

**Supplementary material**

Differentially expressed proteins in *Aspergillus niger* IOC 4687

Table 1: Differentially identified proteins by *A.niger* IOC 4687 fungus mass spectrometry in the absence of Cu<sup>2+</sup> (Uniprot, <http://www.uniprot.org>).

#Acesso	-10lgP	Convergência (%)	#Peptídeos	Proteins
A0A117DYT5	44342	52	37	Cobalamin-independent methionine synthase
A0A100IED2	42355	46	36	Elongation factor
A0A117DXF8	41556	34	26	2-oxoglutarate dehydrogenase E1 component
A5AB29	41030	49	22	Glutamate decarboxylase (EC 4.1.1.15)
A0A117E173	34101	38	22	Hsp70 chaperone
A0A100IAD1	34517	25	16	Aminopeptidase C
A0A100IFA7	30427	22	13	Aconitase family protein
A0A124BUR9	24060	6	13	Glycogen debranching enzyme Gdb1
A2QUW9	24336	38	12	Aspergillus niger contig An10c0020, genomic contig (EC 1.1.1.-)
A2R8S1	28850	21	12	Aspergillus niger contig An16c0250, genomic contig (EC 3.4.14.-)
A0A100IA47	25819	15	12	Bifunctional purine biosynthesis protein Ade16
A0A117E141	24430	45	10	ATP synthase subunit 4, mitochondrial
G3Y9G5	21056	11	9	Uncharacterized protein
A0A172CE91	22513	26	8	Translation elongation factor 1-alpha (Fragment)
A2R7U3	20162	29	7	Aspergillus niger contig An16c0170, genomic contig (EC 1.1.1.-)
A0A117DZF6	30535	12	7	ER to Golgi transport protein Yif1
A0A100IQI4	16016	11	6	ABC transporter
E2PSQ3	19859	16	6	Aspergillus niger contig An07c0160, genomic contig
A2R070	15895	18	6	Aspergillus niger contig An12c0240, genomic contig
G3XNR9	15823	22	6	Methyltransferase (Fragment)
A0A100IUG8	17191	23	6	Short-chain dehydrogenase/reductase family protein
G3XVV7	15865	30	6	Uncharacterized protein
G3Y3M5	18070	7	6	Uncharacterized protein
G3Y8V4	19884	12	6	Uncharacterized protein

G3XN30	23435	41	6	Uncharacterized protein (Fragment)
G3YG52	13410	18	6	Uncharacterized protein (Fragment)
A2QA24	19439	14	5	Aspergillus niger contig An01c0330, genomic contig
A2QLH0	13842	14	5	Aspergillus niger contig An06c0070, genomic contig
A2R9C5	17031	13	5	Aspergillus niger contig An17c0040, genomic contig
A0A124BY94	14760	29	5	Uncharacterized protein
A2QJ58	14808	6	5	Uncharacterized protein
G3XUS2	16232	5	5	Uncharacterized protein
G3YG69	13457	29	5	Uncharacterized protein (Fragment)
A2QLN6	13543	11	4	Aspergillus niger contig An06c0090, genomic contig
A2QSZ5	15832	14	4	Aspergillus niger contig An09c0020, genomic contig (EC 2.1.1.-)
A2R040	16212	21	4	Aspergillus niger contig An12c0220, genomic contig
A2R6K2	17243	17	4	Aspergillus niger contig An16c0010, genomic contig (EC 2.1.1.41)
A2R7Q2	16451	17	4	Aspergillus niger contig An16c0160, genomic contig (EC 2.4.1.83)
A0A100IN43	11767	11	4	Survival factor 1
G3XZZ8	12283	10	4	Uncharacterized protein
G3Y0V9	14251	18	4	V-type proton ATPase subunit
A0A124BXJ2	9164	12	3	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase
A0A124BUY0	17585	9	3	2-methylcitrate dehydratase
A0A100ILE8	17337	14	3	3-hydroxybutyryl-CoA dehydrogenase
A2Q988	13440	11	3	Aspergillus niger contig An01c0250, genomic contig (EC 1.2.1.-)
A2Q9M7	14515	10	3	Aspergillus niger contig An01c0290, genomic contig
A2QF99	8924	6	3	Aspergillus niger contig An02c0450, genomic contig
A2QPJ6	13181	17	3	Aspergillus niger contig An07c0340, genomic contig (EC 3.1.1.45)
A2QPK9	9380	5	3	Aspergillus niger contig An07c0370, genomic contig
A2R469	9522	12	3	Aspergillus niger contig An14c0200, genomic contig
E2PSW1	15301	11	3	Aspergillus niger contig An17c0060, genomic contig (EC 2.7.1.20)
A2RAC5	11531	8	3	Aspergillus niger contig An18c0080, genomic contig (EC 1.14.-.-)

A0A100IK26	19784	7	3	Cytochrome P450 monooxygenase
A0A117DZE0	8134	9	3	Glutamine synthetase
A0A100I2M0	8923	9	3	Mitochondrial protein import protein Mas5
P55804	13684	49	3	NADP(+)-dependent glycerol dehydrogenase (EC 1.1.1.72) (Fragments)
G3Y6S2	12580	2	3	Pre-mRNA splicing helicase
G3XPH6	9417	48	3	Profilin
A0A117E1L4	15559	12	3	Proteasome component PRE2
A0A124BWC0	8520	5	3	SPX domain protein
A0A100IQF6	14953	9	3	Uncharacterized protein
G3XMQ1	16611	7	3	Uncharacterized protein
G3XNM7	11762	38	3	Uncharacterized protein
G3XXV3	14109	12	3	Uncharacterized protein
G3YAH5	13996	2	3	Uncharacterized protein
A0A117E1H1	15384	4	2	Acetyl-CoA-acetyltransferase
Q00217	14156	6	2	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 2 (EC 2.4.1.15) (Trehalose-6-phosphate synthase) (UDP-glucose-glucosephosphate glucosyltransferase)
A2QEV0	11465	11	2	Altered inheritance of mitochondria protein 24, mitochondrial
G3Y3K5	7436	6	2	Arginase (EC 3.5.3.1)
D8FSP0	5446	9	2	Arylamine N-acetyltransferase 2
A2QAY4	8539	3	2	Aspergillus niger contig An01c0400, genomic contig
A2QDZ5	8616	4	2	Aspergillus niger contig An02c0270, genomic contig
A2QP65	7010	11	2	Aspergillus niger contig An07c0260, genomic contig (EC 3.5.1.19)
A2QUB8	12235	5	2	Aspergillus niger contig An09c0150, genomic contig (EC 2.6.1.5)
A2QUT4	8790	9	2	Aspergillus niger contig An09c0220, genomic contig (EC 2.5.1.49)
A2QV31	6375	8	2	Aspergillus niger contig An10c0050, genomic contig (EC 2.7.8.23)
A2QVE0	14178	6	2	Aspergillus niger contig An11c0040, genomic contig (EC 3.5.4.3)
A2QWZ5	7891	5	2	Aspergillus niger contig An11c0240, genomic contig (EC 1.14.14.3)

A5ABQ5	7628	3	2	Aspergillus niger contig An11c0340, genomic contig
A2QYI1	11595	3	2	Aspergillus niger contig An12c0050, genomic contig (EC 1.14.-.-)
A2R093	8994	26	2	Aspergillus niger contig An12c0260, genomic contig (EC 6.3.2.19)
A2R0Z5	7851	2	2	Aspergillus niger contig An12c0350, genomic contig (EC 2.4.1.16)
A2R7M4	9894	16	2	Aspergillus niger contig An16c0150, genomic contig
A2RAW5	13525	19	2	Aspergillus niger contig An18c0160, genomic contig
A0A100IAI5	7751	7	2	AT DNA binding protein
A0A100I5M3	9296	4	2	Autophagy protein Atg20
A0A117E1A3	7335	2	2	Chitin synthase G
A0A124BXP0	9409	4	2	Cytochrome P450 alkane hydroxylase
A0A100IAY7	10332	3	2	Glycerol kinase
A0A124BUT2	10627	6	2	Glyoxylate reductase
A0A117E0Z1	14142	7	2	Guanine deaminase
G3Y376	10223	4	2	Imidazoleglycerol phosphate synthase (EC 2.4.2.-) (EC 4.1.3.-)
A0A100IF33	7836	3	2	Mitochondrial carrier protein
A0A100IIK0	5442	1	2	Pentafunctional AROM polypeptide [Includes: 3-dehydroquinone dehydratase (3-dehydroquinase) (EC 4.2.1.10); 3-dehydroquinone synthase (DHQS) (EC 4.2.3.4); 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS); Shikimate dehydrogenase (EC 1.1.1.25); Shikimate kinase (SK) (EC 2.7.1.71)]
G3YHN0	4955	2	2	Pentafunctional AROM polypeptide [Includes: 3-dehydroquinone dehydratase (3-dehydroquinase) (EC 4.2.1.10); 3-dehydroquinone synthase (DHQS) (EC 4.2.3.4); 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS); Shikimate dehydrogenase (EC 1.1.1.25); Shikimate kinase (SK) (EC 2.7.1.71)]
G3Y6C3	7253	13	2	Phosphoglycerate mutase (EC 5.4.2.-)
A2QHM1	9657	8	2	Protein transport protein sec13
A0A100IBY6	7675	2	2	PT repeat family protein

A0A100INZ0	12228	19	2	Rho GDP-dissociation inhibitor
G3Y1A2	11186	4	2	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit
A0A100IGK5	11015	8	2	Short-chain dehydrogenases/reductase
G3Y384	11607	4	2	Ubiquitinyl hydrolase 1 (EC 3.4.19.12)
A0A117DWH9	9675	4	2	Uncharacterized protein
A0A124BYS2	11374	3	2	Uncharacterized protein
G3XPL1	4939	2	2	Uncharacterized protein
G3Y1D3	7777	2	2	Uncharacterized protein
G3YBW1	13660	7	2	Uncharacterized protein
G3XVI7	5197	13	2	Uncharacterized protein (Fragment)
G3Y1T0	9354	1	2	Uncharacterized protein (Fragment)
A0A100IRD4	3450	4	1	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase
A0A100IJM4	4447	3	1	3'(2'),5'-bisphosphate nucleotidase
G3YDC2	4562	7	1	30kD heat shock protein
A2QCE1	6484	2	1	3-isopropylmalate dehydratase (EC 4.2.1.33) (Alpha-IPM isomerase) (Isopropylmalate isomerase)
A0A100IIB7	8173	4	1	3-ketoacyl-CoA ketothiolase
A0A117E4B2	8964	4	1	3-ketoacyl-CoA thiolase
A0A100IB61	4838	3	1	3-ketoacyl-coA thiolase peroxisomal A
A0A124BWJ7	3803	1	1	3-methylcrotonyl-CoA carboxylase subunit alpha
A0A100ICL4	6905	2	1	6-phosphofructo-2-kinase 1
A0A100IJH8	8847	3	1	AAA family ATPase
A0A100ICU6	3477	1	1	ABC transporter
A0A100IST5	6953	2	1	Acetolactate synthase
A0A124BZ14	5028	4	1	Actin-bundling protein Sac6
A0A117E1J6	4019	6	1	ADP-ribose pyrophosphatase

A0A117DY12	3198	2	1	Alpha/beta hydrolase
A0A100IT77	3896	2	1	Alpha-ketoglutarate dependent xanthine dioxygenase
A0A100I735	4259	2	1	Amino adipic semialdehyde synthase
A0A117DWN7	3268	4	1	Anthranilate phosphoribosyltransferase
A0A100IHG1	4304	1	1	Anucleate primary sterigmata protein A
A0A100IMZ2	4065	3	1	Arginase family protein
A2Q7C2	4484	5	1	Aspergillus niger contig An01c0020, genomic contig
A2Q7W4	6259	4	1	Aspergillus niger contig An01c0080, genomic contig
A2Q878	5311	6	1	Aspergillus niger contig An01c0100, genomic contig (EC 5.3.3.-)
A2QA94	7558	3	1	Aspergillus niger contig An01c0330, genomic contig (EC 3.5.2.3)
A2QBA2	15111	5	1	Aspergillus niger contig An01c0470, genomic contig
A2QCH0	3524	3	1	Aspergillus niger contig An02c0090, genomic contig
A5AAH4	6361	2	1	Aspergillus niger contig An02c0310, genomic contig (EC 1.1.2.4)
A2QEN3	6491	4	1	Aspergillus niger contig An02c0360, genomic contig
A2QGD7	7178	4	1	Aspergillus niger contig An03c0080, genomic contig
A2QGV0	3710	6	1	Aspergillus niger contig An03c0130, genomic contig
A2QHC2	5183	1	1	Aspergillus niger contig An03c0200, genomic contig (EC 2.4.1.16)
A2QHU7	3660	4	1	Aspergillus niger contig An04c0070, genomic contig
A2QIG3	4466	3	1	Aspergillus niger contig An04c0140, genomic contig
A2QIL1	7092	2	1	Aspergillus niger contig An04c0140, genomic contig
A2QMT8	8564	4	1	Aspergillus niger contig An07c0080, genomic contig
A2QMV4	6618	2	1	Aspergillus niger contig An07c0080, genomic contig
A2QMW7	8395	5	1	Aspergillus niger contig An07c0090, genomic contig (EC 1.1.1.-)
A2QMY3	3282	2	1	Aspergillus niger contig An07c0100, genomic contig
A2QPA1	8536	1	1	Aspergillus niger contig An07c0300, genomic contig
A2QPL2	4663	4	1	Aspergillus niger contig An07c0370, genomic contig
A2QQR8	3750	2	1	Aspergillus niger contig An08c0100, genomic contig (EC 3.4.21.-)
A2QRB1	8981	4	1	Aspergillus niger contig An08c0130, genomic contig (EC 2.3.1.16)

A2QTP3	3318	2	1	Aspergillus niger contig An09c0070, genomic contig
A2QUW6	4982	1	1	Aspergillus niger contig An10c0020, genomic contig
A5ABF6	5734	2	1	Aspergillus niger contig An11c0010, genomic contig
A2QVT6	8488	6	1	Aspergillus niger contig An11c0090, genomic contig
A2QWF8	8209	2	1	Aspergillus niger contig An11c0200, genomic contig (Fragment)
A5ABR4	4825	3	1	Aspergillus niger contig An11c0340, genomic contig
A2QYN6	3300	2	1	Aspergillus niger contig An12c0060, genomic contig (EC 2.5.1.29)
A2R0E9	12159	3	1	Aspergillus niger contig An12c0280, genomic contig (EC 3.4.-.-)
A2R1M5	3687	2	1	Aspergillus niger contig An13c0060, genomic contig
A2R3K0	4049	1	1	Aspergillus niger contig An14c0160, genomic contig
A2R3M8	3285	1	1	Aspergillus niger contig An14c0170, genomic contig
A2R3P5	4230	2	1	Aspergillus niger contig An14c0170, genomic contig
A2R3T5	6436	5	1	Aspergillus niger contig An14c0180, genomic contig
A2R3U3	4230	2	1	Aspergillus niger contig An14c0180, genomic contig
A2R424	3765	2	1	Aspergillus niger contig An14c0190, genomic contig
A2R5V8	5229	1	1	Aspergillus niger contig An15c0200, genomic contig
A2R620	3808	1	1	Aspergillus niger contig An15c0210, genomic contig
A2R8L9	4274	2	1	Aspergillus niger contig An16c0230, genomic contig
A2R9B0	11854	6	1	Aspergillus niger contig An17c0030, genomic contig
A2RB76	7983	3	1	Aspergillus niger contig An18c0170, genomic contig
A2QPN1	3656	14	1	Autophagy-related protein 8 (Autophagy-related ubiquitin-like modifier atg8)
A0A100ILA6	4933	3	1	BNR/Asp-box repeat protein
A0A100IBT0	6822	3	1	Branched-chain amino acid aminotransferase
A0A117DZ96	6696	3	1	Calcium/calmodulin-dependent protein kinase
G3Y5W3	4845	1	1	cAMP-dependent protein kinase regulatory subunit
A2QKY5	3571	2	1	Carboxypeptidase (EC 3.4.16.-)
A0A100INJ4	4470	2	1	CBS domain protein



A0A100IP67	10485	4	1	Chitin synthase activator
T1SGS1	7370	3	1	Citrate synthase (Fragment)
A0A0H5ARK2	5654	6	1	Citrate transport protein (Mitochondrial tricarboxylate transporter)
A0A100IKL7	3675	2	1	CMGC/SRPK protein kinase
A0A117DXV8	4594	6	1	Coiled-coil domain-containing protein
A0A124BWT6	4742	2	1	Cyanate hydratase (Cyanase) (EC 4.2.1.104) (Cyanate hydrolase) (Cyanate lyase)
A0A100IAM4	7092	1	1	Dead box ATP-dependent rna helicase
G3Y417	8674	4	1	Decarboxylase yanB (EC 4.1.1.-) (Yanuthone D synthesis protein B)
G3XN75	4707	5	1	Dehydrogenase
A2QAJ5	5625	4	1	Dipeptidase (EC 3.4.13.19)
G3XMY2	7405	1	1	DNA helicase (EC 3.6.4.12)
A0A117DXI6	3456	1	1	DNA polymerase epsilon subunit C
A0A100ITR6	6887	4	1	DnaJ domain protein
A0A117E1K1	5384	3	1	Endo-1,3-beta-glucanase eglC
A0A124BWC6	4232	9	1	ER-derived vesicles protein ERV14
A0A100IJ67	6664	3	1	Fe-containing alcohol dehydrogenase
A0A100INL7	5856	8	1	Fumarylacetoacetate hydrolase family protein
A0A100I3X8	3440	3	1	Gamma-glutamyltranspeptidase
A0A100IPJ9	5786	5	1	GDSL lipase/acylhydrolase family protein
A0A100I6Y8	3675	3	1	Glucooligosaccharide oxidase
G3Y3M0	8507	5	1	Homoserine dehydrogenase (HDH) (EC 1.1.1.3)
A0A100IH16	8444	6	1	Imidazoleglycerol-phosphate dehydratase
E2PSZ3	4726	2	1	IMP-specific 5'-nucleotidase 1 (EC 3.1.3.-)
A0A100IU80	8320	5	1	Inorganic diphosphatase
G3XMB9	3642	3	1	Ketoreductase azaE (EC 1.-.-) (Azaphilone biosynthesis cluster protein azaE)
A0A100I9T7	3660	3	1	Kinase-related protein

A0A100IB39	7093	3	1	Kynurenine aminotransferase
A0A100IPR3	7964	3	1	Lysosomal protective protein
A0A100IGU3	7653	2	1	Mannosyl-oligosaccharide glucosidase
A0A117E128	3847	2	1	Metabolite transport protein
G3XLM4	6559	2	1	Methylenetetrahydrofolate reductase (EC 1.5.1.20)
A0A100IGC7	7893	5	1	Monothiol glutaredoxin-4
A0A117DY30	8155	2	1	mRNA splicing factor
A0A100INU6	7316	2	1	NADH-ubiquinone oxidoreductase 64 kDa subunit
A0A117E493	7020	2	1	Nitrogen assimilation transcription factor NirA
G3Y421	7258	4	1	O-Mevalon transferase yanI (EC 2.-.-) (Yanuthone D synthesis protein I)
A0A100IJZ0	5235	3	1	Oxidoreductase
A0A100I9K6	8329	5	1	Peptide alpha-N-acetyltransferase Nat2
A0A100IL90	3425	1	1	Phosphatidylinositol 3-kinase Tor2
A0A100ILE0	4141	4	1	Phosphoglycerate mutase
A0A117DUZ4	5037	4	1	Phosphoserine phosphatase
A0A100IJ11	8488	2	1	Plasma membrane antiporter
A2RBC2	3468	2	1	Probable carboxypeptidase An18g06210 (EC 3.4.17.-) (Peptidase M20 domain-containing protein An18g06210)
A2RA98	3783	1	1	Protein kinase C (EC 2.7.11.13)
Q00078	4985	1	1	Protein kinase C-like (EC 2.7.11.13)
A0A117E2X4	3555	3	1	RNA-splicing protein MRS3
A0A100IUG1	7195	2	1	Ser/Thr protein phosphatase family
A0A117E3Q4	3197	4	1	SH3 domain protein
A0A100I2E9	4025	2	1	Siderophore biosynthesis protein
Q00179	4189	2	1	Signal recognition particle 54 kDa protein homolog
A2QJF4	6496	2	1	Signal recognition particle subunit SRP72
A0A124BV10	6349	4	1	Similar to An02g04850

A0A100IKI6	4801	6	1	Small nuclear ribonucleoprotein U2, A
A0A100II23	4026	5	1	Suppressor/enhancer of lin-12 protein 9
A0A100IK93	3143	1	1	Transporter mch1
A0A124BWL4	9366	5	1	tRNA methyltransferase subunit GCD14
A2QTW3	3550	13	1	U6 snRNA-associated Sm-like protein LSm2
A0A117DX56	3348	2	1	Ubiquitin fusion degradation protein UfdB
A0A100IGC5	9992	1	1	Uncharacterized protein
A0A100IRC0	4230	2	1	Uncharacterized protein
A0A100ITS4	4960	0	1	Uncharacterized protein
A0A117E225	7857	15	1	Uncharacterized protein
A2R2V5	3201	5	1	Uncharacterized protein
G3XTD1	6203	1	1	Uncharacterized protein
G3XU92	3368	2	1	Uncharacterized protein
G3XVP9	4660	2	1	Uncharacterized protein
G3XY19	9992	4	1	Uncharacterized protein
G3XZP8	4366	4	1	Uncharacterized protein
G3Y822	5546	14	1	Uncharacterized protein
G3YAF7	3379	8	1	Uncharacterized protein
G3YBM9	6027	1	1	Uncharacterized protein
G3YC04	8064	1	1	Uncharacterized protein
G3YC44	3337	1	1	Uncharacterized protein
G3YFP7	4386	5	1	Uncharacterized protein
G3YG83	3270	0	1	Uncharacterized protein
G3YHM6	3451	0	1	Uncharacterized protein
G3XVT5	4785	1	1	Uncharacterized protein (Fragment)
G3Y9V6	8329	10	1	Uncharacterized protein (Fragment)
G3YFM4	3535	1	1	Uncharacterized protein (Fragment)
A0A100I3G4	5317	4	1	Vacuolar protein sorting-associated protein 26

A0A100IHM8	3505	2	1	Vacuolar protein sorting-associated protein 29
A0A100ING1	4359	5	1	Vacuolar protein sorting-associated protein 74
A0A100IKX4	5523	6	1	Xanthine phosphoribosyltransferase 1

Table 2: Differentially identified proteins by *A.niger* IOC 4687 fungus mass spectrometry in presence of Cu<sup>2+</sup> (Uniprot, <http://www.uniprot.org>).

#Acesso	-10lgP	Convergencia (%)	#Peptideos	Proteinas
G3XZT4	39087	46	25	Uncharacterized protein
D7GAW3	36317	57	17	Translation elongation factor 1-alpha (Fragment)
A0A100INN3	26592	36	14	14-3-3 protein
I7B155	25053	53	12	Calmodulin (Fragment)
A2R121	28732	39	11	Aspergillus niger contig An12c0380, genomic contig (EC 1.3.1.-)
A0A100IQ03	27053	35	10	NADH-ubiquinone oxidoreductase 39 kDa subunit
A2R8G7	26480	37	8	Aspergillus niger contig An16c0230, genomic contig (EC 1.1.1.100)
A5ABB4	21941	24	7	Aspergillus niger contig An08c0230, genomic contig (EC 1.1.1.91)
A0A100IPI0	17412	18	7	Heat shock protein 60
A0A100IU47	25347	25	7	Norsolorinic acid reductase
A0A124BW23	16998	14	6	Aminotransferase, classes I and II
A0A100IJG5	16692	18	5	Aflatoxin B1-aldehyde reductase GliO-like
A2Q8R5	17300	19	5	Aspergillus niger contig An01c0190, genomic contig
A2QYU0	17592	19	5	Aspergillus niger contig An12c0070, genomic contig (EC 1.3.1.-)
G3XVT2	21786	12	5	Uncharacterized protein
A2QCS1	18715	4	4	Aspergillus niger contig An02c0120, genomic contig
A2QLM3	14786	8	4	Aspergillus niger contig An06c0090, genomic contig
A2QN65	17996	13	4	Aspergillus niger contig An07c0110, genomic contig (EC 1.1.1.-)
A2QW33	17009	15	4	Aspergillus niger contig An11c0150, genomic contig (EC 1.1.1.195)
A0A117DYG4	14373	7	4	Eukaryotic translation initiation factor eIF-4A subunit, putative [Aspergillus flavus ATP-dependent RNA helicase FAL1 [Aspe
A0A100IAS4	22207	15	4	Uncharacterized protein
G3XUII	16349	14	4	Uncharacterized protein
A0A100IMW8	12331	12	3	Aldo-keto reductase

A2QSY9	13478	14	3	Aspergillus niger contig An09c0020, genomic contig
A2R501	11315	7	3	Aspergillus niger contig An15c0100, genomic contig (EC 1.1.3.13)
A0A100IAW6	16037	9	3	Chitinase
A0A117E3H5	10345	6	3	EH domain binding protein epsin 2
G3XLZ5	13459	15	3	Uncharacterized protein (Fragment)
G3YGP4	9309	6	2	Aldehyde dehydrogenase (EC 1.2.1.3)
A2Q9J5	6576	2	2	Aspergillus niger contig An01c0290, genomic contig (EC 4.1.1.21)
A2QBX5	9255	15	2	Aspergillus niger contig An02c0010, genomic contig (EC 3.4.21.-)
A2QMN7	10199	8	2	Aspergillus niger contig An07c0070, genomic contig
A2QSI3	8992	6	2	Aspergillus niger contig An08c0280, genomic contig (EC 1.2.1.3)
A2QYU3	9242	6	2	Aspergillus niger contig An12c0070, genomic contig (EC 1.3.1.-)
A0A100IJ50	11196	1	2	Cell wall biogenesis protein phosphatase Ssd1
A0A117DX85	5277	10	2	Lectin family integral membrane protein
A0A100IFU7	9654	11	2	Ras family protein (Ras-related protein Rab-6A)
Q078W8	9654	11	2	Secretion related GTPase C
A0A100IFI2	6758	4	2	Translation initiation factor 4B
G3XP29	10868	3	2	Uncharacterized protein
G3Y355	10518	1	2	Uncharacterized protein (Fragment)
A0A117E3A2	6666	2	1	14-alpha sterol demethylase Cyp51B
A0A100ICS8	5832	0	1	1-phosphatidylinositol-3-phosphate 5-kinase
A2Q7G2	5985	2	1	Aspergillus niger contig An01c0030, genomic contig
A2Q9K1	5071	3	1	Aspergillus niger contig An01c0290, genomic contig (EC 1.1.1.184)
A2QBD3	8046	6	1	Aspergillus niger contig An01c0470, genomic contig
A2QC57	4795	1	1	Aspergillus niger contig An02c0040, genomic contig (Fragment)
A2QES6	4827	3	1	Aspergillus niger contig An02c0390, genomic contig
A2QGA4	4585	4	1	Aspergillus niger contig An03c0070, genomic contig
A2QIK6	6057	3	1	Aspergillus niger contig An04c0140, genomic contig
A2QMJ4	8589	5	1	Aspergillus niger contig An07c0050, genomic contig (EC 2.5.1.18)

A2QMP0	4712	4	1	Aspergillus niger contig An07c0080, genomic contig
A2QMR9	4203	0	1	Aspergillus niger contig An07c0080, genomic contig
A2QQP7	3931	7	1	Aspergillus niger contig An08c0100, genomic contig
A2QT31	11510	3	1	Aspergillus niger contig An09c0030, genomic contig (EC 1.14.13.1)
A2QU00	4214	6	1	Aspergillus niger contig An09c0100, genomic contig
A2QUJ9	4227	3	1	Aspergillus niger contig An09c0180, genomic contig
A2QW14	5173	3	1	Aspergillus niger contig An11c0150, genomic contig
A2QY47	5938	9	1	Aspergillus niger contig An11c0400, genomic contig
A2QZJ8	6169	3	1	Aspergillus niger contig An12c0160, genomic contig
A2R113	5553	3	1	Aspergillus niger contig An12c0380, genomic contig (EC 1.-.-)
A2R162	7268	2	1	Aspergillus niger contig An13c0010, genomic contig (EC 1.14.14.-)
A2R2K2	9417	3	1	Aspergillus niger contig An14c0030, genomic contig (Fragment)
A2R2M7	6856	4	1	Aspergillus niger contig An14c0060, genomic contig (EC 1.-.-)
A2R359	4522	1	1	Aspergillus niger contig An14c0130, genomic contig
A2R447	6662	0	1	Aspergillus niger contig An14c0190, genomic contig (Fragment)
A2R455	7921	10	1	Aspergillus niger contig An14c0200, genomic contig
A2R4Z4	6067	0	1	Aspergillus niger contig An15c0100, genomic contig (EC 2.1.1.-)
A2R5T3	6381	3	1	Aspergillus niger contig An15c0190, genomic contig
A2RAX5	6911	1	1	Aspergillus niger contig An18c0160, genomic contig
A2RAX9	5496	1	1	Aspergillus niger contig An18c0160, genomic contig
A0A117E1A8	6650	3	1	BAR adaptor protein RVS167
A0A100I6D3	4228	0	1	Chitin synthase ChsE
A0A100IME7	7402	6	1	Citrate and oxoglutarate carrier protein (DNA replication protein YHM2)
G3Y702	4341	13	1	Cyclin-dependent kinases regulatory subunit
G3XT55	4950	3	1	Dehydrogenase
A0A100IU38	4540	1	1	DNA-binding protein HGH1
A0A100IFR6	6580	5	1	DUF92 domain protein
A0A100I6B8	3970	1	1	Exocyst complex component Exo70

G3XWH2	3658	3	1	Ferulic acid decarboxylase 1 (EC 4.1.1.102) (Phenacrylate decarboxylase)
A0A100ITN0	58,85	2	1	Flavin-binding monooxygenase
Q5F4N6	6938	2	1	Flavo-hemoglobin
A0A100I3C3	5537	2	1	Glutathione transferase
A0A100IUZ3	6257	17	1	Import inner membrane translocase subunit TIM9 (Tim10/DDP family zinc finger family protein)
A0A124BY48	6108	1	1	LMBR1 domain protein
A0A117E0V4	4096	4	1	L-PSP endoribonuclease family protein
A0A100IJX6	3908	8	1	LSM domain family protein (Small nuclear ribonucleoprotein Sm D2)
A0A124BW51	5762	9	1	LSM domain family protein (Small nuclear ribonucleoprotein SmD3)
A0A117E2F8	6766	1	1	MFS transporter
A0A100IMC6	4149	3	1	Mitochondrial fusion protein
P05328	5687	2	1	Multifunctional tryptophan biosynthesis protein [Includes: Anthranilate synthase component 2 (AS) (EC 4.1.3.27) (Anthranilate synthase, glutamine amidotransferase component); Indole-3-glycerol phosphate synthase (IGPS) (EC 4.1.1.48); N-(5'-phosphoribosyl)anthranilate isomerase (PRAI) (EC 5.3.1.24)]
A0A100I973	10135	3	1	NADH oxidase
G3XZG5	3794	2	1	NADH:flavin oxidoreductase
G3XW35	3442	0	1	Non-ribosomal peptide synthetase
A0A100IL69	5865	5	1	Nuclear transport factor 2
A0A100IJE3	4125	1	1	Patched sphingolipid transporter
A0A100I3A5	7972	4	1	Phosphatidyl synthase
A0A100I3L3	3733	1	1	Phosphoribosylaminoimidazole carboxylase
A0A100ISL2	3763	0	1	Polyketide synthase
A0A100IQ55	4532	5	1	Seryl-tRNA synthetase
A0A117DZC7	4295	1	1	Similar to An15g02770
A0A124BZ28	3665	2	1	Sulfite reductase



A0A100IT00	4151	3	1	Tetratricopeptide repeat domain protein
A0A100I5N0	12061	3	1	Translation initiation factor eIF-2B subunit family protein
A2QP99	3486	3	1	Trehalose-6-phosphate synthase (EC 2.4.1.15) (UDP-glucose-glucosephosphate glucosyltransferase)
A0A100IR20	5157	6	1	TrkA-N domain dehydrogenase
A0A124BVK0	3456	0	1	tRNA processing endoribonuclease Trz1
A0A117DWN1	4953	6	1	Ubiquitin conjugating enzyme
A0A100I6G1	9169	1	1	Uncharacterized protein
A0A100IG69	6281	3	1	Uncharacterized protein
A0A100ILR8	5928	4	1	Uncharacterized protein
A0A100IQA7	11002	2	1	Uncharacterized protein
A0A100IUH7	4839	1	1	Uncharacterized protein
A2QR37	10225	6	1	Uncharacterized protein
G3XLR0	4443	3	1	Uncharacterized protein
G3XM24	5785	6	1	Uncharacterized protein
G3XMP2	5877	2	1	Uncharacterized protein
G3XRI8	5816	2	1	Uncharacterized protein
G3XTP0	5433	7	1	Uncharacterized protein
G3XW01	3764	4	1	Uncharacterized protein
G3XW65	4766	3	1	Uncharacterized protein
G3XWJ2	5252	2	1	Uncharacterized protein
G3XXU4	5476	0	1	Uncharacterized protein
G3Y528	5279	6	1	Uncharacterized protein
G3Y6V8	5121	4	1	Uncharacterized protein
G3Y7G1	4791	1	1	Uncharacterized protein
G3YCH9	6051	5	1	Uncharacterized protein
G3YDW1	5299	6	1	Uncharacterized protein
G3YFA3	3734	4	1	Uncharacterized protein

G3Y164	3598	2	1	Uncharacterized protein (Fragment)
G3Y2V8	5003	1	1	Uncharacterized protein (Fragment)
G3Y377	9939	2	1	Uncharacterized protein (Fragment)
G3Y8E7	5167	2	1	Uncharacterized protein (Fragment)
G3YG09	6732	2	1	Uncharacterized protein (Fragment)

