

## Supporting Information

### **Identifying biochemical constituents involved in the mycosynthesis of zinc oxide nanoparticles**

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**Table S1.** Proteome of *Aspergillus niger* following 1 mM Zn challenge.

#	Accession	Description	Coverage [%]	# Peptides
1	A0A124BW99	3-isopropylmalate dehydrogenase OS= <i>Aspergillus niger</i> OX=5061 GN=ABL_02721 PE=3 SV=1	2	1
2	A0A100I9W6	4-hydroxyphenylpyruvate dioxygenase OS= <i>Aspergillus niger</i> OX=5061 GN=ABL_02088 PE=3 SV=1	10	1
3	A0A117DYT5	5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase OS= <i>Aspergillus niger</i> OX=5061 GN=ABL_02132 PE=3 SV=1	1	1
4	A0A319A3N3	AB hydrolase-1 domain-containing protein OS= <i>Aspergillus lacticoffeatus</i> (strain CBS 101883) OX=1450533 GN=BO96DRAFT_342582 PE=4 SV=1	5	1
5	A0A505HX38	ABC transporter family protein OS= <i>Aspergillus niger</i> OX=5061 GN=CAN33_0042725 PE=4 SV=1	7	1
6	A0A100IQI4	ABC transporter OS= <i>Aspergillus niger</i> OX=5061 GN=ABL_08150 PE=4 SV=1	4	1
7	Q1JTV6	Acetyl-CoA carboxylase OS= <i>Aspergillus niger</i> OX=5061 GN=accA PE=4 SV=1	0	1
8	A0A370BHM8	Alcohol dehydrogenase OS= <i>Aspergillus niger</i> ATCC 13496 OX=1353008 GN=M747DRAFT_335378 PE=4 SV=1	3	1
9	A0A100IRC6	Alcohol dehydrogenase OS= <i>Aspergillus niger</i> OX=5061 GN=ABL_08421 PE=3 SV=1	6	1
10	A0A370BGA4	Alcohol oxidase OS= <i>Aspergillus niger</i> ATCC 13496 OX=1353008 GN=M747DRAFT_362794 PE=3 SV=1	4	1
11	A0A319AH66	Aldo/keto reductase OS= <i>Aspergillus</i> <i>lacticoffeatus</i> (strain CBS 101883) OX=1450533 GN=BO96DRAFT_226298 PE=4 SV=1	8	1
12	A0A319A7L9	Aldo/keto reductase OS= <i>Aspergillus</i> <i>lacticoffeatus</i> (strain CBS 101883) OX=1450533 GN=BO96DRAFT_395911 PE=4 SV=1	6	1
13	A0A117DWV8	alpha-galactosidase OS= <i>Aspergillus niger</i> OX=5061 GN=ABL_01986 PE=4 SV=1	5	1
14	A0A254TL69	Alpha/beta hydrolase family protein OS= <i>Aspergillus niger</i> OX=5061 GN=ATCC64974_109640 PE=4 SV=1	1	1
15	A0A100ISX4	Amidohydrolase family protein OS= <i>Aspergillus niger</i> OX=5061 GN=ABL_09395 PE=4 SV=1	7	1
16	A0A117E0L8	AMP dependent CoA ligase OS= <i>Aspergillus</i> <i>niger</i> OX=5061 GN=ABL_05403 PE=4 SV=1	4	1
17	A0A319AKQ2	ANK_REP_REGION domain-containing	3	1

		protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_497773 PE=4 SV=1		
18	A0A10011T8	Ankyrin repeat-containing protein, putative OS=Aspergillus niger OX=5061 GN=ABL_00023 PE=4 SV=1	3	1
19	A0A117E351	APH domain-containing protein OS=Aspergillus niger OX=5061 GN=ABL_09199 PE=4 SV=1	6	1
20	A0A505IE24	ATP synthase F1, beta subunit OS=Aspergillus niger OX=5061 GN=CAN33_0027245 PE=4 SV=1	7	1
21	A0A370C3R5	ATP synthase subunit d, mitochondrial OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_294127 PE=3 SV=1	16	1
22	A0A370BYZ1	ATP-dependent RNA helicase DED1 OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_235958 PE=3 SV=1	2	1
23	A0A254UFH6	beta-glucosidase OS=Aspergillus niger OX=5061 GN=ATCC64974_91770 PE=3 SV=1	5	1
24	A0A319AA60	BZIP domain-containing protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_456833 PE=4 SV=1	2	1
25	A0A100IGA6	BZIP-type transcription factor OS=Aspergillus niger OX=5061 GN=ABL_03762 PE=4 SV=1	3	1
26	G3Y1Z3	CAP-Gly domain-containing protein OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_206560 PE=3 SV=1	1	1
27	A0A100IJ86	Carboxylic ester hydrolase OS=Aspergillus niger OX=5061 GN=ABL_04880 PE=3 SV=1	4	1
28	A0A370C5Q8	CHAT domain-containing protein OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_235560 PE=3 SV=1	2	2
29	A0A117E1A3	chitin synthase OS=Aspergillus niger OX=5061 GN=ABL_06376 PE=4 SV=1	1	1
30	A0A117E2D8	Chromatin-remodeling ATPase INO80 OS=Aspergillus niger OX=5061 GN=ABL_08056 PE=3 SV=1	1	1
31	A2Q8M3	Contig An01c0170, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An01g04860 PE=4 SV=1	8	1
32	A2Q917	Contig An01c0230, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An01g06320	4	1

		PE=4 SV=1		
33	A2QAK7	Contig An01c0350, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An01g11860 PE=4 SV=1	2	1
34	A2QAZ0	Contig An01c0400, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An01g13280 PE=4 SV=1	1	1
35	A2QKD4	Contig An04c0390, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An04g10230 PE=3 SV=1	2	1
36	A2QLH1	Contig An06c0070, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An06g01180 PE=4 SV=1	5	1
37	A2QSN4	Contig An08c0280, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An08g11350 PE=4 SV=1	5	1
38	A2QTH2	Contig An09c0050, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An09g02100 PE=4 SV=1	1	1
39	A2QYD0	Contig An12c0030, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An12g00800 PE=4 SV=1	1	1
40	A2QZW5	Contig An12c0190, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An12g06470 PE=4 SV=1	3	1
41	A2R110	Contig An12c0370, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An12g10530 PE=4 SV=1	2	1
42	A2R248	Contig An13c0110, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An13g03520 PE=4 SV=1	3	1
43	A2R3X7	Contig An14c0180, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An14g05840 PE=4 SV=1	4	1
44	A2R4R4	Contig An15c0090, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An15g01320 PE=3 SV=1	1	1
45	A2R5X6	Contig An15c0200, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An15g05900	8	1

		PE=4 SV=1		
46	A2R701	Contig An16c0070, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An16g01800 PE=4 SV=1	3	1
47	A2R8G7	Contig An16c0230, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An16g07090 PE=4 SV=1	6	1
48	A2R984	Contig An17c0020, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An17g00470 PE=4 SV=1	11	1
49	A2RAU5	Contig An18c0150, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An18g04370 PE=4 SV=1	81	1
50	A0A117DXJ9	CrpH protein OS=Aspergillus niger OX=5061 GN=ABL_02506 PE=3 SV=1	2	1
51	A0A505IPU9	Cyclic nucleotide-binding domain family protein OS=Aspergillus niger OX=5061 GN=CAN33_0035860 PE=4 SV=1	5	1
52	A0A370BPR4	Cytochrome P450 OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_335399 PE=4 SV=1	3	1
53	A0A3F3RRN7	Cytoplasmic protein OS=Aspergillus niger OX=5061 GN=ATCC64974_83590 PE=4 SV=1	18	1
54	A2QGI9	D-arabinono-1,4-lactone oxidase OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An03g03460 PE=3 SV=1	4	1
55	A0A319AA99	Delta-aminolevulinic acid dehydratase OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_412557 PE=3 SV=1	7	1
56	A0A100INU1	Dihydroxy-acid dehydratase OS=Aspergillus niger OX=5061 GN=ABL_07287 PE=3 SV=1	5	1
57	A0A319A6B3	Dipeptidyl-peptidase V OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_415625 PE=3 SV=1	3	1
58	A0A254UH30	DNA polymerase kappa OS=Aspergillus niger OX=5061 GN=ATCC64974_40550 PE=4 SV=1	2	1
59	A0A3F3R8X9	DNA repair protein RAD16 OS=Aspergillus niger OX=5061 GN=ATCC64974_23690 PE=3 SV=1	4	1
60	A0A100I3M4	DNA repair protein Rad50 OS=Aspergillus niger OX=5061 GN=ABL_00526 PE=3 SV=1	1	1
61	A0A100ICF8	Dolichyl-phosphate-mannose--protein mannosyltransferase OS=Aspergillus niger OX=5061 GN=ABL_02731 PE=3 SV=1	3	1
62	G3XU68	DUF2007 domain-containing protein	5	1

		OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_43889 PE=4 SV=1		
63	G3XYR9	Dynein light intermediate chain OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_181494 PE=4 SV=1	2	1
64	A2R4M7	E3 ubiquitin protein ligase OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An15g00950 PE=3 SV=1	2	1
65	A0A100I6Z2	Efflux pump antibiotic resistance protein OS=Aspergillus niger OX=5061 GN=ABL_01342 PE=4 SV=1	2	1
66	A0A319AXN7	ELMO domain-containing protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_428019 PE=4 SV=1	3	1
67	A0A100IGB1	Enoyl-CoA hydratase/isomerase family protein OS=Aspergillus niger OX=5061 GN=ABL_03776 PE=4 SV=1	6	1
68	A0A319AWI5	Eukaryotic translation initiation factor 3 subunit A OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=TIF32 PE=3 SV=1	2	1
69	A0A319AS46	Eukaryotic translation initiation factor 3 subunit E OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=INT6 PE=3 SV=1	5	1
70	G3Y7T4	FAD_binding_3 domain-containing protein OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_44604 PE=4 SV=1	7	1
71	A0A505ILT5	Fatty acid synthase OS=Aspergillus niger OX=5061 GN=CAN33_0051120 PE=4 SV=1	0	1
72	A0A254UE40	Flavin containing amine oxidoreductase family protein OS=Aspergillus niger OX=5061 GN=ATCC64974_33860 PE=4 SV=1	2	1
73	A0A100IDC3	FSH1 domain-containing protein OS=Aspergillus niger OX=5061 GN=ABL_02989 PE=4 SV=1	4	1
74	G3XPX6	Fungal_trans domain-containing protein OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_44761 PE=4 SV=1	4	1

75	G3Y0E5	G_PROTEIN_RECEP_F2_4 domain-containing protein (Fragment) OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_181551 PE=4 SV=1	7	1
76	A0A370C116	General substrate transporter OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_296052 PE=3 SV=1	3	1
77	A0A319A327	Glutamine synthetase/guanido kinase OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_343380 PE=3 SV=1	4	1
78	A0A124BUR9	Glycogen debranching enzyme Gdb1 OS=Aspergillus niger OX=5061 GN=ABL_00375 PE=4 SV=1	1	1
79	G3Y3Q0	Glycos_transf_1 domain-containing protein OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_52318 PE=4 SV=1	1	1
80	A0A3F3R6T1	Glycosidase OS=Aspergillus niger OX=5061 GN=ATCC64974_14620 PE=3 SV=1	2	1
81	A0A370BT40	GTP-binding protein Obg OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_297006 PE=4 SV=1	4	1
82	A0A100IIZ3	HEAT repeat protein OS=Aspergillus niger OX=5061 GN=ABL_04748 PE=4 SV=1	1	1
83	A0A319BB09	HET domain-containing protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_502130 PE=4 SV=1	4	1
84	A0A100IUP3	HET domain-containing protein OS=Aspergillus niger OX=5061 GN=ABL_10193 PE=4 SV=1	3	1
85	A0A370BUC2	IPT/TIG domain-containing protein OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_66209 PE=4 SV=1	2	1
86	Q6RZ15	Ketosynthase (Fragment) OS=Aspergillus niger OX=5061 PE=4 SV=1	11	1
87	A0A370BVT3	Kinase-like protein (Fragment) OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_284773 PE=4 SV=1	9	1
88	G3Y1G7	Kinesin-like protein OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_206452 PE=3 SV=1	3	1
89	A0A100I5M6	Kinesin-like protein OS=Aspergillus niger OX=5061 GN=ABL_01077 PE=3 SV=1	3	1

90	A0A254UGL8	Mediator of RNA polymerase II transcription subunit 12 OS=Aspergillus niger OX=5061 GN=ATCC64974_94900 PE=3 SV=1	1	1
91	A0A117DUP2	MesA OS=Aspergillus niger OX=5061 GN=ABL_00298 PE=4 SV=1	3	1
92	A0A370BVA2	Metallo-dependent hydrolase OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_282090 PE=4 SV=1	4	1
93	A0A319AKK6	MFS domain-containing protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_497262 PE=3 SV=1	3	1
94	A0A319AK89	MFS general substrate transporter OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_435090 PE=4 SV=1	3	1
95	A0A100ICG2	MFS monosaccharide transporter OS=Aspergillus niger OX=5061 GN=ABL_02730 PE=3 SV=1	2	1
96	A0A117E3H1	MFS transporter OS=Aspergillus niger OX=5061 GN=ABL_09739 PE=4 SV=1	5	1
97	A0A505HXE4	Mitochondrial 54S ribosomal protein YmL24/YmL14 OS=Aspergillus niger OX=5061 GN=CAN33_002395 PE=3 SV=1	4	1
98	A0A100IFQ1	Mitochondrial thiamine pyrophosphate carrier 1 OS=Aspergillus niger OX=5061 GN=ABL_03598 PE=3 SV=1	4	1
99	A0A117DZQ5	N-acetyltransferase complex ARD1 subunit OS=Aspergillus niger OX=5061 GN=ABL_04136 PE=3 SV=1	9	1
100	A0A100IU28	N2,N2-dimethylguanosine tRNA methyltransferase OS=Aspergillus niger OX=5061 GN=ABL_09986 PE=3 SV=1	4	1
101	A0A100I720	NAD_binding_9 domain-containing protein OS=Aspergillus niger OX=5061 GN=ABL_01165 PE=4 SV=1	5	1
102	A0A319ACJ4	NB-ARC domain-containing protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_392709 PE=4 SV=1	1	1
103	A0A319AIT3	Ntox15 domain-containing protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_486782 PE=4 SV=1	5	1
104	A0A100I939	Nuclear condensin complex subunit 3 OS=Aspergillus niger OX=5061 GN=ABL_01943 PE=3 SV=1	2	1
105	A0A370CBX7	Nuclear protein export protein Yrb2 OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_301174 PE=4 SV=1	5	1
106	A0A319AHF5	Nuclear RNA binding protein OS=Aspergillus	2	1



		lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_410156 PE=4 SV=1		
107	A0A370BT93	Nucleolar protein 12 OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_266812 PE=3 SV=1	4	1
108	A2QIU5	oxoglutarate dehydrogenase (succinyl- transferring) OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An04g04750 PE=3 SV=1	1	1
109	A0A319AHX1	P-loop containing nucleoside triphosphate hydrolase protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_386832 PE=4 SV=1	3	1
110	A0A100IPC8	P-loop containing nucleoside triphosphate hydrolase protein OS=Aspergillus niger OX=5061 GN=ABL_07557 PE=4 SV=1	5	1
111	A0A319A823	Peptidase inhibitor I78 family protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_53946 PE=4 SV=1	29	1
112	A0A3F3RNC4	peptidylprolyl isomerase OS=Aspergillus niger OX=5061 GN=ATCC64974_72870 PE=4 SV=1	3	1
113	A0A254U6F1	Permease for cytosine/purine, uracil, thiamine, allantoin family protein OS=Aspergillus niger OX=5061 GN=ATCC64974_26260 PE=3 SV=1	21	2
114	A0A254TPQ3	Peroxidase, 2 family protein OS=Aspergillus niger OX=5061 GN=ATCC64974_97090 PE=4 SV=1	1	1
115	A0A100IP08	PHD finger domain protein OS=Aspergillus niger OX=5061 GN=ABL_07072 PE=3 SV=1	2	1
116	A0A124BWL5	Phospholipase/carboxylesterase superfamily OS=Aspergillus niger OX=5061 GN=ABL_03207 PE=4 SV=1	13	1
117	G3XXP5	Phospholipid-transporting ATPase OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_182985 PE=3 SV=1	1	1
118	G3XZA5	Polarized growth protein Boi2 OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_209479 PE=4 SV=1	1	1
119	A0A117E1C4	Polyketide synthase P OS=Aspergillus niger OX=5061 GN=ABL_06494 PE=4 SV=1	2	1
120	A0A370C821	polynucleotide adenyllyltransferase OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_171340 PE=3	2	1

		SV=1		
121	G3Y7J6	Probable glucan endo-1,3-beta-glucosidase eglC OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_44517 PE=3 SV=1	3	1
122	A0A100IK34	Probable vacuolar protein sorting-associated protein 16 homolog OS=Aspergillus niger OX=5061 GN=ABL_05364 PE=3 SV=1	1	1
123	A0A117E1S8	Protein kinase domain-containing protein OS=Aspergillus niger OX=5061 GN=ABL_07156 PE=4 SV=1	1	1
124	A0A319A1X1	Protein kinase Scy1 OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_374092 PE=4 SV=1	3	1
125	A0A254TYY7	Putative endo-1, 4-beta-xylanase B domain protein OS=Aspergillus niger OX=5061 GN=ATCC64974_22520 PE=4 SV=1	7	1
126	A0A370CDI9	Putative mitochondria protein Fmp29 OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_336513 PE=4 SV=1	5	1
127	A0A100IDS0	Proline-5-carboxylate reductase OS=Aspergillus niger OX=5061 GN=ABL_03113 PE=3 SV=1	8	1
128	A0A254UBC1	Raptor N-terminal CASPase like domain family protein OS=Aspergillus niger OX=5061 GN=ATCC64974_47480 PE=4 SV=1	9	1
129	A0A100IN58	Related to regulatory protein amdA OS=Aspergillus niger OX=5061 GN=ABL_06592 PE=4 SV=1	4	1
130	A0A254UE20	Retinol dehydrogenase 12 OS=Aspergillus niger OX=5061 GN=ATCC64974_26640 PE=4 SV=1	5	1
131	A0A319AGZ1	Rho guanyl nucleotide exchange factor OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_397420 PE=4 SV=1	3	1
132	A0A117DV89	Ribosome biogenesis protein OS=Aspergillus niger OX=5061 GN=ABL_00747 PE=4 SV=1	1	1
133	A0A370CFT5	RING finger domain protein OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_301143 PE=4 SV=1	5	1
134	A0A370BZ11	RraA-like protein OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_238911 PE=4 SV=1	3	1
135	A0A505IGI7	rRNA processing/ribosome biogenesis family protein OS=Aspergillus niger OX=5061 GN=CAN33_0036120 PE=3 SV=1	1	1
136	A0A100I4A7	RTA1 domain protein OS=Aspergillus niger	7	1

		OX=5061 GN=ABL_00705 PE=4 SV=1		
137	A0A370CBS1	SEC7 domain-containing protein OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_154736 PE=4 SV=1	2	1
138	A0A100I343	Secretion pathway protein Sls2/Rcy1 OS=Aspergillus niger OX=5061 GN=ABL_00381 PE=4 SV=1	3	1
139	A0A370CG90	Serine/threonine-protein kinase Tel1 OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_365830 PE=3 SV=1	1	1
140	A0A100IUG8	Short-chain dehydrogenase/reductase family protein OS=Aspergillus niger OX=5061 GN=ABL_10235 PE=4 SV=1	8	1
141	A0A100IRB0	Similar to alanine racemase domain protein OS=Aspergillus niger OX=5061 GN=ABL_08575 PE=3 SV=1	5	1
142	A0A100I7L7	Similar to An01g11830 OS=Aspergillus niger OX=5061 GN=ABL_01534 PE=4 SV=1	5	1
143	A0A100I8R1	Similar to An02g09040 OS=Aspergillus niger OX=5061 GN=ABL_01827 PE=4 SV=1	5	1
144	A0A100I8R3	Similar to An02g09290 OS=Aspergillus niger OX=5061 GN=ABL_01848 PE=4 SV=1	5	1
145	A0A100IBH3	Similar to An04g07160 OS=Aspergillus niger OX=5061 GN=ABL_02535 PE=4 SV=1	8	1
146	A0A100IDW3	Similar to An07g04590 OS=Aspergillus niger OX=5061 GN=ABL_03147 PE=4 SV=1	1	1
147	A0A100INV3	Similar to An11g09480 OS=Aspergillus niger OX=5061 GN=ABL_07314 PE=4 SV=1	16	1
148	A0A100IKK4	Similar to An14g01950 OS=Aspergillus niger OX=5061 GN=ABL_05603 PE=4 SV=1	9	1
149	A0A117DZ24	Similar to An15g05930 OS=Aspergillus niger OX=5061 GN=ABL_03604 PE=4 SV=1	25	1
150	A0A319A4R6	Similar to OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_425271 PE=4 SV=1	10	1
151	A0A100ICIO	Similar to OS=Aspergillus niger OX=5061 GN=ABL_02761 PE=4 SV=1	8	1
152	A0A319BAR4	Solid-state culture specific protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_397855 PE=4 SV=1	4	1
153	A0A319ATM9	Superoxide dismutase [Cu-Zn] OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_495966 PE=3 SV=1	6	1
154	A2R622	T-complex protein 1 subunit alpha OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An15g06370 PE=3 SV=1	5	1
155	G3Y5R8	T-complex protein 1 subunit zeta	2	1

		OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_201109 PE=3 SV=1		
156	A0A319AS63	Tetratricopeptide repeat domain protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_436346 PE=4 SV=1	2	1
157	A0A100IDC9	Thiolase-like protein OS=Aspergillus niger OX=5061 GN=ABL_02716 PE=4 SV=1	1	1
158	A0A319AFH4	Thioredox_DsbH domain-containing protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_332328 PE=4 SV=1	2	1
159	A0A318ZU33	TPR-like protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_353132 PE=4 SV=1	2	1
160	A0A319AME1	TPR-like protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_492219 PE=4 SV=1	3	1
161	A0A319ALC4	Transcription factor hoxa13 OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_338958 PE=4 SV=1	3	1
162	A0A117DW75	Transcription factor TFIIA complex subunit Toa1 OS=Aspergillus niger OX=5061 GN=ABL_01455 PE=3 SV=1	9	1
163	A0A124BVE9	tRNA wybutosine-synthesizing protein 4 OS=Aspergillus niger OX=5061 GN=ABL_01386 PE=4 SV=1	4	1
164	A0A319BDK2	type II protein arginine methyltransferase OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_453273 PE=3 SV=1	2	1
165	A0A505IBB1	U3 snoRNA associated family protein OS=Aspergillus niger OX=5061 GN=CAN33_008050 PE=4 SV=1	5	1
166	A0A319C263	Uncharacterized protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_496195 PE=4 SV=1	2	1
167	A2QBQ4	Uncharacterized protein OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An02g00860 PE=4 SV=1	6	1
168	A2QC66	Uncharacterized protein OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An02g02450 PE=4 SV=1	3	1
169	A2QIV1	Uncharacterized protein OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) OX=425011 GN=An04g04830 PE=4 SV=1	46	1
170	A2QX72	Uncharacterized protein OS=Aspergillus niger	7	1

		(strain CBS 513.88 / FGSC A1513) OX=425011 GN=An11g07870 PE=4 SV=1		
171	A0A370C924	Uncharacterized protein OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_293410 PE=4 SV=1	4	1
172	A0A370C9G4	Uncharacterized protein OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_294057 PE=4 SV=1	7	1
173	A0A100IL12	Unnamed protein product OS=Aspergillus niger OX=5061 GN=ABL_05820 PE=3 SV=1	6	1
174	A0A124BXQ9	Unnamed protein product OS=Aspergillus niger OX=5061 GN=ABL_05838 PE=4 SV=1	5	1
175	A0A100IS93	Unnamed protein product OS=Aspergillus niger OX=5061 GN=ABL_08842 PE=3 SV=1	3	1
176	A0A124BYV6	Unnamed protein product OS=Aspergillus niger OX=5061 GN=ABL_09407 PE=4 SV=1	1	1
177	A0A100IU45	Unnamed protein product OS=Aspergillus niger OX=5061 GN=ABL_10000 PE=4 SV=1	7	1
178	A0A100IUI7	Unnamed protein product OS=Aspergillus niger OX=5061 GN=ABL_10258 PE=4 SV=1	9	1
179	A0A117E491	Unnamed protein product OS=Aspergillus niger OX=5061 GN=ABL_10276 PE=4 SV=1	2	1
180	G3Y0X4	Vacuolar segregation protein OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) OX=380704 GN=ASPNIDRAFT_207173 PE=4 SV=1	1	1
181	A0A100IKN8	Vegetative cell wall protein gp1 OS=Aspergillus niger OX=5061 GN=ABL_05301 PE=4 SV=1	10	1
182	A0A100IJN2	VHS domain protein OS=Aspergillus niger OX=5061 GN=ABL_05127 PE=4 SV=1	8	1
183	A0A124BXS5	WD domain containing protein OS=Aspergillus niger OX=5061 GN=ABL_05972 PE=4 SV=1	3	1
184	A0A318ZVS9	WD domain protein OS=Aspergillus lacticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_427533 PE=4 SV=1	5	1
185	A0A117DV01	Zinc knuckle transcription factor OS=Aspergillus niger OX=5061 GN=ABL_00565 PE=4 SV=1	1	1
186	A0A254TW09	Zinc-binding dehydrogenase family protein OS=Aspergillus niger OX=5061 GN=ATCC64974_52450 PE=4 SV=1	3	1
187	A0A370C4R8	Zn(2)-C6 fungal-type domain-containing protein OS=Aspergillus niger ATCC 13496 OX=1353008 GN=M747DRAFT_26933 PE=4 SV=1	9	1
188	A0A100I4L5	Zn(2)-C6 fungal-type domain-containing protein OS=Aspergillus niger OX=5061 GN=ABL_00793 PE=4 SV=1	6	1

189	A0A319A7T1	Zn(II)2Cys6 transcription factor OS=Aspergillus laticoffeatus (strain CBS 101883) OX=1450533 GN=BO96DRAFT_136839 PE=4 SV=1	3	1
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OS = Organism Name; OX = Organism Identifier; GN = Gene Name; PE = Protein Existence; SV = Sequence Version.

**Table S2.** Proteome of *Aspergillus versicolor* following 1 mM Zn challenge.

#	Accession	Description	Coverage [%]	# Peptides
1	A0A1L9PMT1	3-ketosteroid reductase OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_132993 PE=4 SV=1	2	1
2	A0A1L9PRL7	3-oxoacid CoA-transferase OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_63628 PE=3 SV=1	5	2
3	A0A1L9PYK9	Abhydrolase_4 domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_32920 PE=4 SV=1	14	1
4	A0A1L9PUZ2	Actin cytoskeleton-regulatory complex protein PAN1 OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_55278 PE=3 SV=1	1	1
5	A0A1L9PI02	ANK_REP_REGION domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_40727 PE=4 SV=1	4	1
6	A0A1L9PEG7	AT DNA binding protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_127334 PE=4 SV=1	1	1
7	A0A1L9P4F3	ATP-dependent Clp protease OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_23400 PE=4 SV=1	4	1
8	A0A1L9PZX6	Cell pattern formation-associated protein stuA OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_56565 PE=4 SV=1	4	1
9	A0A1L9PM18	CRAL-TRIO domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_683286 PE=4 SV=1	3	1
10	A0A1L9P378	CULLIN_2 domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_48278 PE=3 SV=1	1	1
11	A0A1L9PBX4	Cytochrome P450 OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_50570 PE=3 SV=1	4	1
12	A0A1L9P543	Double-strand break repair protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_182449 PE=3 SV=1	3	1
13	A0A1L9P7S5	EHN domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_59247 PE=3 SV=1	3	1

14	A0A1L9P7A6	Elongation factor 1-beta OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_36821 PE=3 SV=1	9	1
15	A0A1L9Q041	FAD_binding_3 domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_201722 PE=4 SV=1	3	1
16	A0A1L9PXR6	FAD-binding PCMH-type domain- containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_32615 PE=3 SV=1	4	1
17	A0A1L9Q0H0	FAD-binding PCMH-type domain- containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_56697 PE=4 SV=1	3	1
18	A0A1L9PHA0	Fatty acid synthase subunit alpha OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_593098 PE=3 SV=1	2	2
19	A0A1L9PYD8	Fungal_trans domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_87828 PE=4 SV=1	5	1
20	A0A1L9PQJ6	G-patch domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_133656 PE=4 SV=1	6	1
21	A0A1L9Q109	Glycos_transf_1 domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_46734 PE=4 SV=1	1	1
22	A0A1L9P6X7	Gmp synthase OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_277587 PE=4 SV=1	8	1
23	A0A1L9PAC7	Helicase C-terminal domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_161747 PE=4 SV=1	2	1
24	A0A1L9PNN3	HET domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_42645 PE=4 SV=1	3	1
25	A0A1L9PSL1	histone acetyltransferase OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_54661 PE=3 SV=1	1	1
26	A0A1L9PA07	hydroxyacid-oxoacid transhydrogenase OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_124745 PE=3 SV=1	3	1
27	A0A1L9PB22	Importin N-terminal domain-containing	2	1



		protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_38167 PE=4 SV=1		
28	A0A1L9PHK9	J domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_40513 PE=4 SV=1	3	1
29	A0A1L9PTS2	Magnesium transporter OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_44450 PE=3 SV=1	5	1
30	A0A1L9PPK9	MFS domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_134352 PE=4 SV=1	2	1
31	A0A1L9Q1B0	MFS domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_370275 PE=4 SV=1	4	1
32	A0A1L9Q5E2	MFS domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_48072 PE=4 SV=1	7	1
33	A0A1L9P4E8	MYB family conidiophore development protein F1bD OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_157666 PE=4 SV=1	5	1
34	A0A1L9P463	MYND-type zinc finger protein samB OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_231328 PE=3 SV=1	7	2
35	A0A1L9PB84	NAD(P)-binding protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_147977 PE=4 SV=1	10	1
36	A0A1L9PUT3	NAD(P)-binding protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_55240 PE=3 SV=1	10	1
37	A0A1L9PZW1	Nucleoporin POM33 OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_354776 PE=3 SV=1	8	1
38	A0A1L9PVH6	Oxidoreductase OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_86892 PE=4 SV=1	9	1
39	A0A1L9PHE0	Piwi domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_82417 PE=4 SV=1	2	1
40	A0A1L9P620	PKS_ER domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_183056 PE=3 SV=1	10	1
41	A0A1L9P4I2	Plasma membrane ATPase OS=Aspergillus versicolor CBS 583.65	2	1

		OX=1036611 GN=ASPVEDRAFT_35829 PE=3 SV=1		
42	A0A1L9PN34	PNK3P-domain-containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_42469 PE=4 SV=1	5	1
43	A0A1L9P7X2	Pre-mRNA splicing factor clf1 OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_120958 PE=4 SV=1	4	1
44	A0A1L9PN68	Proteasome component OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_72741 PE=4 SV=1	1	1
45	A0A1L9PQE3	Protein ecm33 OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_133806 PE=4 SV=1	6	1
46	A0A1L9PJ13	Rad4 transglutaminase-like domain- containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_41066 PE=3 SV=1	4	1
47	A0A1L9P806	RNA polymerase-associated protein LEO1 OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_122579 PE=4 SV=1	4	1
48	A0A1L9PEM7	Similar to OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_51191 PE=4 SV=1	5	1
49	A0A1L9PMB1	Spindle pole body component alp14 OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_131415 PE=4 SV=1	2	1
50	A0A1L9PIR4	Threonylcarbamoyl-AMP synthase OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_52330 PE=3 SV=1	2	1
51	A0A1L9P6M2	tRNA-dihydrouridine(47) synthase [NAD(P)(+)] OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_24145 PE=3 SV=1	3	1
52	A0A1L9Q280	Uncharacterized protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_47078 PE=4 SV=1	13	1
53	A0A1L9Q453	Zn(2)-C6 fungal-type domain- containing protein OS=Aspergillus versicolor CBS 583.65 OX=1036611 GN=ASPVEDRAFT_57603 PE=4 SV=1	5	1

OS = Organism Name; OX = Organism Identifier; GN = Gene Name; PE = Protein Existence; SV = Sequence Version.

**Table S3.** Proteome of *Cladosporium cladosporioides* following 1 mM Zn challenge.

#	Accession	Description	Coverage [%]	# Peptides
1	A0A0Y0M151	Highly reducing polyketide synthase cla2 OS=Cladosporium cladosporioides OX=29917 GN=cla2 PE=1 SV=1	2	2
2	A8C2B6	Histone H3 (Fragment) OS=Cladosporium aff. cladosporioides CBS 673.69 OX=470196 PE=3 SV=1	28	1
3	A0A076JS36	Methyltransferase domain-containing protein OS=Cladosporium cladosporioides virus 1 OX=1529605 PE=4 SV=1	6	1
4	G9FT48	Polyketide synthase (Fragment) OS=Cladosporium cladosporioides OX=29917 GN=pks1 PE=4 SV=1	28	2
5	A0A0X8DS88	Putative glycoside hydrolase OS=Cladosporium cladosporioides OX=29917 PE=2 SV=1	5	1
6	A0A076JYE6	Putative RNA-dependent RNA polymerase OS=Cladosporium cladosporioides virus 1 OX=1529605 PE=4 SV=1	1	1
7	B0L807	Vacuolar serine protease (Fragment) OS=Cladosporium cladosporioides OX=29917 PE=2 SV=1	6	1

OS = Organism Name; OX = Organism Identifier; GN = Gene Name; PE = Protein Existence; SV = Sequence Version.

**Table S4.** Proteome of *Paecilomyces variotii* following 1 mM Zn challenge.

#	Accession	Description	Coverage [%]	# Peptides
1	A0A443HXN1	Acetyl-CoA carboxylase OS=Byssoschlamys spectabilis OX=264951 GN=C8Q69DRAFT_526400 PE=4 SV=1	0	1
2	V5FU02	Acyl-CoA thioester hydrolase OS=Byssoschlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_4171 PE=4 SV=1	3	1
3	A0A443HP93	Acyl-CoA thioesterase OS=Byssoschlamys spectabilis OX=264951 GN=C8Q69DRAFT_474121 PE=3 SV=1	10	1
4	A0A443I5L1	ADP-ribose 1''-phosphate phosphatase OS=Byssoschlamys spectabilis OX=264951 GN=C8Q69DRAFT_425998 PE=3 SV=1	8	1
5	A0A443HMS9	ADP-ribosylation factor GTPase- activating protein OS=Byssoschlamys spectabilis OX=264951 GN=C8Q69DRAFT_59829 PE=4 SV=1	1	1
6	A0A443HJL3	ANK_REP_REGION domain-containing protein OS=Byssoschlamys spectabilis OX=264951 GN=C8Q69DRAFT_448048 PE=4 SV=1	1	1
7	V5HW50	Aspartokinase OS=Byssoschlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_2605 PE=3 SV=1	5	1
8	V5I0P8	BTB domain and ankyrin repeat protein OS=Byssoschlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_4744 PE=4 SV=1	2	1
9	V5FM31	Carboxymethylenebutenolidase OS=Byssoschlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_1527 PE=3 SV=1	1	1
10	A0A443I8E9	Carboxypeptidase OS=Byssoschlamys spectabilis OX=264951 GN=C8Q69DRAFT_484887 PE=3 SV=1	3	1
11	A0A443I3X2	Cerato-platanin OS=Byssoschlamys spectabilis OX=264951 GN=C8Q69DRAFT_183704 PE=3 SV=1	10	1
12	V5FV50	chitinase OS=Byssoschlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_4576 PE=3 SV=1	2	1
13	V5GCB6	CMGC/CDK/CDK5 protein kinase OS=Byssoschlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009	3	1

		GN=PVAR5_8425 PE=3 SV=1		
14	V5I3X8	DNA-directed RNA polymerase subunit beta OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_6663 PE=3 SV=1	2	1
15	A0A443HM53	DUF2088 domain-containing protein OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_500729 PE=4 SV=1	7	1
16	A0A443HV26	DUF2236 domain-containing protein OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_486643 PE=4 SV=1	5	1
17	V5I5G2	FAD binding domain protein OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_8011 PE=3 SV=1	3	1
18	V5FW90	Flavin-nucleotide-binding protein OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_1468 PE=4 SV=1	7	1
19	A0A443HK18	glutamine--tRNA ligase OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_480150 PE=3 SV=1	2	1
20	V5G6T2	Involucrin repeat protein, putative (Fragment) OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_8926 PE=4 SV=1	0	1
21	A0A443HXM7	Lipa and NB-ARC domain protein OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_248774 PE=4 SV=1	1	1
22	A0A443I4B5	Nucleoporin NUP37 OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_396353 PE=4 SV=1	4	1
23	V5G4V1	Oxalate decarboxylase OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_8183 PE=4 SV=1	6	1
24	A0A443HWF7	Pentatricopeptide repeat protein OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_464253 PE=4 SV=1	3	1
25	V5I1X2	Phosphatidate cytidyltransferase, putative OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_5455 PE=4 SV=1	6	1
26	A0A443HW63	Phosphatidylinositol 3-kinase VPS34	3	1

		OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_230358 PE=3 SV=1		
27	A0A443HJC8	Phosphotransferase enzyme family protein OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_501658 PE=4 SV=1	4	1
28	V5FXF2	Protein kinase domain-containing protein OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_5443 PE=4 SV=1	2	1
29	A0A443HMA6	Protein transport protein SEC22 OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_513969 PE=3 SV=1	11	1
30	A0A443I8H4	Putative ABC transporter OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_513375 PE=4 SV=1	2	1
31	A0A443HYS5	Putative ribonuclease P complex subunit Pop1 OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_461649 PE=4 SV=1	3	1
32	A0A443HR32	Putative ubiquitin-conjugating enzyme Ubc6 OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_404844 PE=4 SV=1	10	1
33	A0A443HQ17	SCD domain-containing protein OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_472050 PE=4 SV=1	1	1
34	V5FQ97	SH3 domain-containing protein OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_9000 PE=4 SV=1	1	1
35	V5FJF1	Shugoshin OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_6657 PE=3 SV=1	4	1
36	A0A443HSQ9	Small secreted protein OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_508163 PE=4 SV=1	21	3
37	A0A443HXA5	Spindle pole body component OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_431804 PE=3 SV=1	2	1
38	V5FYX7	Sugar transporter family protein OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_3560 PE=3 SV=1	5	1

39	V5F844	Terpenoid synthase OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_0620 PE=4 SV=1	3	1
40	A0A443I8M7	THO complex subunit 2 OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_495578 PE=3 SV=1	1	1
41	V5HTS4	Uncharacterized protein OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_1539 PE=4 SV=1	15	1
42	V5GDD7	Uncharacterized protein OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) OX=1356009 GN=PVAR5_7640 PE=4 SV=1	10	1
43	A0A443HKJ7	ZT_dimer domain-containing protein OS=Byssochlamys spectabilis OX=264951 GN=C8Q69DRAFT_94699 PE=4 SV=1	6	1

OS = Organism Name; OX = Organism Identifier; GN = Gene Name; PE = Protein Existence; SV = Sequence Version.

**Table S5.** Proteome of *Penicillium chrysogenum* following 1 mM Zn challenge.

#	Accession	Description	Coverage [%]	# Peptides
1	AOA167T7D6	Chromatin assembly factor 1 subunit OS=Penicillium chrysogenum OX=5076 GN=EN45_065260 PE=4 SV=1	4	1
2	AOA167UIR0	Chromatin structure-remodeling complex subunit OS=Penicillium chrysogenum OX=5076 GN=EN45_079080 PE=4 SV=1	1	1
3	AOA167SX13	Fidgetin-like protein OS=Penicillium chrysogenum OX=5076 GN=EN45_062170 PE=4 SV=1	4	1
4	AOA167TPR9	GPI-anchored cell surface glycoprotein OS=Penicillium chrysogenum OX=5076 GN=EN45_070670 PE=4 SV=1	2	1
5	AOA167QFB8	HET domain-containing protein OS=Penicillium chrysogenum OX=5076 GN=EN45_088330 PE=4 SV=1	3	1
6	AOA162BDK5	Interferon-induced GTP-binding protein OS=Penicillium chrysogenum OX=5076 GN=EN45_108450 PE=4 SV=1	3	1
7	B6GYS0	Pc12g01310 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc12g01310 PE=4 SV=1	9	1
8	B6H0V6	Pc12g03270 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc12g03270 PE=4 SV=1	5	1
9	B6H1E9	Pc13g02790 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc13g02790 PE=4 SV=1	5	1
10	B6H314	Pc13g15820 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc13g15820 PE=3 SV=1	5	1
11	B6HDE3	Pc20g07370 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc20g07370 PE=4 SV=1	5	1
12	B6HGB8	Pc20g11840 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc20g11840 PE=4 SV=1	5	1



13	B6HHI3	Pc21g05370 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc21g05370 PE=4 SV=1	7	1
14	B6HKG0	Pc21g07340 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc21g07340 PE=4 SV=1	9	1
15	B6HJ37	Pc21g19250 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc21g19250 PE=4 SV=1	2	1
16	B6HPZ0	Pc22g15540 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc22g15540 PE=4 SV=1	4	1
17	B6HSF4	Pc22g17300 protein OS=Penicillium rubens (strain ATCC 28089 / DSM 1075 / NRRL 1951 / Wisconsin 54-1255) OX=500485 GN=Pc22g17300 PE=4 SV=1	2	1
18	AOA167SKS7	Protein NipSnap-like protein OS=Penicillium chrysogenum OX=5076 GN=EN45_058600 PE=3 SV=1	2	1
19	AOA167TKX5	Putative quinone oxidoreductase OS=Penicillium chrysogenum OX=5076 GN=EN45_069590 PE=4 SV=1	5	1
20	AOA167WFH0	Vacuolar calcium ion transporter OS=Penicillium chrysogenum OX=5076 GN=EN45_017260 PE=3 SV=1	5	1

OS = Organism Name; OX = Organism Identifier; GN = Gene Name; PE = Protein Existence; SV = Sequence Version.

**Table S6.** Comparison across five fungal proteomes (like proteins highlighted in yellow).

Protein Identifier	<i>Aspergillus niger</i>	<i>Aspergillus versicolor</i>	<i>Cladosporium cladosporioides</i>	<i>Paecilomyces variotii</i>	<i>Penicillium chrysogenum</i>
3-isopropylmalate dehydrogenase	X				
3-ketosteroid reductase		X			
3-oxoacid CoA-transferase		X			
4-hydroxyphenylpyruvate dioxygenase	X				
5-methyltetrahydropteroyl-triglutamate-homocysteine S-methyltransferase	X				
AB hydrolase-1 domain-containing protein	X				
ABC transporter	X				
ABC transporter family protein	X				
Abhydrolase_4 domain-containing protein		X			
Acetyl-CoA carboxylase	X			X	
Actin cytoskeleton-regulatory complex protein PAN1		X			
Acyl-CoA thioester hydrolase				X	
Acyl-CoA thioesterase				X	
ADP-ribose 1"-phosphate phosphatase				X	
ADP-ribosylation factor GTPase-activating protein				X	
Alcohol dehydrogenase	X				
Alcohol oxidase	X				
Aldo/keto reductase	X				
Alpha/beta hydrolase family protein	X				
Alpha-galactosidase	X				
Amidohydrolase family protein	X				
AMP dependent CoA ligase	X				
ANK_REP_REGION domain-containing protein	X	X		X	
Ankyrin repeat-containing protein, putative	X				
APH domain-containing protein	X				
Aspartokinase				X	
AT DNA binding protein		X			

<b>Protein Identifier</b>	<b><i>Aspergillus niger</i></b>	<b><i>Aspergillus versicolor</i></b>	<b><i>Cladosporium cladosporioides</i></b>	<b><i>Paecilomyces variotii</i></b>	<b><i>Penicillium chrysogenum</i></b>
ATP synthase F1, beta subunit	X				
ATP synthase subunit d, mitochondrial	X				
ATP-dependent Clp protease		X			
ATP-dependent RNA helicase DED1	X				
Beta-glucosidase	X				
BTB domain and ankyrin repeat protein				X	
BZIP domain-containing protein	X				
BZIP-type transcription factor	X				
CAP-Gly domain-containing protein	X				
Carboxylic ester hydrolase	X				
Carboxymethylenebutenolidase				X	
Carboxypeptidase				X	
Cell pattern formation-associated protein stuA		X			
Cerato-platanin				X	
CHAT domain-containing protein	X				
Chitin synthase	X				
Chitinase				X	
Chromatin assembly factor 1 subunit					
Chromatin structure-remodeling complex subunit					
Chromatin-remodeling ATPase INO80	X				X
CMGC/CDK/CDK5 protein kinase				X	X
CRAL-TRIO domain-containing protein		X			
CrpH protein	X				
CULLIN_2 domain-containing protein		X			
Cyclic nucleotide-binding domain family protein	X				
Cytochrome P450	X	X			
Cytoplasmic protein	X				
D-arabinono-1,4-lactone oxidase	X				
Delta-aminolevulinic acid dehydratase	X				
Dihydroxy-acid dehydratase	X				
Dipeptidyl-peptidase V	X				

<b>Protein Identifier</b>	<b><i>Aspergillus niger</i></b>	<b><i>Aspergillus versicolor</i></b>	<b><i>Cladosporium cladosporioides</i></b>	<b><i>Paecilomyces variotii</i></b>	<b><i>Penicillium chrysogenum</i></b>
DNA polymerase kappa	X				
DNA repair protein RAD16	X				
DNA repair protein Rad50	X				
DNA-directed RNA polymerase subunit beta				X	
Dolichyl-phosphate-mannose--protein mannosyltransferase	X				
Double-strand break repair protein		X			
DUF2007 domain-containing protein	X				
DUF2088 domain-containing protein				X	
DUF2236 domain-containing protein				X	
Dynein light intermediate chain	X				
E3 ubiquitin protein ligase	X				
Efflux pump antibiotic resistance protein	X				
EHN domain-containing protein		X			
ELMO domain-containing protein	X				
Elongation factor 1-beta		X			
Enoyl-CoA hydratase/isomerase family protein	X				
Eukaryotic translation initiation factor 3 subunit A & E	X				
FAD binding domain protein				X	
FAD_binding_3 domain-containing protein	X	X			
FAD-binding PCMH-type domain-containing protein		X			
Fatty acid synthase	X	X			
Fidgetin-like protein					
Flavin containing amine oxidoreductase family protein	X				
Flavin-nucleotide-binding protein				X	X
FSH1 domain-containing protein	X				
Fungal trans domain-containing protein	X	X			
G_Protein_Recep_F2_4 domain-containing protein (Fragment)	X				
General substrate transporter	X				

Protein Identifier	<i>Aspergillus niger</i>	<i>Aspergillus versicolor</i>	<i>Cladosporium cladosporioides</i>	<i>Paecilomyces variotii</i>	<i>Penicillium chrysogenum</i>
Glutamine synthetase/guanido kinase	X				
Glutamine--tRNA ligase				X	
Glycogen debranching enzyme Gdb1	X				
Glycos_transf_1 domain-containing protein	X	X			
Glycosidase	X				
GMP synthase		X			
G-patch domain-containing protein		X			
GPI-anchored cell surface glycoprotein					
GTP-binding protein Obg	X				
HEAT repeat protein	X				X
Helicase C-terminal domain-containing protein		X			
HET domain-containing protein	X	X			
Highly reducing polyketide synthase cla2			X		
Histone acetyltransferase		X			
Histone H3 (Fragment)			X		X
Hydroxyacid-oxoacid transhydrogenase		X			
Importin N-terminal domain-containing protein		X			
Interferon-induced GTP-binding protein					
Involucrin repeat protein, putative (Fragment)				X	
IPT/TIG domain-containing protein	X				X
J domain-containing protein		X			
Ketosynthase (Fragment)	X				
Kinase-like protein (Fragment)	X				
Kinesin-like protein	X				
Lipa and NB-ARC domain protein				X	
Magnesium transporter		X			
Mediator of RNA polymerase II transcription subunit 12	X				
MesA	X				
Metallo-dependent hydrolase	X				

Protein Identifier	<i>Aspergillus niger</i>	<i>Aspergillus versicolor</i>	<i>Cladosporium cladosporioides</i>	<i>Paecilomyces variotii</i>	<i>Penicillium chrysogenum</i>
Methyltransferase domain-containing protein			X		
MFS domain-containing protein	X	X			
MFS general substrate transporter	X				
MFS monosaccharide transporter	X				
MFS transporter	X				
Mitochondrial 54S ribosomal protein YmL24/YmL14	X				
Mitochondrial thiamine pyrophosphate carrier 1	X				
MYB family conidiophore development protein FlbD		X			
MYND-type zinc finger protein samB		X			
N2,N2-dimethylguanosine tRNA methyltransferase	X				
N-acetyltransferase complex ARD1 subunit	X				
NAD(P)-binding protein	X	X			
NB-ARC domain-containing protein	X				
Ntox15 domain-containing protein	X				
Nuclear condensin complex subunit 3	X				
Nuclear protein export protein Yrb2	X				
Nuclear RNA binding protein	X				
Nucleolar protein 12	X				
Nucleoporin NUP37				X	
Nucleoporin POM33		X			
Oxalate decarboxylase				X	
Oxidoreductase		X			
Oxoglutarate dehydrogenase (succinyl-transferring)	X				
Pentatricopeptide repeat protein				X	
Peptidase inhibitor I78 family protein	X				
Peptidylprolyl isomerase	X				
Permease for cytosine/purine, uracil, thiamine, allantoin family protein	X				
Peroxidase, 2 family protein	X				
PHD finger domain protein	X				
Phosphatidate cytidyltransferase,				X	

Protein Identifier	<i>Aspergillus niger</i>	<i>Aspergillus versicolor</i>	<i>Cladosporium cladosporioides</i>	<i>Paecilomyces variotii</i>	<i>Penicillium chrysogenum</i>
putative					
Phosphatidylinositol 3-kinase VPS34				X	
Phospholipase/carboxylesterase superfamily	X				
Phospholipid-transporting ATPase	X				
Phosphotransferase enzyme family protein				X	
Piwi domain-containing protein		X			
PKS_ER domain-containing protein		X			
Plasma membrane ATPase		X			
P-loop containing nucleoside triphosphate hydrolase protein	X				
PNK3P-domain-containing protein		X			
Polarized growth protein Boi2	X				
Polyketide synthase	X		X		
Polynucleotide adenylyltransferase	X				
Pre-mRNA splicing factor clf1		X			
Probable glucan endo-1,3-beta-glucosidase eglC	X				
Probable vacuolar protein sorting-associated protein 16 homolog	X				
Proteasome component		X			
Protein ecm33		X			
Protein kinase domain-containing protein	X			X	
Protein kinase Scy1	X				
Protein NipSnap-like protein					
Protein transport protein SEC22				X	
Putative ABC transporter				X	X
Putative endo-1, 4-beta-xylanase B domain protein	X				
Putative glycoside hydrolase			X		
Putative mitochondria protein Fmp29	X				
Putative quinone oxidoreductase					X
Putative ribonuclease P complex subunit Pop1				X	
Putative RNA-dependent RNA polymerase			X		X

<b>Protein Identifier</b>	<b><i>Aspergillus niger</i></b>	<b><i>Aspergillus versicolor</i></b>	<b><i>Cladosporium cladosporioides</i></b>	<b><i>Paecilomyces variotii</i></b>	<b><i>Penicillium chrysogenum</i></b>
Putative ubiquitin-conjugating enzyme Ubc6				X	
Pyrroline-5-carboxylate reductase	X				
Rad4 transglutaminase-like domain-containing protein		X			
Raptor N-terminal CASPase like domain family protein	X				
Related to regulatory protein amdA	X				
Retinol dehydrogenase 12	X				
Rho guanyl nucleotide exchange factor	X				
Ribosome biogenesis protein	X				
RING finger domain protein	X				
RNA polymerase-associated protein LEO1		X			
RraA-like protein	X				
rRNA processing/ribosome biogenesis family protein	X				
RTA1 domain protein	X				
SCD domain-containing protein				X	
SEC7 domain-containing protein	X				
Secretion pathway protein Sls2/Rcy1	X				
Serine/threonine-protein kinase Tel1	X				
SH3 domain-containing protein				X	
Short-chain dehydrogenase/reductase family protein	X				
Shugoshin				X	
Spindle pole body component		X		X	
Sugar transporter family protein				X	
Superoxide dismutase [Cu-Zn]	X				
T-complex protein 1 subunit alpha	X				
T-complex protein 1 subunit zeta	X				
Terpenoid synthase				X	
Tetratricopeptide repeat domain protein	X				
Thiolase-like protein	X				
Thioredox_DsbH domain-containing protein	X				



<b>Protein Identifier</b>	<i>Aspergillus niger</i>	<i>Aspergillus versicolor</i>	<i>Cladosporium cladosporioides</i>	<i>Paecilomyces variotii</i>	<i>Penicillium chrysogenum</i>
THO complex subunit 2				X	
Threonylcarbamoyl-AMP synthase		X			
TPR-like protein	X				
Transcription factor hoxa13	X				
Transcription factor TFIIA complex subunit Toa1	X				
tRNA wybutosine-synthesizing protein 4	X				
tRNA-dihydrouridine(47) synthase [NAD(P)(+)]		X			
Type II protein arginine methyltransferase	X				
U3 snoRNA associated family protein	X				
Vacuolar calcium ion transporter					
Vacuolar segregation protein	X				
Vacuolar serine protease (Fragment)			X		X
Vegetative cell wall protein gp1	X				
VHS domain protein	X				
WD domain containing protein	X				
Zinc knuckle transcription factor	X				
Zinc-binding dehydrogenase family protein	X				
Zn(2)-C6 fungal-type domain-containing protein	X	X			
Zn(II)2Cys6 transcription factor	X				
ZT dimer domain-containing protein				X	
<b>Total Count = 222</b>	<b>135</b>	<b>47</b>	<b>7</b>	<b>40</b>	<b>9</b>

**Table S7.** Mean and SE for two fungi at each of four stages.

<b>Fungus</b>	<b>Group</b>	<b>Mean</b>	<b>SEM</b>
<i>A. versicolor</i>	Post-Growth	24.2	1.4
	Before Filtration	40.1	1.4
	After Filtration	18.6	1.8
	48 h Post-Spike	18.2	1.4
<i>C. cladosporioides</i>	Post-Growth	20.1	1.4
	Before Filtration	20.8	1.4
	After Filtration	18.0	1.8
	48 h Post-Spike	17.2	1.4

**Table S8.** Comparisons for factor: Stage within *A. versicolor*.

<b>Comparison</b>	<b>Diff of Means</b>	<b>t</b>	<b>P</b>	<b>P&lt;0.050</b>
Before Filtration vs. 48 h post-spike	22.0	10.830	<0.001	Yes
Before Filtration vs. After Filtration	21.5	9.497	<0.001	Yes
Before Filtration vs. Post-Growth	16.0	7.886	<0.001	Yes
Post-Growth vs. 48 h Post-Spike	6.0	2.945	0.016	Yes
Post-Growth vs. After Filtration	5.5	2.444	0.037	Yes
After Filtration vs. 48 h Post-Spike	0.4	0.190	0.850	No

**Table S9.** Comparisons for factor: Stage within *C. cladosporioides*.

<b>Comparison</b>	<b>Diff of Means</b>	<b>t</b>	<b>P</b>	<b>P&lt;0.050</b>
Before Filtration vs. 48 h Post-Spike	3.6	1.758	0.417	No
Post-Growth vs. 48 h Post-Spike	2.8	1.406	0.599	No
Before Filtration vs. After Filtration	2.8	1.244	0.631	No
Post-Growth vs. After Filtration	2.1	0.928	0.736	No
Before Filtration vs. Post-Growth	0.7	0.353	0.925	No
After Filtration vs. 48 h Post-Spike	0.7	0.329	0.925	No

**Table S10.** Protein levels between both fungi compared at each stage in the process.

<b>Factors compared between fungi</b>	<b>Diff of Means</b>	<b>t</b>	<b>P</b>	<b>P&lt;0.050</b>
Post-Growth	4.1	2.022	0.050	Yes
Before Filtration	19.3	9.555	<0.001	Yes
After Filtration	0.7	0.267	0.791	No
48 h Post-Spike	1.0	0.483	0.632	No

**Table S11.** Top 25 metabolites in *Aspergillus niger* exudate following 1 mM Zn challenge.

Number of Metabolite	<i>Aspergillus niger</i>	
	Name of metabolite	% of total
1	Hexylamine	12.63
2	Sulfamic acid	6.07
3	4-Imidazolemethanol	5.60
4	(1S,4S)-4-Hydroxy-3-oxocyclohexanecarboxylic acid	4.94
5	N6-Acetyl-L-lysine*	3.52
6	L-Pyroglutamic acid*	2.50
7	N6,N6,N6-Trimethyl-L-lysine*	1.77
8	Cyclohexane	1.71
9	2'-O-Methyladenosine*	1.62
10	N-(Carboxymethyl)norleucine	1.45
11	⊖*	1.02
12	NP-012972*	0.93
13	Palmitoleic Acid*	0.90
14	13(S)-HOTrE*	0.88
15	Pyrimidine	0.86
16	Allysine	0.85
17	[Similar to: Thiamine; ΔMass: -0.2644 Da]*	0.78
18	2-Heptyl-4,5-dimethyl-1,3-oxazole	0.74
19	Triacetin	0.67
20	Dichloroacetic acid	0.63
21	16±-Hydroxydehydroepiandrosterone 3-sulfate	0.61
22	Bis(methylbenzylidene)sorbitol*	0.61
23	2-Hydroxyfelbamate	0.60
24	1-(1H-Imidazol-5-yl)-3-(phosphonoxy)-2-propanone	0.59
25	(12Z)-9,10,11-trihydroxyoctadec-12-enoic acid*	0.57
<b>% of Metabolome By Top 25 Hits (Grand Total)</b>		<b>53.05</b>

LEGEND	
*	MS2-based match (higher confidence level)
⊖	[Similar to: 2-[3-chloro-2-hydroxy-4-methoxy-6-(methoxycarbonyl)phenoxy]-6-hydroxy-4-methylbenzoic acid; ΔMass: -6.7938 Da]
ψ	4-(2,6-dimethylphenyl)-5-(7-oxabicyclo[2.2.1]hept-2-yl)-2,4-dihydro-3H-1,2,4-triazole-3-thione
Ω	5,7-dihydroxy-2-(4-hydroxy-3-methoxyphenyl)-3,4-dihydro-2H-1-benzopyran-4-one
Λ	(2S)-4-Methyl-2-(((3S,4S,5R)-2,3,4-trihydroxy-5-(hydroxymethyl)tetrahydro-2-furanyl)methyl)amino)pentanoic acid
⊕	2-[[2Z)-2-((4-[(3-Aminopropyl)amino]butyl)imino)-2-hydroxyethyl]-2-hydroxysuccinic acid

**Table S12.** Top 25 metabolites in *Aspergillus versicolor* exudate following 1 mM Zn challenge.

Number of Metabolite	<i>Aspergillus versicolor</i>	
	Name of metabolite	% of total
1	Sulfamic acid	12.47
2	Hexylamine	8.79
3	4-Imidazolemethanol	5.40
4	δ-Valerolactam*	4.44
5	Aminopyrrolnitrin	2.70
6	Thiamine*	2.66
7	2'-O-Methyladenosine*	1.96
8	O-ureido-D-serine	1.93
9	Isovalerylglutamic acid*	1.49
10	Fomepizole	1.41
11	[Similar to: Thiamine; ΔMass: -0.2644 Da]*	1.41
12	L-alpha-Glycerolphosphorylcholine	1.28
13	1-(1H-Imidazol-5-yl)-3-(phosphonoxy)-2-propanone	1.25
14	cGMP	1.24
15	Pyrimidine	1.20
16	Ω*	1.20
17	Θ*	1.05
18	Hexamethylenetetramine*	0.75
19	Apocynin	0.73
20	L-Pyroglutamic acid*	0.71
21	Ψ*	0.68
22	Acetylcholine*	0.64
23	S-(-)-Raclopride*	0.63
24	D-ribosylnicotinate	0.62
25	Guvacine	0.59
Percentage of metabolome covered by top 25 hits		57.22

LEGEND	
*	MS2-based match (higher confidence level)
Θ	[Similar to: 2-[3-chloro-2-hydroxy-4-methoxy-6-(methoxycarbonyl)phenoxy]-6-hydroxy-4-methylbenzoic acid; ΔMass: -6.7938 Da]
Ψ	4-(2,6-dimethylphenyl)-5-(7-oxabicyclo[2.2.1]hept-2-yl)-2,4-dihydro-3H-1,2,4-triazole-3-thione
Ω	5,7-dihydroxy-2-(4-hydroxy-3-methoxyphenyl)-3,4-dihydro-2H-1-benzopyran-4-one
Λ	(2S)-4-Methyl-2-(((3S,4S,5R)-2,3,4-trihydroxy-5-(hydroxymethyl)tetrahydro-2-furanyl)methyl)amino)pentanoic acid
Φ	2-[[[2Z]-2-[[4-[[[3-Aminopropyl]amino]butyl]imino]-2-hydroxyethyl]-2-hydroxysuccinic acid

**Table S13.** Top 25 metabolites in *Cladosporium cladosporioides* exudate following 1 mM Zn challenge.

<i>Cladosporium cladosporioides</i>		
Number of Metabolite	Name of metabolite	% of total
1	Sulfamic acid	24.18
2	Hexylamine	10.10
3	Ω*	8.63
4	[Similar to: Thiamine; ΔMass: -0.2644 Da]*	4.07
5	(1S,4S)-4-Hydroxy-3-oxocyclohexanecarboxylic acid	3.74
6	Pyrimidine	3.61
7	4-Imidazolemethanol	3.47
8	PD-0333941*	1.11
9	Apocynin	0.99
10	1-(1H-Imidazol-5-yl)-3-(phosphonoxy)-2-propanone	0.92
11	Θ*	0.84
12	Deanol	0.83
13	δ-Valerolactam*	0.76
14	Butyryl-L-homoserine lactone	0.60
15	N6-Acetyl-L-lysine*	0.60
16	NLK*	0.60
17	Λ	0.58
18	NP-005394*	0.57
19	L-Pyroglutamic acid*	0.57
20	Φ	0.56
21	N6,N6,N6-Trimethyl-L-lysine*	0.53
22	Triacetin	0.51
23	16 <sup>±</sup> -Hydroxydehydroepiandrosterone 3-sulfate	0.48
24	Bis(methylbenzylidene)sorbitol*	0.48
25	ZV4	0.46
Percentage of metabolome covered by top 25 hits		69.79

LEGEND	
*	MS2-based match (higher confidence level)
Θ	[Similar to: 2-[3-chloro-2-hydroxy-4-methoxy-6-(methoxycarbonyl)phenoxy]-6-hydroxy-4-methylbenzoic acid; ΔMass: -6.7938 Da]
Ψ	4-(2,6-dimethylphenyl)-5-(7-oxabicyclo[2.2.1]hept-2-yl)-2,4-dihydro-3H-1,2,4-triazole-3-thione
Ω	5,7-dihydroxy-2-(4-hydroxy-3-methoxyphenyl)-3,4-dihydro-2H-1-benzopyran-4-one
Λ	(2S)-4-Methyl-2-(((3S,4S,5R)-2,3,4-trihydroxy-5-(hydroxymethyl)tetrahydro-2-furanyl)methyl)amino)pentanoic acid
Φ	2-((2Z)-2-((4-((3-Aminopropyl)amino)butyl)imino)-2-hydroxyethyl)-2-hydroxysuccinic acid



**Table S14.** Top 25 metabolites in *Paecilomyces variotii* exudate following 1 mM Zn challenge.

Number of Metabolite	<i>Paecilomyces variotii</i>	
	Name of metabolite	% of total
1	Hexylamine	16.25
2	Sulfamic acid	13.47
3	4-Imidazolemethanol	2.85
4	5-chloro-2,8-dimethyl-4-[(3-nitro-2-pyridyl)oxy]quinoline*	2.84
5	g-Butyrobetaine	2.24
6	cGMP	1.93
7	[Similar to: Thiamine; ΔMass: -0.2644 Da]*	1.90
8	δ-Valerolactam*	1.63
9	2'-O-Methyladenosine*	1.38
10	Cytidine 3',5'-cyclic monophosphate	1.24
11	N-valeryl-Glycine	1.22
12	N-(Carboxymethyl)norleucine	1.06
13	(1S,4S)-4-Hydroxy-3-oxocyclohexanecarboxylic acid	1.03
14	2',3'-Cyclic UMP	0.92
15	2-amino-2,3,7-trideoxy-D-lyxo-hept-6-ulosonic acid	0.91
16	1H-Imidazol-2-ol	0.83
17	NLK*	0.78
18	N6-Acetyl-L-lysine*	0.78
19	N6,N6,N6-Trimethyl-L-lysine*	0.78
20	Amfepramone*	0.71
21	⊖*	0.70
22	D-PANTOTHENIC ACID	0.69
23	NP-019722*	0.69
24	5,7-Dihydroxy-4-methylcoumarin*	0.64
25	b-Ala-Lys	0.61
Percentage of metabolome covered by top 25 hits		58.07

LEGEND	
*	MS2-based match (higher confidence level)
⊖	[Similar to: 2-[3-chloro-2-hydroxy-4-methoxy-6-(methoxycarbonyl)phenoxy]-6-hydroxy-4-methylbenzoic acid; ΔMass: -6.7938 Da]
ψ	4-(2,6-dimethylphenyl)-5-(7-oxabicyclo[2.2.1]hept-2-yl)-2,4-dihydro-3H-1,2,4-triazole-3-thione
Ω	5,7-dihydroxy-2-(4-hydroxy-3-methoxyphenyl)-3,4-dihydro-2H-1-benzopyran-4-one
Λ	(2S)-4-Methyl-2-(((3S,4S,5R)-2,3,4-trihydroxy-5-(hydroxymethyl)tetrahydro-2-furanyl)methyl)amino)pentanoic acid
⊕	2-[(2Z)-2-((4-[(3-Aminopropyl)amino]butyl)imino)-2-hydroxyethyl]-2-hydroxysuccinic acid

**Table S15.** Top 25 metabolites in *Penicillium chrysogenum* exudate following 1 mM Zn challenge.

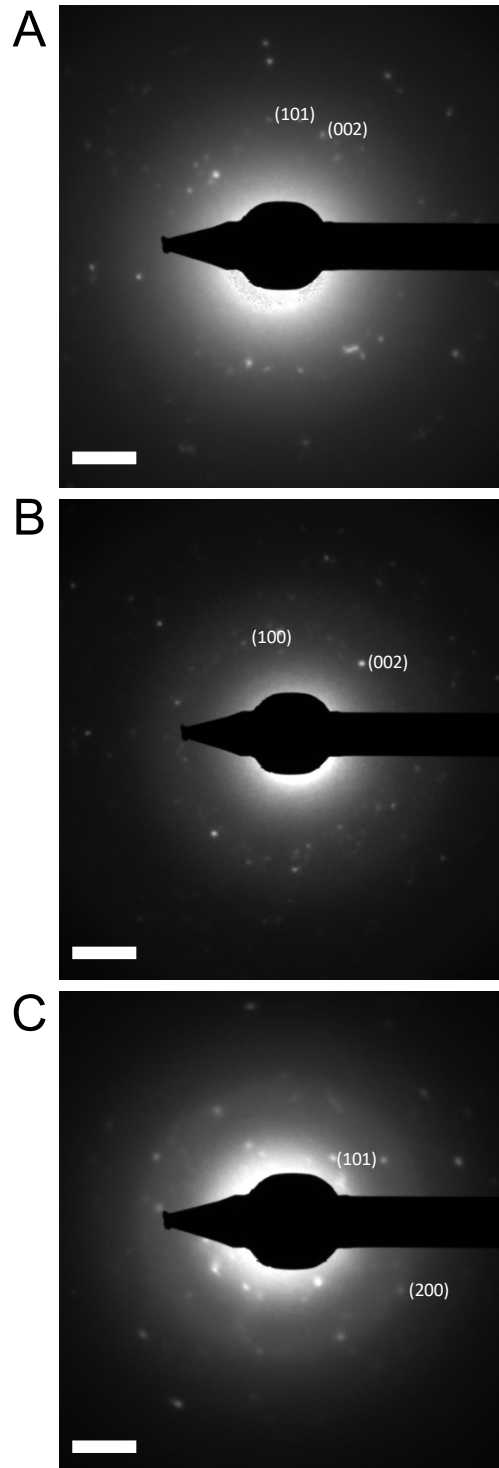
Number of Metabolite	<i>Penicillium chrysogenum</i>	
	Name of metabolite	% of total
1	Hexylamine	17.22
2	Sulfamic acid	13.57
3	Ω*	9.35
4	4-Imidazolmethanol	5.10
5	[Similar to: Thiamine; ΔMass: -0.2644 Da]*	1.94
6	δ-Valerolactam*	1.64
7	N-valeryl-Glycine	1.43
8	(3S)-3-(Pentanoyloxy)-4-(trimethylammonio)butanoate	1.41
9	PD-0333941*	1.14
10	Pyrimidine	1.05
11	D-PANTOTHENIC ACID	0.93
12	NP-019722*	0.93
13	1-Nitrosopyrrolidine (NPYR)*	0.92
14	D-ribosylnicotinate	0.92
15	Fomepizole	0.84
16	Nicotinic acid*	0.82
17	2',3'-Cyclic UMP	0.81
18	cGMP	0.81
19	DL-Mevalonic acid	0.77
20	Mevalonolactone*	0.76
21	Θ*	0.74
22	Pyridoxine*	0.74
23	l-Histidinal	0.70
24	Thiamine*	0.66
25	Sorbic acid*	0.65
Percentage of metabolome covered by top 25 hits		65.85

LEGEND	
*	MS2-based match (higher confidence level)
Θ	[Similar to: 2-[3-chloro-2-hydroxy-4-methoxy-6-(methoxycarbonyl)phenoxy]-6-hydroxy-4-methylbenzoic acid; ΔMass: -6.7938 Da]
Ψ	4-(2,6-dimethylphenyl)-5-(7-oxabicyclo[2.2.1]hept-2-yl)-2,4-dihydro-3H-1,2,4-triazole-3-thione
Ω	5,7-dihydroxy-2-(4-hydroxy-3-methoxyphenyl)-3,4-dihydro-2H-1-benzopyran-4-one
Λ	(2S)-4-Methyl-2-(((3S,4S,5R)-2,3,4-trihydroxy-5-(hydroxymethyl)tetrahydro-2-furanyl)methyl)amino)pentanoic acid
Φ	2-[[2Z]-2-(4-[[3-Aminopropyl]amino]butyl)imino]-2-hydroxyethyl]-2-hydroxysuccinic acid

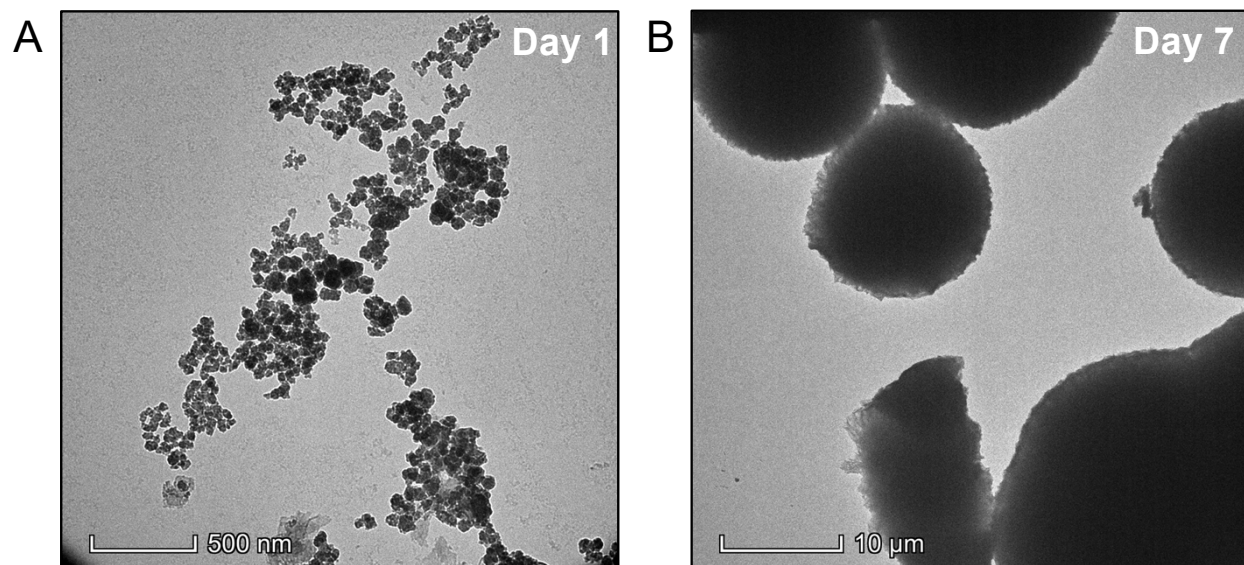
**Table S16.** Top 25 metabolites in *Aspergillus versicolor* exudate without Zn challenge.

Number of Metabolite	<i>Aspergillus versicolor</i> (no Zn challenge)	
	Name of metabolite	% of total
1	Betaine*	26.4
2	Cinnamic acid	7.4
3	L-Norleucine*	6.6
4	Betaine*	5.0
5	Carbamazepine*	3.9
6	DL-Tryptophan*	3.4
7	Phosphoric acid	2.7
8	Isoleucine*	2.7
9	Choline O-Sulfate	2.6
10	oxazolidinone	2.4
11	$\delta$ -Valerolactam*	2.3
12	N-valeryl-Glycine	1.8
13	3-(3,4-dihydroxyphenyl)propanoic acid*	1.5
14	THTC*	1.2
15	DL-Arginine*	1.1
16	Piperidine	1.1
17	Proline*	1.1
18	Hexylamine	1.0
19	Piperidine	1.0
20	Uric acid*	0.9
21	Propamocarb	0.9
22	Choline*	0.7
23	2'-O-Methyladenosine*	0.7
24	3-Buten-1-amine	0.7
25	Thiamine*	0.7
Percentage of metabolome covered by top 25 hits		79.7

\* MS2-based match (higher confidence level)



**Figure S1.** Electron diffraction patterns of ZnO obtained from challenged *A. versicolor* exudate (A), HMTA non-biological control (B), and unchallenged *A. versicolor* exudate (C). Indexed spots correspond to hexagonal confirmation of ZnO, ICDD#: 00-036-1451.



**Figure S2.** Non-biological control containing HMTA and Zn only, drop casted 24 h after synthesis (A), and following one week in solution at room temperature (B).