, F. W. Hemming, and J. F. Peberdy. Galactofuranoic-oligomannose N-linked glycans of α -galactosidase A from *Aspergillus niger*. *Eur. J. Biochem.*, 268(15):4134–4143, 2001.
- G. Weidner, B. Steffan, and A.A. Brakhage. The *Aspergillus nidulans* *lysF* gene encodes homoaconitase, an enzyme involved in the fungus-specific lysine biosynthesis pathway. *Molecular and General Genetics*, 255:237–247, 1997.
- L. M. Wennekes, T. Goosen, P. J. van den Broek, and H. W. van den Broek. Purification and characterization of glucose-6-phosphate dehydrogenase from *Aspergillus niger* and *Aspergillus nidulans*. *J. Gen. Microbiol.*, 139(11):2793–2800, 1993.
- F. Widmer and J. L. Leuba. beta-Galactosidase from *Aspergillus niger*. Separation and characterization of three multiple forms. *Eur. J. Biochem.*, 100(2):559–567, 1979.
- B. A. Williams, S. Sillaots, A. Tsang, and R. Storms. Isolation by genetic complementation of two differentially expressed genes for β -isopropylmalate dehydrogenase from *Aspergillus niger*. *Curr. Genet.*, 30(4):305–311, 1996.
- C. F. Witteveen, P. van de Vondervoort, C. Dijkema, K. Swart, and J. Visser. Characterization of a glycerol kinase mutant of *Aspergillus niger*. *J. Gen. Microbiol.*, 136(7):1299–1305, 1990.
- C. F. B. Witteveen and J. Visser. Polyol pools in *Aspergillus niger*. *FEMS Microbiology Letters*, 134:57–62, 1995.
- C. F. B. Witteveen, R. Busink, P. van de Vondervoort, C. Dijkema, K. Swart, and J. Visser. L-Arabinose and D-xylose catabolism in *Aspergillus niger*. *Journal of General Microbiology*, 135:2163–2171, 1989.
- C. F. B. Witteveen, F. Weber, R. Busink, and J. Visser. Isolation and characterization of two xylitol dehydrogenases from *Aspergillus niger*. *Microbiology*, 140:1679–1685, 1994.
- C.F.B. Witteveen, M. Veenhuis, and J. Visser. Localization of glucose oxidase and catalase activities in *Aspergillus niger*. *Applied and Environmental Microbiology*, 58(4):1190–1194, 1992.

- F. B. Witteveen, V de van, H. C. van den Broeck, A. C. van Engelenburg, L. H. de Graaff, M. H. Hillebrand, P. J. Schaap, and J. Visser. Induction of glucose oxidase, catalase, and lactonase in *Aspergillus niger*. *Curr. Genet.*, 24(5):408–416, 1993.
- W. S. Wold and I. Suzuki. Demonstration in *Aspergillus niger* of adenylyl cyclase, a cyclic adenosine 3',5'-monophosphate-binding protein, and studies on intracellular and extracellular phosphodiesterases. *Can. J. Microbiol.*, 20(11):1567–1576, 1974.
- M. F. Wolschek and C. P. Kubicek. The filamentous fungus *Aspergillus niger* contains two "differentially regulated" trehalose-6-phosphate synthase-encoding genes, tpsA and tpsB. *J. Biol. Chem.*, 272(5):2729–2735, 1997.
- C. L. Woronick and M. J. Johnson. Carbon dioxide fixation by cell-free extracts of *Aspergillus niger*. *Journal of Biological Chemistry*, 235(1):9–15, 1960.
- J. C. Wriston, Jr. and T. O. Yelling. L-asparaginase: a review. *Advances in Enzymology and Related Areas of Molecular Biology*, 39:185–248, 1973.
- T. Wunder, S. Kremer, O. Sterner, and H. Anke. Metabolism of the polycyclic aromatic hydrocarbon pyrene by *Aspergillus niger* SK 9317. *Appl. Microbiol. Biotechnol.*, 42(4):636–641, 1994.
- M. Wyss, L. Pasamontes, R. Remy, J. Kohler, E. Kuszniir, M. Gadiant, F. Muller, and A. P. G. M. van Loon. Comparison of the thermostability properties of three acid phosphatases from molds: *Aspergillus fumigatus* phytase, *A. niger* phytase, and *A. niger* pH 2.5 acid phosphatase. *Appl. Environ. Microbiol.*, 64(11):4446–4451, 1998.
- M. Wyss, R. Brugger, A. Kronenberger, R. Remy, R. Fimbel, G. Oesterheld, M. Lehmann, and A. P. van Loon. Biochemical characterization of fungal phytases (myo-inositol hexakisphosphate phosphohydrolases): catalytic properties. *Appl. Environ. Microbiol.*, 65(2):367–373, 1999.
- Y. H. Xiong, J. Z. Liu, and H. Y. Song. Purification and partial characterization of an extracellular ribonuclease from a mutant of *Aspergillus niger*. *Appl. Biochem. Biotechnol.*, 125(3):201–210, 2005.
- K. Yanai, A. Nakane, A. Kawate, and M. Hirayama. Molecular cloning and characterization of the fructooligosaccharide-producing β -fructofuranosidase gene from *Aspergillus niger* ATCC 20611. *Biosci. Biotechnol. Biochem.*, 65(4):766–773, 2001.

- M.E. Yelton, J.E. Hamer, E.R. de Souza, E.J. Mullaney, and W.E. Timberlake. Developmental regulation of the *Aspergillus nidulans trpC* gene. *Proc. Natl. Acad. Sci. USA*, 80:7576–7580, 1983.
- R. K. Yogambal and T. B. Karegoudar. Metabolism of polycyclic aromatic hydrocarbons by *Aspergillus niger*. *Indian J. Exp. Biol.*, 35(9):1021–1023, 1997.
- M. Yukioka and T. Winnick. Synthesis of malformin by an enzyme preparation from *Aspergillus niger*. *J. Bacteriol.*, 91(6):2237–2244, 1966.
- T.M. Zabriskie and M.D. Jackson. Lysine biosynthesis and metabolism in fungi. *Nat. Prod. Rep.*, 17:85–97, 2000.
- W. Zhong, M. W. Jeffries, and N. H. Georgopapadakou. Inhibition of inositol phosphorylceramide synthase by aureobasidin A in *Candida* and *Aspergillus* species. *Antimicrob. Agents Chemother.*, 44(3):651–653, 2000.