

Additional file 2. All identified intracellular proteins. Classification of intracellular proteins of *A. niger* AB1.13 grown on defined medium with xylose or maltose as carbon substrate that were identified via 2-D GE followed by MALDI ToF MS.

Locus ID ¹	NCBI Accession-No ¹	Gene protein ¹	Function and homolog ¹	MW [Da] ²	pI ³	Macot Score	Spot-No ⁴
Functional classification ¹							
1. Metabolism							
1.1 Carbohydrate metabolism							
Glycolysis / gluconeogenesis							
An03g04530	XP_001390334	beta-PGM	Beta-phosphoglucomutase beta-PGM - <i>L. lactis</i>	27,128	4.92	70	15
An02g07470	XP_001399881	fba1	Fructose-bisphosphate aldolase Fba1 - <i>S. cerevisiae</i>	39,515	5.52	235	39a,b
An14g04920	XP_001401115	tpiA	Triose-phosphate-isomerase tpiA from patent WO8704464-A - <i>A. niger</i>	26,909	5.6	186	44
An16g01830	XP_001397496	gpdA	Glyceraldehyde-3-phosphate dehydrogenase gpdA - <i>A. niger</i>	36,187	6.61	194	75
An08g02260	XP_001392342	pgkA	Phosphoglycerate kinase pgkA - <i>A. nidulans</i>	44,360	6.17	134	66a,b
An18g06250	XP_001399078	eno1	Phosphopyruvate hydratase ENO1 - <i>C. albicans</i>	47,359	5.24	181	27a,b
An07g09530	XP_001392027	pda1	Alpha subunit E1 of the pyruvate dehydrogenase complex Pda1 - <i>S. cerevisiae</i>	45,167	7.64	211	81
An07g06840	XP_001391760	lpd1	Precursor of dihydrolipoamide dehydrogenase Lpd1 - <i>S. cerevisiae</i>	54,924	8.25	164	86
An17g01530	XP_001398382	adhA	Alcohol-dehydrogenase adhA from patent WO8704464-A - <i>A. niger</i>	37,132	6.67	244	76
Citrate cycle (TCA cycle)							
An08g10530	XP_001393157	aco1	Mitochondrial aconitate hydratase Aco1 - <i>S. cerevisiae</i>	84,408	6.18	383	67a,b
An06g00990	XP_001390926	YEL047c	Soluble cytoplasmic fumarate reductase YEL047c - <i>S. cerevisiae</i>	51,722	6.08	75	61
An12g07850	XP_001395836	fumR	Fumarate hydratase fumR - <i>R. oryzae</i>	57,624	8.11	111	85
An07g02160	XP_001391302	mdh1	Mitochondrial malate dehydrogenase Mdh1 - <i>S. cerevisiae</i>	35,735	8.92	262	98a,b
An15g00070	XP_001396546	mdh	Malate dehydrogenase precursor MDH - <i>M. musculus</i>	34,378	6.46	262	72
Pentose phosphate pathway							
An01g14740	XP_001389862	goxC, god	Glucose oxidase precursor goxC - <i>A. niger</i>	65,495	4.94	63	16

An02g02930	XP_001399433	rpiB	Ribose-5-phosphate isomerase rpiB - <i>E. coli</i>	17,157	7.68	68	82
An07g03850	XP_001391467	tal1	Transaldolase Tal1 - <i>S. cerevisiae</i>	35,429	5.57	243	40
Pyruvate metabolism							
An16g07110	XP_001398011	ach1	Acetyl-CoA hydrolase Ach1 - <i>S. cerevisiae</i>	58,145	6.04	129	60
An14g06340	XP_001401257	rsp29	Hydroxyacylglutathione hydrolase RSP29 - <i>R. norvegicus</i>	32,796	6.82	123	78
An08g07290	XP_001392844	aldA	Aldehyde dehydrogenase aldA - <i>A. niger</i>	53,868	6.15	268	65
An11g01120	XP_001394119	alr	NADPH-dependent aldehyde reductase - <i>S. salmonicolor</i>	42,155	6.32	113	71a,b
Sugar metabolism and others							
An01g09960	XP_001389416	xlnD	Xylosidase xlnD - <i>A. niger</i>	87,211	4.76	81	10
An18g03570	XP_001398816	bgl1	Beta-glucosidase bgl1 - <i>A. niger</i>	93,230	4.64	76	8
An01g03740	XP_001388804	xyrA	D-xylose reductase xyrA - <i>A. niger</i>	36,095	5.86	97	52
An01g03480	XP_001388778	gutB	Sorbitol dehydrogenase gutB - <i>B. subtilis</i>	36,901	5.88	85	53
An01g05800	XP_001389004	estf1	Lactone-specific esterase estf1 - <i>P. fluorescens</i>	32,921	8.96	190	100
An01g06970	XP_001389120	ara1	D-arabinose dehydrogenase Ara1 - <i>S. cerevisiae</i>	36,746	5.97	188	57
An15g02300	XP_001396769	abfB	Arabinofuranosidase B abfB - <i>A. niger</i>	52,509	4.23	70	2
An08g01740	XP_001392293	gcy1	Uronate dehydrogenase from patent DE19604798-A1 - <i>S. cerevisiae</i>	33,470	6.1	178	64
1.2 Energy metabolism							
Oxidative phosphorylation and ATP synthesis							
An02g12010	XP_001400329	ipp1	Inorganic pyrophosphatase Ipp1 - <i>S. cerevisiae</i>	32,313	5.23	160	24
An01g03570	XP_001388787	mcr1	Cytochrome-b5 reductase Mcr1 - <i>S. cerevisiae</i>	36,091	8.93	81	99a,b
An09g06650	XP_001393980	-	Core protein II of ubiquinol-cytochrome c reductase CAA42214.1 - <i>B. taurus</i>	47,626	8.83	138	93
An02g04520	XP_001399589	atp5	H ⁺ -transporting ATP synthase delta chain precursor Atp5 - <i>S. cerevisiae</i>	24,326	9.47	136	102
An15g01710	XP_001396710	atp7	F1Fo-ATP synthase subunit 7 ATP7 - <i>K. lactis</i>	19,417	8.73	190	90
Methane metabolism							
An18g05480	XP_001398998	aox1	Alcohol oxidase AOX1 - <i>P. pastoris</i>	74,594	6.57	159	74a,b
An15g02200	XP_001396759	aod1	Alcohol oxidase AOD1 - <i>C. boidinii</i>	65,079	5.44	161	32

An15g00410	XP_001396580	aciA	Acetate-inducible gene aciA - <i>A. nidulans</i> [1-3] (aciA = fdh)	39,510	6.08	187	62
Sulfur metabolism							
An03g00660	XP_001389970	tauD	Taurine dioxygenase tauD - <i>E. coli</i>	41,284	6.1	169	63
An03g02280	XP_001390126	ssuD	FMNH ₂ -dependent aliphatic sulfonate monooxygenase ssuD - <i>E. coli</i>	49,929	8.34	65	88
1.3 Lipid metabolism							
An02g02960	XP_001399436	acbp	Acyl-CoA-binding type 2 protein Acbp - <i>S. carlsbergensis</i>	15,839	5.59	159	43
An04g03360	XP_001401704	aiPLA2	Acidic Ca(2+)-independent phospholipase A2 aiPLA2 - <i>R. norvegicus</i>	23,328	5.2	140	22
1.4 Nucleotide metabolism							
An07g10100	XP_001392085	adk1	Adenylate kinase Adk1 - <i>S. cerevisiae</i>	28,630	8.32	68	87
An02g06030	XP_001399739	uaz	Urate oxidase uaz - <i>A. flavus</i>	34,059	6.84	127	79
An02g10320	XP_001400160	nmt1	Protein nmt1 - <i>A. parasiticus</i>	38,116	5.81	160	51a,b
An09g05870	XP_001393898	ndk-1	Nucleoside-diphosphate kinase NDK-1 - <i>N. crassa</i>	17,008	8.45	86	89
An01g08570	XP_001389279	trxB	Thioredoxin reductase TrxB - <i>P. chrysogenum</i>	39,140	5.19	109	21a,b
1.5 Amino acid metabolism							
An04g06380	XP_001402002	mAspAT	Mitochondrial aspartate aminotransferase mAspAT - <i>M. musculus</i>	47,037	8.92	189	97a,b,c
An02g07430	XP_001399877	YJR139c	Homoserine dehydrogenase YJR139c - <i>S. cerevisiae</i>	38,916	5.49	142	36
An02g07500	XP_001399884	lys1	Saccharopine dehydrogenase LYS1 - <i>C. albicans</i>	41,382	5.12	118	20
An09g03940	XP_001393710	ilv-2	Ketol-acid reductoisomerase ilv-2 - <i>N. crassa</i>	44,559	8.91	166	95
An04g01750	XP_001401543	met6	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase Met6 - <i>S. cerevisiae</i>	87,066	6.23	180	70a,b,c
An08g02700	XP_001392387	eth-1	S-adenosylmethionine synthase eth-1 - <i>N. crassa</i>	42,128	5.7	270	47
An02g12060	XP_001400334	cysB	Hypothetical cystathione beta-synthase cysB - <i>D. discoideum</i>	19,852	5.57	78	41
1.6 Metabolism of cofactors and vitamins							
An11g01630	XP_001394167	nmt2	Thiazole biosynthesis protein nmt2 - <i>S. pombe</i>	35,585	5.48	177	35
An14g02460	XP_001400872	fhbA	Flavohemoglobin FhbA - <i>A. niger</i> [4] (NCBI = fhg = Flavohemoglobin Fhp - <i>A. eutrophus</i>)	45,706	5.44	214	33a,b
1.7 Biodegradation of xenobiotics							
An03g04560	XP_001390337	morA	Morphine dehydrogenase - <i>P. putida</i>	31,387	5.93	55	55

An02g04580	XP_001399596	YAL049c	Hypothetical protein YAL049c - <i>S. cerevisiae</i>	27,613	5.99	77	59
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2. Genetic information processing

2.1 Transcription

An18g02140	XP_001398673	sbp1p	Spi1-GTPase binding protein sbp1p - <i>S. pombe</i>	28,200	4.86	79	12
An01g02880	XP_001388722	cep52	Cytoplasmic ubiquitin / ribosomal fusion protein Cep52 - <i>S. cerevisiae</i>	14,554	9.84	78	104
An11g04510	XP_001394443	sup2	Suppressor 2 Sup2 - <i>S. cerevisiae</i>	77,978	8.83	62	92

2.2 Translation

An08g03490	XP_001392465	ef-1	Elongation factor 1 beta EF-1 - <i>O. cuniculus</i>	33,466	4.55	82	7
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2.3 Sorting and degradation

An12g03910	XP_001395465	pinA	Peptidyl-prolyl cis/trans isomerase pinA - <i>A. nidulans</i>	19,786	6.18	105	68
An02g14800	XP_001400609	pdiA	Protein disulfide isomerase A pdiA - <i>A. niger</i>	56,306	4.48	231	6
An04g02020	XP_001401570	cypB	Cyclophilin cypB - <i>A. nidulans</i>	29,658	6.55	154	73
An14g00850	XP_001400714	fpr1	Peptidyl-prolyl isomerase Fpr1 - <i>S. cerevisiae</i>	11,345	8.79	59	91
An07g08300	XP_001391905	cypA	Cyclophilin-like peptidyl prolyl cis-trans isomerase cypA - <i>A. niger</i>	18,873	8.87	159	94a,b,c
An12g04940	XP_001395564	hsp60	Mitochondrial heat shock protein Hsp60 - <i>S. cerevisiae</i>	61,890	5.51	260	38
An14g04160	XP_001401040	cof1	Cofilin Cof1 - <i>S. cerevisiae</i>	17,090	5.47	72	34
An16g09260	XP_001398224	ssb2	DnaK-type molecular chaperone Ssb2 - <i>S. cerevisiae</i>	66,884	5.24	185	26
An11g04180	XP_001394413	bipA	DnaK-type molecular chaperone bipA - <i>A. niger</i>	73,459	4.96	163	18
An05g00810	XP_001390658	TbcA	Tubulin-specific chaperone A TBCA - <i>O. cuniculus</i>	13,369	5.57	91	42
An07g05920	XP_001391670	cypD	Estrogen receptor-binding cyclophilin cypD - <i>B. taurus</i>	41,129	5.91	188	54
An18g02020	XP_001398661	tigA	Disulfide isomerase tigA - <i>A. niger</i>	38,592	5.49	128	37a,b
An02g07210	XP_001399855	pepE	Aspartic protease pepE - <i>A. niger</i>	43,395	4.85	66	11
An08g11190	XP_001393220	ank1	Ankyrin Ank1 - <i>M. musculus</i>	97,785	5.67	58	46
An02g01550	XP_001399295	CS-Ag	Secreted serine protease 19 kDa CS antigen CS-Ag - <i>C. immitis</i>	15,163	4.24	91	3
An07g03880	XP_001391470	pepC	Serine proteinase pepC - <i>A. niger</i>	52,803	5.23	72	23

An13g00760	XP_001396216	tpm1	Tropomyosin Tpm1 - <i>S. cerevisiae</i>	18,873	4.94	59	17
An12g08760	XP_001395927	vma-4	Vacuolar ATPase subunit E Vma-4 - <i>N. crassa</i>	26,037	5.33	188	29
An02g06360	XP_001399773	arc16	Arp2/3 complex 16kD subunit arc16 - <i>H. sapiens</i>	20,395	5.43	70	31a,b

3. Cellular processes (cell cycle and morphogenesis)

An14g03180	XP_001400943	cdc3p	Profilin cdc3p - <i>S. pombe</i>	13,772	5.72	57	48
An16g05020	XP_001397810	vip1p	Protein vip1p - <i>S. pombe</i>	27,778	5.73	118	49
An04g07010	XP_001402062	caM	Calmodulin caM - <i>A. nidulans</i>	17,013	4.11	77	1
An01g11960	XP_001389605	bfr1	Brefeldin A resistance protein Bfr1 - <i>S. cerevisiae</i>	56,744	8.98	112	101
An02g06710	XP_001399806	mpt4	Suppressor of tom1 protein Mpt4 - <i>S. cerevisiae</i>	33,399	9.65	144	103
An14g05320	XP_001401155	wos2p	Cell cycle regulator p21 protein wos2p - <i>S. pombe</i>	21,937	4.44	81	5
An02g09550	XP_001400085	het-c2	Protein het-c2 - <i>P. anserina</i>	22,105	6.93	68	80
An16g03740	XP_001397686	pkaR	cAMP-dependent protein kinase regulatory subunit pkaR - <i>A. niger</i>	44,536	4.89	77	14

4. Others

4.1 Stress response

An04g04060	XP_001401773	ccp1	Cytochrome-c peroxidase precursor Ccp1 - <i>S. cerevisiae</i>	40,220	7.73	93	83a,b
An16g00920	XP_001397405	pmp20	Peroxisomal membrane protein PMP20 - <i>C. boidinii</i>	17,828	5.63	78	45
An01g02500	XP_001388687	-	Thioredoxin - <i>A. nidulans</i>	11,914	5.32	82	28
An02g12270	XP_001400355	grrbp2	Glycine-rich RNA-binding protein grrbp2 - <i>E. esula</i>	12,842	5.79	68	50a,b
An12g00790	XP_001395168	sti1	Stress-induced protein Sti1 - <i>S. cerevisiae</i>	69,875	5.98	119	58
An07g04570	XP_001391539	hex1	Hex1 - <i>A. nidulans</i>	24,123	6.76	164	77a,b,c
An01g01830	XP_001388622	cpeB	Catalase/peroxidase cpeB - <i>S. reticuli</i>	84,251	6.19	151	69
An07g03770	XP_001391459	sodC	Cu,Zn superoxide dismutase sodC - <i>A. fumigatus</i>	15,960	5.94	97	56a,b
An12g08570	XP_001395908	prxII	Type 2 peroxiredoxin PrxII - <i>B. napus</i>	18,586	5.38	127	30a,b,c

4.2 Virulence factors

An01g09980	XP_001389418	Asp-HS	Hemolysin Asp-HS - <i>A. fumigatus</i>	16,259	7.81	91	84
An01g10050	XP_001389424	IgE-HRF	IgE-dependent histamine-releasing factor - <i>H. sapiens</i>	20,275	4.72	65	9

4.3 Unclassified

An02g05620	XP_001399698	-	Hypothetical protein encoded by An07g10060 - <i>A. niger</i>	7,972	4.86	82	13
An07g03660	XP_001391449	-	Hypothetical protein CAD37045.1 - <i>N. crassa</i> (similar to An09g00630)	28,769	8.91	92	96
An08g10030	XP_001393111	-	Hypothetical MF-7 antigenic protein from patent WO9721817-A1 - <i>M. sp.</i>	12,710	5.23	76	25
An09g00630	XP_001393387	cipC	Hypothetical cipC - <i>A. nidulans</i>	12,607	5.09	76	19
An09g06410	XP_001393955	-	Hypothetical protein EAA66742.1 - <i>A. nidulans</i>	27,897	4.32	98	4a,b

¹ Accession numbers and gene/protein names are according to the sequenced genome of *A. niger* [5] and the NCBI Reference Sequence database (<http://www.ncbi.nlm.nih.gov/refseq/>). For those proteins annotated as “hypothetical protein” (most proteins of *A. niger*), the similarity information provided in the NCBI annotation in the section “CDS” is shown instead. Genes/proteins in bold are proven genes/proteins of *A. niger*. Functional classification is mostly according to KEGG PATHWAY database (<http://www.genome.jp/kegg/metabolism.html>). Annotations deviating from the current NCBI Reference Sequence database (status 2010-03-26) are indicated with a reference proving annotation.

² Theoretical pI not considering potential posttranslational modifications (determined using: http://www.expasy.ch/cgi-bin/pi_tool).

³ Theoretical average mass not considering potential posttranslational modifications (determined using: http://www.expasy.ch/cgi-bin/pi_tool).

⁴ “Spot-No” indicates the serial number of all identified protein spots of the intracellular proteome of *A. niger* AB1.13 from xylose and maltose grown cultures on the interactive and searchable 2-D gels (Additional files 3 and 4, respectively).

References

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- 2 Chow CM, RajBhandary UL: **Developmental regulation of the gene for formate dehydrogenase in *Neurospora crassa*.** *J Bacteriol* 1993, **175**: 3703-3709.
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