

Table 1. *A. fumigatus* Af293 pathways.

Pathway name	No. Steps ¹	Level ²			
2-amino-3-carboxymuconate semialdehyde degradation to glutaryl-CoA	4 (1)	4	asparagine degradation I	1	3
2-ketoglutarate dehydrogenase complex	3	3	aspartate biosynthesis	1	3
2-methylcitrate cycle I	5 (2)	4	aspartate degradation II	2	3
3-dehydroquinate biosynthesis I	2	3	beta-alanine biosynthesis V	2 (1)	4
4-aminobutyrate degradation I	3	3	betacyanin biosynthesis	7 (1)	4
4-hydroxybenzoate biosynthesis I (eukaryotes)	5 (1)	4	betanidin degradation	1	3
4-hydroxymandelate degradation³	5	1	betaxanthin biosynthesis	3 (2)	3
5-aminoimidazole ribonucleotide biosynthesis I	5	3	betaxanthin biosynthesis (via dopamine)	2 (1)	3
6-hydroxymethyl-dihydropterin diphosphate biosynthesis	5 (3)	4	branched-chain alpha-keto acid dehydrogenase complex	3	2
acetate conversion to acetyl-CoA	1	3	butanediol biosynthesis	1	3
acetoin biosynthesis I	3 (1)	4	butanediol degradation	1	3
acetyl-CoA biosynthesis (from citrate)	1	3	C30 botryococcene biosynthesis	3	2
acetyl-CoA biosynthesis (from pyruvate)	3	3	calcium transport I	2	3
acyl-CoA hydrolysis	1	3	cardiolipin biosynthesis II	3 (2)	2
aerobic respiration -- electron donor II	4	3	CDP-diacylglycerol biosynthesis I	4	2
aerobic respiration -- electron donor III	4 (2)	4	choline biosynthesis III	3	3
allantoin degradation to ureidoglycolate I (urea producing)	2	3	choline degradation I	2	3
alternative ergosterol biosynthesis pathway (A. fumigatus)⁴	17	1	choline degradation II	2	3
arginine biosynthesis II (acetyl cycle)	9	3	chorismate biosynthesis I	7	2
arginine degradation I (arginase pathway)	4 (3)	3	citrulline degradation	2 (1)	4
arginine degradation VI (arginase 2 pathway)	4 (3)	3	coenzyme A biosynthesis	5	2
arginine degradation VII (arginase 3 pathway)	2	3	copper transport II	1	3
arginine degradation X (arginine monooxygenase pathway)	3 (1)	4	cyanate degradation	3	3
arsenate detoxification II	1	3	cyclopropane fatty acid (CFA) biosynthesis	1	3
asparagine biosynthesis I	1	3	degradation of purine ribonucleosides	6 (3)	4
			DIMBOA-glucoside degradation	1	3
			di-trans,poly-cis-undecaprenyl diphosphate biosynthesis	8	3
			D-mannose degradation	1	3
			dolichyl-diphosphooligosaccharide biosynthesis	16	2
			dTDP-L-rhamnose biosynthesis I	4 (1)	4
			epoxysqualene biosynthesis	3	3
			fatty acid activation	1	3
			fatty acid beta-oxidation I⁵	7	1
			fatty acid beta-oxidation II (core pathway)⁵	5	1
			fatty acid biosynthesis initiation II	2	3
			fatty acid omega-oxidation⁶	6	1

flavin biosynthesis III (eukaryotes)	9 (8)	2	glycolysis II	10	3
folate polyglutamylation I	5	3	glyoxylate cycle	6	1
folate polyglutamylation II	2 (1)	4	heme biosynthesis from uroporphyrinogen-III I	4	3
folate transformations	12 (10)	2	heptaprenyl diphosphate biosynthesis	4 (3)	2
formaldehyde assimilation III (dihydroxyacetone cycle)	12		histidine biosynthesis	10	2
formate oxidation to CO ₂	1	3	homocysteine and cysteine interconversion	4 (3)	4
formate to nitrate electron transfer	2	3	homocysteine biosynthesis	2	3
formylTHF biosynthesis I	11	2	homogalacturonan degradation	2	3
formylTHF biosynthesis II	12 (11)	2	homoserine biosynthesis	3	3
gamma-linolenate biosynthesis II (animals)	2 (1)	4	hyperforin biosynthesis	4 (2)	4
GDP-glucose biosynthesis	4 (2)	4	IAA biosynthesis V	1	3
GDP-mannose biosynthesis	4	3	inosine-5'-phosphate biosynthesis II	5	3
geranyldiphosphate biosynthesis	1	3	isoleucine biosynthesis I (from threonine)	5	3
geranylgeranyldiphosphate biosynthesis	1	3	isoleucine degradation I	6	2
gluconeogenesis I	12		isoleucine degradation II	3	2
glucose and glucose-1-phosphate degradation	4 (2)	4	itaconate biosynthesis	4 (3)	4
glutamate biosynthesis I	1	3	itaconate degradation	3 (1)	4
glutamate biosynthesis III	1	3	lactose degradation III	1	3
glutamate biosynthesis IV	1	3	lanosterol biosynthesis	1	3
glutamate degradation I	1	3	L-arabinose degradation II	3 (1)	4
glutamate dependent acid resistance	1	3	L-cysteine degradation I	3 (2)	3
glutamine biosynthesis I	1	3	L-cysteine degradation II	1	3
glutamine degradation II	1	3	leucine biosynthesis	6 (5)	3
glutaryl-CoA degradation	5	2	leucine degradation I	7	2
glutathione biosynthesis	2	3	leucine degradation III	3	3
glutathione redox reactions I	3	2	lysine biosynthesis IV	8	2
glutathione redox reactions II	2 (1)	3	mannitol degradation I	1	3
glutathione-mediated detoxification	1	2	melibiose degradation	1	3
glycerol degradation I	3	3	methionine degradation I (to homocysteine)	3	3
glycerol degradation IV	2	3	methionine degradation III	3 (2)	2
glycerol-3-phosphate shuttle	2	3	methyl parathion degradation	1	3
glycine betaine biosynthesis I (Gram-negative bacteria)	2	3	methylglyoxal degradation I	3	3
glycine betaine biosynthesis II (Gram-positive bacteria)	2	3	methylglyoxal degradation V	3 (2)	4
glycine biosynthesis I	1	3	methylsalicylate degradation	2	3
glycine biosynthesis III	1	3	mevalonate pathway I	7	3
glycine biosynthesis IV	1	3	mixed acid fermentation	11	4
glycine cleavage complex	3	3	myo-inositol biosynthesis	2	3
glycogen biosynthesis II (from UDP-D-Glucose)	5	3	N-acetylglucosamine degradation	2	3
glycogen degradation I	7	3	N-acetylneuraminic acid and N-acetylmannosamine degradation	3 (1)	4
glycogen degradation II	5	3	NAD biosynthesis from 2-amino-3-carboxymuconate semialdehyde	4 (3)	3
			NAD biosynthesis I (from aspartate)	6 (3)	4

NAD salvage pathway I	8 (6)	2	purine	7 (1)	4
NAD/NADH	6 (4)	4	deoxyribonucleosides		
phosphorylation and			degradation		
dephosphorylation			putrescine biosynthesis III	1	3
nitrate reduction III	2 (1)	4	pyridoxal 5'-phosphate	8 (2)	4
(dissimilatory)			biosynthesis		
nitrate reduction V	5 (4)	3	pyridoxal 5'-phosphate	5	1
(assimilatory)			salvage pathway		
oleate beta-oxidation	3	2	pyrimidine	6 (2)	4
oleate biosynthesis II	2 (1)	4	deoxyribonucleosides		
(animals)			degradation		
ornithine biosynthesis	5	3	pyrimidine	11	4
ornithine degradation	1	3	deoxyribonucleotides de	(8)	
(proline biosynthesis)			novo biosynthesis		
oxidative ethanol	3	3	pyrimidine ribonucleotides	4	2
degradation I			interconversion		
oxidative ethanol	3	3	pyruvate fermentation to	2	3
degradation III			ethanol II		
palmitate biosynthesis I	29	1	pyruvate fermentation to	1	3
(animals)	(27)		lactate		
pantothenate biosynthesis I	3	3	removal of superoxide	2	3
paraoxon degradation	1	3	radicals		
pentose phosphate	5	3	respiration (anaerobic)	7	2
pathway (non-oxidative			S-adenosyl-L-methionine	4 (3)	4
branch)			cycle II		
pentose phosphate	3	3	S-adenosylmethionine	1	3
pathway (oxidative branch)			biosynthesis		
pentose phosphate	3	3	salicylate degradation I	1	3
pathway (partial)			salvage pathways of	12	4
phenol degradation I	1	3	adenine, hypoxanthine, and	(3)	
(aerobic)			their nucleosides		
phenylalanine biosynthesis	3	3	salvage pathways of	7 (4)	2
I			guanine, xanthine, and their		
phenylalanine degradation	4 (2)	4	nucleosides		
III			salvage pathways of	8 (7)	2
phenylethanol biosynthesis	3 (2)	2	pyrimidine ribonucleotides		
phenylethylamine	2 (1)	4	seed germination protein	1	3
degradation			turnover		
phosphatidylcholine	3	3	selenocysteine biosynthesis	4 (1)	4
biosynthesis I			II (archaea and eukaryotes)		
phosphatidylcholine	5	3	serine biosynthesis	3	3
biosynthesis II			siroheme biosynthesis	4	2
phosphatidylcholine	5 (3)	4	sorbitol biosynthesis II	3	3
biosynthesis III			sorbitol degradation I	1	3
phosphatidylcholine	5 (3)	4	spermidine biosynthesis	2	3
biosynthesis IV			sphingolipid metabolism ⁷	13	1
phosphatidylethanolamine	2	3	sphingomyelin metabolism	1	2
biosynthesis I			sphingosine and	5 (4)	2
phosphatidylethanolamine	3	3	sphingosine-1-phosphate		
biosynthesis II			metabolism		
phospholipases	5	2	sulfate activation for	2	3
proline biosynthesis I	4 (3)	3	sulfonation		
proline biosynthesis II (from	6 (3)	4	sulfite oxidation IV	1	3
arginine)			taurine degradation IV	1	3
proline degradation I	2	3	TCA cycle variation III	9	2
proline degradation II	2	3	(eukaryotic)		
PRPP biosynthesis I	1	3	tetrapyrrole biosynthesis II	4	3
			thioredoxin pathway	2 (1)	4

thiosulfate	1	3
disproportionation III (rhodanese)		
threonine biosynthesis from homoserine	2	3
trans,trans-farnesyl diphosphate biosynthesis	3	3
trehalose biosynthesis I	2	3
trehalose degradation I (low osmolarity)	2	3
trehalose degradation II (trehalase)	2	3
triacylglycerol biosynthesis	5	3
triacylglycerol degradation	4 (1)	4
tRNA charging pathway	20	3
tryptophan biosynthesis	6	2
tryptophan degradation I (via anthranilate)	3	3
tryptophan degradation to 2-amino-3- carboxymuconate semialdehyde	5	3
tryptophan degradation X (mammalian, via tryptamine)	4	3
tyrosine biosynthesis I	3	3
tyrosine degradation I	5	2
tyrosine degradation III	4 (2)	4
ubiquinone-10 biosynthesis (eukaryotic)	9 (6)	1
ubiquinone-6 biosynthesis (eukaryotic)	9 (6)	1
ubiquinone-7 biosynthesis (eukaryotic)	9 (6)	1
ubiquinone-8 biosynthesis (eukaryotic)	9 (6)	1
ubiquinone-9 biosynthesis (eukaryotic)	9 (6)	1
UDP-N-acetyl-D- glucosamine biosynthesis II	4	3
urate degradation to allantoin	3	2
urea degradation I	2	3
urea degradation II	1	3
uridine-5'-phosphate biosynthesis	6	2
valine biosynthesis	4	3
valine degradation I	7	2
valine degradation II	3	3
very long chain fatty acid biosynthesis⁸	4	1
wax esters biosynthesis II	2 (1)	4
wound-induced proteolysis I	1	3
xylitol degradation	2	3
zymosterol biosynthesis	12	3

¹Number of reactions in pathway. The number of reactions annotated/present in *A. fumigatus* Af293 is identical to this unless indicated otherwise by a bracketed figure. Some 'missing' reactions are spontaneous and do therefore not have an enzyme assigned.

²Levels of annotation are as follows: 1= manual annotation of entire pathway; 2 = automatic annotation followed by successful/predominantly successful manual hole filling; 3 = automatic annotated to completion/near completion; 4 = automatic annotation with holes unresolved.

³Literature [13-15].

⁴Literature [16-18]

⁵Literature [19-23]

⁶Literature [24]

⁷Literature [25,26]

⁸Literature [27]