

Table S2. Complete list of proteins identified by MASCOT in *O. maius* Zn samples after shotgun proteomics. The organism of the nearest protein match is indicated, together with the accession number, the protein score and the number of matching peptides. Further description based on conserved protein regions is provided, if available in GenBank

Protein matches uniquely found in the control sample

Accession number	Protein Description	Protein regions	Organism	Protein score	Peptide matches
gi 261196736	40S ribosomal protein S19		<i>Ajiellomyces dermatitidis</i> SLH14081	96	2
gi 573064061	40S ribosomal protein S19		<i>Pestalotiopsis fici</i> W106-1	86	2
gi 406865979	60S acidic ribosomal protein P2		<i>Marssonina brunnea</i> f. sp. ~multigermutubi~ MB_m1	51	2
gi 302306830	ACL196Wp	Transaldolase	<i>Ashbya gossypii</i> ATCC 10895	104	5
gi 512204104	Actin-like ATPase		<i>Glarea lozoyensis</i> ATCC 20868	462	14
gi 584136457	acyl-protein thioesterase I		<i>Fusarium verticillioides</i> 7600	62	2
gi 119406412	aldehyde dehydrogenase		<i>Neosartorya fischeri</i> NRRL 181	65	3
gi 119472009	aldehyde dehydrogenase		<i>Neosartorya fischeri</i> NRRL 181	52	2
gi 225684023	conserved hypothetical protein	Peroxioredoxin	<i>Paracoccidioides brasiliensis</i> Pb03	68	3
gi 146451562	conserved hypothetical protein		<i>Lodderomyces elongisporus</i> NRRL YB-4239	64	2
gi 70993478	conserved lysine-rich protein		<i>Aspergillus fumigatus</i> Af293	50	3
gi 401886738	cytoplasm protein		<i>Trichosporon asahii</i> var. asahii CBS 2479	52	3
gi 398394555	FKBP peptidyl-prolyl cis-trans isomerase		<i>Zymoseptoria tritici</i> IPO323	70	4
gi 406866984	FKBP-type peptidyl-prolyl cis-trans isomerase		<i>Marssonina brunnea</i> f. sp. ~multigermutubi~ MB_m1	88	2
gi 154693434	formate dehydrogenase		<i>Sclerotinia sclerotiorum</i> 1980 UF-70	215	17
gi 440635823	formate dehydrogenase		<i>Pseudogymnoascus destructans</i> 20631-21	111	5
gi 50659022	glyceraldehyde-3-phosphate dehydrogenase		<i>Beauveria bassiana</i>	85	2
gi 452846379	glyceraldehyde-3-phosphate dehydrogenase-like protein		<i>Dothistroma septosporum</i> NZE10	52	2
gi 1945628	heat shock protein 70		<i>Cryptococcus curvatus</i>	111	3
gi 341039040	heat shock protein 70-like protein		<i>Chaetomium thermophilum</i> var. thermophilum DSM 1495	374	10
gi 584413640	Histone H2A		<i>Penicillium raoultii</i>	209	8
gi 786617	histone H2A variant		<i>Schizosaccharomyces pombe</i>	82	2
gi 2257481	HISTONE H2A VARIANT		<i>Schizosaccharomyces pombe</i>	102	2
gi 173404	histone H2A-alpha		<i>Schizosaccharomyces pombe</i>	140	5
gi 170100098	histone H2B		<i>Laccaria bicolor</i> S238N-H82	120	8
gi 27531291	histone H2B		<i>Rosellinia necatrix</i>	165	7
gi 164643946	histone H2B		<i>Laccaria bicolor</i> S238N-H82	125	6
gi 20260807	Hsp70 protein 1		<i>Rhizopus stolonifer</i>	207	4
gi 590008059	hsp88-like protein		<i>Capronia coronata</i> CBS 617.96	68	3
gi 590018458	hypothetical protein A101_02049		<i>Capronia coronata</i> CBS 617.96	55	2
gi 409076167	hypothetical protein AGAB1DRAFT_115671	Glyceraldehyde 3-phosphate dehydrogenase	<i>Agaricus bisporus</i> var. burnettii JB137-58	55	3
gi 350635562	hypothetical protein ASPNIDRAFT_209713	transaldolase	<i>Aspergillus niger</i> ATCC 1015	228	6
gi 119188877	hypothetical protein CIMG_04486	cyclophilin	<i>Coccidioides immitis</i> RS	53	2
gi 402468426	hypothetical protein EDEG_02098		<i>Edwardsiella aedis</i> USNM 41457	53	2
gi 46116894	hypothetical protein FG04289.1	Histone H4	<i>Fusarium graminearum</i> PH-1	66	2
gi 402079170	hypothetical protein GGTG_08276		<i>Gaeumannomyces graminis</i> var. tritici R3-111a-1	53	2
gi 410075021	hypothetical protein KAFR_0A05230	Histone 2A	<i>Kazachstania africana</i> CBS 2517	51	2
gi 361124132	hypothetical protein M7L_8069		<i>Glarea lozoyensis</i> 74030	68	5
gi 452978820	hypothetical protein MYCFIDRAFT_56853	aldehyde dehydrogenase	<i>Pseudocercospora fijiensis</i> CIRAD86	83	2
gi 525587278	hypothetical protein PDE_08490		<i>Penicillium oxalicum</i> 114-2	50	3
gi 300101770	hypothetical protein SCHCODRAFT_85988	malate dehydrogenase	<i>Schizophyllum commune</i> H4-8	79	2
gi 387513779	hypothetical protein TBLA_0E01600	heat shock 70 kDa protein	<i>Tetrapispora blattae</i> CBS 6284	218	5
gi 347004715	hypothetical protein THITE_2123173	aldehyde dehydrogenase	<i>Thielavia terrestris</i> NRRL 8126	91	3
gi 367054142	hypothetical protein THITE_2123173	aldehyde dehydrogenase	<i>Thielavia terrestris</i> NRRL 8126	73	2
gi 347000918	hypothetical protein THITE_66001	malate dehydrogenase	<i>Thielavia terrestris</i> NRRL 8126	221	5

gi 71024353	hypothetical protein UM06259.1	cyclophilin	<i>Ustilago maydis</i> 521	53	2
gi 238933890	KLTH0C06556p	heat shock 70 kDa protein	<i>Lachancea thermotolerans</i> CBS 6340	229	4
gi 558860618	L-xylulose reductase		<i>Fusarium graminearum</i> PH-1	111	3
gi 261360051	malate dehydrogenase		<i>Verticillium alfalfae</i> VaMs.102	221	5
gi 591493978	malate dehydrogenase, mitochondrial		<i>Fusarium oxysporum</i> f. sp. vasinfectum 25433	156	5
gi 114191202	malate dehydrogenase, mitochondrial precursor		<i>Aspergillus terreus</i> NIH2624	213	6
gi 242810201	malate dehydrogenase, NAD-dependent		<i>Talaromyces stipitatus</i> ATCC 10500	129	4
gi 309302318	malate dehydrogenase, NAD-dependent		<i>Puccinia graminis</i> f. sp. tritici CRL 75-36-700-3	89	2
gi 531981682	malate dehydrogenase, variant		<i>Ajellomyces dermatitidis</i> ATCC 26199	113	3
gi 150951593	mitochondrial malate dehydrogenase		<i>Scheffersomyces stipitis</i> CBS 6054	99	3
gi 149388723	mitochondrial malate dehydrogenase		<i>Scheffersomyces stipitis</i> CBS 6054	54	2
gi 295657623	myosin-2		<i>Paracoccidioides</i> sp. ~lutzi~ Pb01	75	2
gi 226283862	myosin-2		<i>Paracoccidioides</i> sp. ~lutzi~ Pb01	74	2
gi 512201152	NAD(P)-binding Rossmann-fold containing protein		<i>Glarea lozoyensis</i> ATCC 20868	219	17
gi 70984134	NAD-dependent formate dehydrogenase AcIA/Fdh		<i>Aspergillus fumigatus</i> AJ293	105	5
gi 391868305	NAD-dependent malate dehydrogenase		<i>Aspergillus oryzae</i> 3.042	146	5
gi 512205210	NAP-like protein	Nucleosome assembly protein	<i>Glarea lozoyensis</i> ATCC 20868	95	2
gi 310792632	nucleosome assembly protein		<i>Colletotrichum graminicola</i> M1.001	70	2
gi 211581920	Pc12g04310	NAD-dependent Formate Dehydrogenase	<i>Penicillium chrysogenum</i> Wisconsin 54-1255	151	5
gi 378725349	peptidyl-prolyl cis-trans isomerase B		<i>Exophiala dermatitidis</i> NIH/UT8656	60	2
gi 512203585	PH		<i>Glarea lozoyensis</i> ATCC 20868	78	2
gi 574142463	phospholipase D1		<i>Kluyveromyces marxianus</i> DMKU3-1042	64	2
gi 399166643	probable ribosomal protein S19.e, cytosolic		<i>Claviceps purpurea</i> 20.1	75	2
gi 110592112	putative enolase		<i>Beauveria bassiana</i>	51	2
gi 361130990	putative Eukaryotic translation initiation factor 5A		<i>Glarea lozoyensis</i> 74030	62	2
gi 472242176	putative malate dehydrogenase protein		<i>Botryotinia fuckeliana</i> BcDW1	245	7
gi 472245582	putative mannitol dehydrogenase protein		<i>Botryotinia fuckeliana</i> BcDW1	76	3
gi 472244911	putative tsa family protein	Peroxiredoxin	<i>Botryotinia fuckeliana</i> BcDW1	54	4
gi 239613220	ribosomal protein L23a		<i>Ajellomyces dermatitidis</i> ER-3	70	2
gi 549054705	Similar to Glycerdehyde-3-phosphate dehydrogenase; acc. no. Q9P8C0		<i>Pyronema omphalodes</i> CBS 100304	75	2
gi 312221561	similar to nucleoside diphosphate kinase		<i>Leptosphaeria maculans</i> JN3	124	3
gi 210070767	sorbitol/xylulose reductase Sou1-like, putative		<i>Talaromyces marneffei</i> ATCC 18224	95	3
gi 323337548	Sut1p		<i>Saccharomyces cerevisiae</i> Vin13	49	3
gi 114191388	transaldolase		<i>Aspergillus terreus</i> NIH2624	228	6
gi 558864501	transaldolase		<i>Fusarium graminearum</i> PH-1	187	4
gi 238879833	transaldolase		<i>Candida albicans</i> W0-1	69	3
gi 170947976	unnamed protein product	Hsp70 protein	<i>Podospira anserina</i> S mat+	89	4
gi 170942211	unnamed protein product	transaldolase	<i>Podospira anserina</i> S mat+	140	3
gi 49649016	YALI0D22352p	Hsp70 protein	<i>Yarrowia lipolytica</i> CLIB122	231	6
gi 49649782	YALIOE13706p	Hsp70 protein	<i>Yarrowia lipolytica</i> CLIB122	60	3
gi 199427004	YALIOE35046p	Hsp70 protein	<i>Yarrowia lipolytica</i> CLIB122	217	5
gi 210076308	YALIOE35046p	Hsp70 protein	<i>Yarrowia lipolytica</i>	137	3
gi 238937808	ZYRO0A12914p	Transaldolases	<i>Zygosaccharomyces rouxii</i>	106	5

Protein matches uniquely found in the cadmium treated sample

Accession number	Protein Description		Organism	Protein score	Peptide matches
gi 154303611	10 kDa heat shock protein, mitochondrial		<i>Botryotinia fuckeliana</i> B05.10	64	2
gi 12054276	14-3-3-like protein		<i>Trichoderma reesei</i>	71	2
gi 154298946	40S ribosomal protein S12		<i>Botryotinia fuckeliana</i> B05.10	65	2
gi 116206800	60S ribosomal protein L22		<i>Chaetomium globosum</i> CBS 148.51	86	2
gi 563291817	60S ribosomal protein L25		<i>Sclerotinia borealis</i> F-4157	119	3

gi 16198005	actin		<i>Chaetomium globosum</i> CBS 148.51	78	3
gi 33146374	actin		<i>Phanerochaete chrysosporium</i>	88	3
gi 194739500	actin		<i>Phoma herbarum</i>	69	2
gi 521729675	actin I		<i>Gloeophyllum trabeum</i> ATCC 11539	50	2
gi 589979807	actin, gamma		<i>Cladophialophora yegresii</i> CBS 114405	82	3
gi 298363374	actin, partial		<i>Basidiobolus ranarum</i>	58	2
gi 563298381	agmatinase		<i>Sclerotinia borealis</i> F-4157	50	2
gi 565931545	agmatinase		<i>Cladophialophora carrionii</i> CBS 160.54	53	2
gi 119182499	ATP synthase beta chain, mitochondrial		<i>Coccidioides immitis</i> RS	65	2
gi 149235644	ATP-dependent molecular chaperone HSC82		<i>Lodderomyces elongisporus</i> NRRL YB-4239	126	3
gi 89032159	beta-tubulin		<i>Stereocaulon tomentosum</i>	74	3
gi 186970549	beta-tubulin		<i>Edhazardia aedis</i>	79	2
gi 13569146	beta-tubulin		<i>Physcia caesia</i>	85	2
gi 13569134	beta-tubulin		<i>Physcia alnophila</i>	82	2
gi 530751825	beta-tubulin, partial		<i>Caloplaca</i> sp. CBF5 JV9673	100	3
gi 326788813	beta-tubulin, partial		<i>Xanthoparmelia plittii</i>	85	2
gi 550807217	chaperone DnaK		<i>Sporothrix schenckii</i> ATCC 58251	170	10
gi 255730583	conserved hypothetical protein		<i>Candida tropicalis</i> MYA-3404	50	2
gi 11277118	dnaK-type molecular chaperone BiP		Imported - <i>Aspergillus awamori</i>	61	2
gi 67540320	EF2_NEUCR Elongation factor 2 (EF-2) (Colonial temperature-sensitive 3)		<i>Aspergillus nidulans</i> FGSC A4	80	2
gi 346680885	elongation factor I, alpha		<i>Calvitimela armeniaca</i>	154	4
gi 110666913	elongation factor I, alpha, partial		<i>Pleopsidium chlorophanum</i>	154	4
gi 442024087	Elongation factor I, alpha, partial		<i>Tuber dryophilum</i>	57	2
gi 411025953	elongation factor-I, alpha, partial		<i>Pleosporeles</i> sp. YS-2012	129	3
gi 82571189	Grp1p	Glycine rich protein	<i>Exophiala dermatitidis</i>	65	2
gi 226287383	heat shock protein		<i>Paracoccidioides brasiliensis</i> Pb18	365	8
gi 378728414	heat shock protein 60		<i>Exophiala dermatitidis</i> NIH/UT8656	63	2
gi 539438266	Heat shock protein 60		<i>Endocarpon pusillum</i> Z07020	63	2
gi 328354614	Heat shock protein 60		<i>Komagataella pastoris</i> CBS 7435	77	2
gi 387538371	heat shock protein 70		<i>Blumeria graminis</i> f. sp. <i>tritici</i>	562	19
gi 539433431	Heat shock protein 90		<i>Endocarpon pusillum</i> Z07020	355	8
gi 389623639	heat shock protein 90		<i>Magnaporthe oryzae</i> 70-15	316	8
gi 406867800	heat shock protein 90		<i>Marssonina brunnea</i> f. sp. ~multigermtubi~ MB_m1	225	7
gi 60656557	heat shock protein 90		<i>Paracoccidioides brasiliensis</i>	256	7
gi 320593198	heat shock protein hsp88		<i>Grosmannia clavigera</i> kw1407	54	2
gi 400596766	Heat shock protein Hsp90		<i>Beauveria bassiana</i> ARSEF 2860	192	6
gi 392563662	histone 2A		<i>Trametes versicolor</i> FP-101664 SS1	49	2
gi 225685094	histone H2B		<i>Paracoccidioides brasiliensis</i> Pb03	150	4
gi 169851378	histone H2B		<i>Coprinopsis cinerea</i> okayama7#130	82	3
gi 384483237	hsp83-like protein		<i>Rhizopus delemar</i> RA 99-880	101	2
gi 171682512	hypothetical protein	Hsp70 protein	<i>Podospora anserina</i> S mat+	125	5
gi 296415137	hypothetical protein	malate dehydrogenase	<i>Tuber melanosporum</i> Mel28	81	2
gi 557728807	hypothetical protein ARB_01274	Hsp90 protein	<i>Byssosclamyces spectabilis</i> No. 5	363	9
gi 154309690	hypothetical protein BC1G_07315	Hsp90 protein	<i>Botryotinia fuckeliana</i> B05.10	271	7
gi 154302177	hypothetical protein BC1G_09769	Hsp70 protein	<i>Botryotinia fuckeliana</i> B05.10	72	2
gi 154301968	hypothetical protein BC1G_10221		<i>Botryotinia fuckeliana</i> B05.10	71	2
gi 154298412	hypothetical protein BC1G_11661	similar to 70 kDa heat shock protein	<i>Botryotinia fuckeliana</i> B05.10	56	2
gi 528291302	hypothetical protein BGHDI14_bgh00149	aldehyde dehydrogenase family 2 member	<i>Blumeria graminis</i> f. sp. <i>hordei</i> DH14	52	2
gi 521770382	hypothetical protein BGT96224_ASP20649	Hsp70 protein	<i>Blumeria graminis</i> f. sp. <i>tritici</i> 96224	72	2
gi 448515268	hypothetical protein CORT_0801370		<i>Candida orthopsilosis</i> Co 90-125	59	2
gi 576040010	hypothetical protein CTHT_0034440	RNA-binding protein	<i>Chaetomium thermophilum</i> var. <i>thermophilum</i> DSM 1495	51	2

gi 452846917	hypothetical protein DOTSDRAFT_67793	Hsp90 protein	<i>Dactylostroma septosporum</i> NZE10	293	7
gi 46136081	hypothetical protein FG09556.1		<i>Fusarium graminearum</i> PH-1	50	2
gi 342889878	hypothetical protein FOXB_00653	Hsp90 protein	<i>Fusarium oxysporum</i> Fo5176	268	8
gi 408399646	hypothetical protein FPSE_01112		<i>Fusarium pseudograminearum</i> CS3096	50	2
gi 526194455	hypothetical protein H072_10208	Hsp70 protein	<i>Dactylella haptotyla</i> CBS 200.50	49	2
gi 452987532	hypothetical protein MYCFIDRAFT_209468	Peroxioredoxin	<i>Pseudocercospora fijiensis</i> CIRAD86	58	2
gi 367023138	hypothetical protein MYCTH_59302		<i>Myceliophthora thermophila</i> ATCC 42464	53	2
gi 85068323	hypothetical protein NCU05347	histone H2A	<i>Neurospora crassa</i> OR74A	82	2
gi 470318265	hypothetical protein PNEG_01692	elongation factor 2	<i>Pneumocystis murina</i> B123	80	2
gi 302688337	hypothetical protein SCHCODRAFT_81694	Hsp70 protein	<i>Schizophyllum commune</i> H4-8	67	2
gi 169605883	hypothetical protein SNOG_05974	malate dehydrogenase	<i>Phaeosphaeria nodorum</i> SN15	169	5
gi 344303221	hypothetical protein SPAPADRAFT_71334		<i>Spathaspora passalidarum</i> NRRL Y-27907	52	2
gi 367039979	hypothetical protein THITE_2109740	Hsp70 protein	<i>Thielavia terrestris</i> NRRL 8126	131	6
gi 365764840	Kar2p	Hsp70 protein	<i>Saccharomyces cerevisiae</i> x <i>Saccharomyces kudriavzevii</i> VIN7	72	5
gi 346974341	kinase		<i>Verticillium dahliae</i> VdLS.17	60	2
gi 16197148	malate dehydrogenase, mitochondrial precursor		<i>Chaetomium globosum</i> CBS 148.51	167	3
gi 440636044	molecular chaperone HspG		<i>Pseudogymnoascus destructans</i> 20631-21	339	8
gi 121713454	nitrate reductase, putative		<i>Aspergillus clavatus</i> NRRL 1	63	2
gi 302897479	predicted protein	Hsp90 protein	<i>Nectria haematococca</i> mpVI 77-13-4	287	9
gi 385304371	protein containing sh3- involved in establishing cell polarity and morphogenesis		<i>Dekkera bruxellensis</i> AWRI 1499	53	3
gi 361124895	putative Heat shock protein 90 like protein		<i>Glarea lozoyensis</i> 74030	215	6
gi 500252294	putative heat shock protein 90 protein		<i>Togninia minima</i> UCRPA7	296	7
gi 485915364	putative heat shock protein 90 protein		<i>Neofusicoccum parvum</i> UCRNP2	261	7
gi 563298568	putative Heat shock protein Hsp88		<i>Sclerotinia borealis</i> F-4157	115	3
gi 361127834	putative Heat shock protein Hsp88		<i>Glarea lozoyensis</i> 74030	97	3
gi 471560739	putative malate dehydrogenase protein		<i>Eutypa lata</i> UCREL1	54	2
gi 406866420	putative nucleoside diphosphate kinase		<i>Marssonina brunnea</i> f. sp. ~multigermutubi~ MB_m1	72	2
gi 361129436	putative Single-stranded TGI-3 DNA-binding protein		<i>Glarea lozoyensis</i> 74030	85	2
gi 588900657	RanBP1 domain-containing protein		<i>Colletotrichum fioriniae</i> PJ7	50	2
gi 310791534	ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein		<i>Colletotrichum graminicola</i> M1.001	65	2
gi 528292166	RNP domain protein		<i>Blumeria graminis</i> f. sp. hordei DH14	64	2
gi 389623223	transketolase		<i>Magnaporthe oryzae</i> 70-15	59	2
gi 213990290	translation elongation factor 1 alpha		<i>Oedohysterium insidens</i>	74	2
gi 113129377	translation elongation factor 1 alpha		<i>Beauveria bassiana</i>	93	2
gi 45645235	translation elongation factor 1 alpha, partial		<i>Stachybotrys subcomplex</i>	76	3
gi 156970792	translation elongation factor 1 alpha, partial		<i>Ophiocordyceps nigrella</i>	74	3
gi 154819731	translation elongation factor 1 alpha, partial		<i>Lecanicillium psalliotae</i>	63	2
gi 90103011	translation elongation factor 1-alpha		<i>Trapelia placodioides</i>	113	4
gi 300394616	translation elongation factor 1-alpha, partial		<i>Pleuroflammula flammea</i>	150	4
gi 555235980	translation elongation factor 1-alpha, partial		<i>Sebacina incrustans</i>	150	4
gi 156099602	translation elongation factor 1-alpha, partial		<i>Candida maritima</i>	87	3
gi 159895338	translation elongation factor 1-alpha, partial		<i>Pichia pilisensis</i>	99	3
gi 156099362	translation elongation factor 1-alpha, partial		<i>Candida abiesophila</i>	59	2
gi 116687341	translation elongation factor 1-alpha, partial		<i>Hypocrea microcitina</i>	61	2
gi 290760108	translation elongation factor-1 alpha		<i>Salsuginia ramicola</i>	156	4
gi 406860515	translationally controlled tumor protein		<i>Marssonina brunnea</i> f. sp. ~multigermutubi~ MB_m1	59	2
gi 83773562	unnamed protein product	transaldolase-like protein	<i>Aspergillus oryzae</i> RIB40	134	5
gi 50553006	YALIOE13706p	Hsp70 protein	<i>Yarrowia lipolytica</i>	121	6

Protein matches uniquely found in the zinc treated sample

Accession number	Protein Description		Organism	Protein score	Peptide matches
gi 241949449	2-phospho-D-glycerate hydro-lyase, putative; 2-phosphoglycerate dehydratase, putative; enolase (1), putative		<i>Candida dubliniensis</i> CD36	88	2
gi 607818	70 kDa heat shock protein		<i>Neurospora crassa</i>	71	2
gi 513031274	AaceriACR038VWp	Hsp70 protein	<i>Saccharomycetaceae</i> sp. ~Ashbya aceri~	64	2
gi 406861156	acetamidase/Formamidase		<i>Marssonina brunnea</i> f. sp. ~multigermtubi~ MB_mI	61	2
gi 523422138	BN860_09318g1_1	Hsp70 protein	<i>Zygosaccharomyces bailii</i> CLIB 213	64	2
gi 169769647	enolase		<i>Aspergillus oryzae</i> R1B40	168	8
gi 565940099	enolase		<i>Cladophialaphora carrionii</i> CBS 160.54	132	3
gi 573068210	Enolase		<i>Pestalotiopsis fiji</i> W106-1	132	3
gi 573987885	enolase		<i>Cordyceps militaris</i> CM01	125	3
gi 406862558	enolase		<i>Marssonina brunnea</i> f. sp. ~multigermtubi~ MB_mI	175	3
gi 320592907	enolase		<i>Grosmannia clavigera</i> kw1407	95	2
gi 563295966	formamidase		<i>Sclerotinia borealis</i> F-4157	61	2
gi 47779503	glyceraldehyde 3-phosphate dehydrogenase		<i>Leccinum</i> sp. hdb 317	49	2
gi 588907234	glyceraldehyde-3-phosphate dehydrogenase		<i>Colletotrichum fiorinae</i> PJ7	85	3
gi 146737987	glyceraldehyde-3-phosphate dehydrogenase		<i>Myrothecium gramineum</i>	71	3
gi 12802697	glyceraldehyde-3-phosphate dehydrogenase		<i>Aspergillus oryzae</i>	83	3
gi 338173008	glyceraldehyde-3-phosphate dehydrogenase		<i>Hypogymnia lugubris</i>	56	2
gi 339892218	glyceraldehyde-3-phosphate dehydrogenase		<i>Cavernularia hultenii</i>	84	2
gi 262232642	glyceraldehyde-3-phosphate dehydrogenase		<i>Sporothrix schenckii</i>	51	2
gi 182375361	glyceraldehyde-3-phosphate dehydrogenase		<i>Trichoderma vires</i>	62	2
gi 162311169	glyceraldehyde-3-phosphate dehydrogenase precursor		<i>Venturia inaequalis</i>	82	2
gi 50307323	hypothetical protein		<i>Kluyveromyces lactis</i> NRRL Y-1140	61	2
gi 154289684	hypothetical protein BC1G_15991	Acetamidase/Formamidase family	<i>Botryotinia fuckeliana</i> B05.10	61	2
gi 528297293	hypothetical protein BGHDI14_bgh00007	enolase	<i>Blumeria graminis</i> f. sp. hordei DHI 4	294	11
gi 539440312	hypothetical protein EPUS_01620	malate dehydrogenase	<i>Endocarpon pusillum</i> Z07020	189	6
gi 590024719	hypothetical protein FOMG_16823		<i>Fusarium oxysporum</i> f. sp. melonis 26406	50	2
gi 565934062	hypothetical protein G647_05116		<i>Cladophialaphora carrionii</i> CBS 160.54	52	2
gi 366990381	hypothetical protein NCAS_0805020		<i>Naumovozyma castellii</i> CBS 4309	49	2
gi 367050974	hypothetical protein THITE_2120059	malate dehydrogenase	<i>Thielavia terrestris</i> NRRL 8126	85	2
gi 358400765	hypothetical protein TRIATDRAFT_297423	enolase	<i>Trichoderma atroviride</i> IMI 206040	146	4
gi 550805221	malate dehydrogenase, NAD-dependent		<i>Sporothrix schenckii</i> ATCC 58251	170	4
gi 557996926	molecular chaperones GRP78/BiP/KAR2		<i>Pseudozyma</i> sp. GHG001	71	2
gi 406862757	phosphoglycerate kinase		<i>Marssonina brunnea</i> f. sp. ~multigermtubi~ MB_mI	95	3
gi 563292102	phosphoglycerate kinase		<i>Sclerotinia borealis</i> F-4157	75	2
gi 512202705	Phosphoglycerate kinase		<i>Glarea lozoyensis</i> ATCC 20868	67	2
gi 589106401	predicted protein	malate dehydrogenase	<i>Trichoderma reesei</i> QM6a	132	3
gi 399171850	probable heat shock protein 80		<i>Claviceps purpurea</i> 20.1	72	2
gi 361127169	putative 5-methyltetrahydropteroyltrimethylglutamate--homocysteine methyltransferase		<i>Glarea lozoyensis</i> 74030	88	2
gi 361130974	putative Enolase		<i>Glarea lozoyensis</i> 74030	177	8
gi 361128640	putative Glyceraldehyde-3-phosphate dehydrogenase		<i>Glarea lozoyensis</i> 74030	55	2
gi 417017	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase 2; Short=GAPDH 2		<i>Agaricus bisporus</i>	57	4
gi 462142	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase; Short=GAPDH		<i>Colletotrichum gloeosporioides</i>	66	2
gi 212534546	transaldolase		<i>Talaromyces marneffei</i> ATCC 18224	255	7
gi 380476997	transaldolase		<i>Colletotrichum higginsianum</i>	203	4
gi 453085034	transaldolase		<i>Sphaerulina musiva</i> SO2202	203	4
gi 403158789	transaldolase		<i>Puccinia graminis</i> f. sp. tritici CRL 75-36-700-3	130	4
gi 378754398	ubiquitin		<i>Nematocida</i> sp. 1 ERTm2	54	2

Protein matches shared by the control and the cadmium treated sample

Accession number	Protein Description		Organism	Protein score	Peptide matches	Protein score	Peptide matches
gi 149238177	conserved hypothetical protein		<i>Lodderomyces elongisporus</i> NRRL YB-4239	76	2	58	2
gi 154315635	dnaK-type molecular chaperone BiP		<i>Botryotinia fuckeliana</i> B05.10	129	5	205	9
gi 440635717	glucose-regulated protein		<i>Pseudogymnoascus destructans</i> 20631-21	124	5	189	9
gi 511004672	glucose-regulated protein		<i>Mucor circinelloides</i> f. <i>circinelloides</i> 1006PhL	59	2	91	2
gi 67526021	H2A_EMENI Histone H2A		<i>Aspergillus nidulans</i> FGSC A4	207	5	181	5
gi 4164594	heat shock protein 70		<i>Paracoccidioides brasiliensis</i>	179	5	303	10
gi 357967087	heat shock protein 70a		<i>Paraphaeosphaeria minitans</i>	306	10	574	22
gi 576034802	heat shock protein 70-like protein		<i>Chaetomium thermophilum</i> var. <i>thermophilum</i> DSM 1495	216	8	429	16
gi 511009849	heat shock protein HSS1		<i>Mucor circinelloides</i> f. <i>circinelloides</i> 1006PhL	212	8	252	8
gi 296804852	histone H2A		<i>Arthroderma otae</i> CBS 113480	52	3	50	2
gi 67540658	hypothetical protein AN6499.2	malate dehydrogenase	<i>Aspergillus nidulans</i> FGSC A4	93	2	78	2
gi 154312864	hypothetical protein BC1G_05133	Peroxiredoxin	<i>Botryotinia fuckeliana</i> B05.10	54	4	53	3
gi 116202643	hypothetical protein CHGG_09206	Hsp70 protein	<i>Chaetomium globosum</i> CBS 148.51	68	2	65	2
gi 365984603	hypothetical protein NDA1_OC02310	Hsp70 protein	<i>Naumovozyma dairenensis</i> CBS 421	78	2	79	2
gi 169596076	hypothetical protein SNOG_00787	Peroxiredoxin	<i>Phaeosphaeria nodorum</i> SNI 5	49	2	83	3
gi 255712457	KLTH0C06556p	Hsp70 protein	<i>Lachancea thermotolerans</i>	139	3	259	6
gi 477536579	peptidyl-prolyl cis-trans isomerase		<i>Colletotrichum orbiculare</i> MAFF 240422	115	5	63	2
gi 568113990	phosphoglycerate kinase		<i>Cyphellophora europaea</i> CBS 101466	54	2	55	2
gi 3052	phosphoglycerate kinase		<i>Neurospora crassa</i>	54	2	55	2
gi 361128362	putative Cytochrome c		<i>Glarea lozoyensis</i> 74030	91	8	64	4
gi 361127833	putative Heat shock 70 kDa protein 2		<i>Glarea lozoyensis</i> 74030	299	10	588	21
gi 353236814	related to glucose-regulated protein 78 of hsp70 family		<i>Piriformospora indica</i> DSM 11827	59	2	91	2
gi 396497447	similar to nucleoside diphosphate kinase		<i>Leptosphaeria maculans</i> JN3	105	2	94	2
gi 11078212	translation elongation factor 1-alpha		<i>Mycotypha microspora</i>	66	2	90	3
gi 156099472	translation elongation factor 1-alpha, partial		<i>Kregervanrija pseudodeltensis</i>	58	2	77	3
gi 156099632	translation elongation factor 1-alpha, partial		<i>Nakazawaea holstii</i>	66	2	88	3
gi 50550179	YALI0D08184p	Hsp70 protein	<i>Yarrowia lipolytica</i>	226	8	417	13
gi 50551349	YALI0D22352p	Hsp70 protein	<i>Yarrowia lipolytica</i>	148	5	289	9

Protein matches shared by the control and the zinc treated sample

Accession number	Protein Description		Organism	Protein score	Peptide matches	Protein score	Peptide matches
gi 477530952	formate dehydrogenase		<i>Colletotrichum orbiculare</i> MAFF 240422	54	2	78	5
gi 114228510	glyceraldehyde 3-phosphate dehydrogenase		<i>Lactarius rufus</i>	84	2	66	2
gi 329745035	glyceraldehyde-3-phosphate dehydrogenase		<i>Rhizoctonia solani</i>	55	2	56	2
gi 340543309	glyceraldehyde-3-phosphate dehydrogenase		<i>Rhizoctonia solani</i>	59	2	77	2
gi 575481960	hypothetical protein BATDERAFT_17222	malate dehydrogenase	<i>Batrachochytrium dendrobatidis</i> JAM81	104	2	157	3
gi 451848964	hypothetical protein COCSADRAFT_38228	malate dehydrogenase	<i>Bipolaris sorokiniana</i> ND90Pr	114	5	202	5
gi 255931575	Pc12g04750	malate dehydrogenase	<i>Penicillium chrysogenum</i> Wisconsin 54-1255	90	2	145	3
gi 549047563	Similar to Glyceraldehyde-3-phosphate dehydrogenase; acc. no. Q8WZN0		<i>Pyronema omphalodes</i> CBS 100304	115	2	101	3

Protein matches shared by the cadmium and the zinc treated sample

Accession number	Protein Description		Organism	Protein score	Peptide matches	Protein score	Peptide matches
gi 212526972	agmatinase, putative		<i>Talaromyces marneffei</i> ATCC 18224	80	2	80	3
gi 169665480	copper/zinc superoxide dismutase		<i>Oidiodendron maius</i>	91	3	101	8
gi 302416609	formate dehydrogenase		<i>Verticillium alfalfae</i> VaMs.102	256	14	258	13
gi 550803673	formate dehydrogenase		<i>Sporothrix schenckii</i> ATCC 58251	249	15	219	11
gi 557729377	glyceraldehyde 3-phosphate dehydrogenase GpdA		<i>Byssosclamyces spectabilis</i> No. 5	70	2	86	2

gi 296412186	hypothetical protein	malate dehydrogenase	<i>Tuber melanosporum</i> Mel28	172	4	203	4
gi 345560669	hypothetical protein AOL_s00215g530	NAD-dependent Formate Dehydrogenase	<i>Arthrobotrys oligospora</i> ATCC 24927	160	9	126	6
gi 46110649	hypothetical protein FG02206.1	agmatinase	<i>Fusarium graminearum</i> PH-1	80	2	70	2
gi 398411472	hypothetical protein MYCGRDRAFT_67048	agmatinase	<i>Zymoseptoria tritici</i> IPO323	80	2	70	2
gi 302676798	hypothetical protein SCHCODRAFT_85988	malate dehydrogenase	<i>Schizophyllum commune</i> H4-8	94	2	93	2
gi 452846054	NAD-dependent dehydrogenase-like protein		<i>Dothistroma septosporum</i> NZE110	243	14	245	9
gi 212546267	NAD-dependent formate dehydrogenase AciA/Fdh		<i>Talaromyces marneffei</i> ATCC 18224	224	12	177	7
gi 255931489	Pc12g04310	NAD-dependent Formate Dehydrogenase	<i>Penicillium chrysogenum</i> Wisconsin 54-1255	87	3	176	7
gi 361132319	putative Formate dehydrogenase		<i>Glarea lozoyensis</i> 74030	113	4	272	19
gi 549048520	Similar to Heat shock protein 90 homolog; acc. no. O43109		<i>Pyronema omphalodes</i> CBS 100304	192	5	63	2
gi 385303182	superoxide dismutase		<i>Dekkera bruxellensis</i> AWRI1499	78	2	83	8
gi 378754615	ubiquitin extension protein		<i>Nematocida</i> sp. 1 ERTm2	130	6	101	3
gi 402242	ubiquitin/S27a fusion protein		<i>Neurospora crassa</i>	130	6	101	3
gi 83771677	unnamed protein product	NAD-dependent Formate Dehydrogenase	<i>Aspergillus oryzae</i> R1B40	137	8	116	7

Protein matches shared by all treatments

Accession number	Protein Description		Organism	Protein score	Peptide matches	Protein score	Peptide matches	Protein score	Peptide matches
gi 154309029	conserved hypothetical protein	malate dehydrogenase	<i>Botryotinia fuckeliana</i> B05.10	267	8	190	4	257	6
gi 521778412	Enolase		<i>Blumeria graminis</i> f. sp. tritici 96224	108	3	131	3	233	4
gi 563298754	enolase		<i>Sclerotinia borealis</i> F-4157	96	3	118	3	212	4
gi 512186494	formate dehydrogenase		<i>Ophiostoma piceae</i> UAMH 11346	194	6	184	6	228	10
gi 322704496	formate dehydrogenase		<i>Metarhizium anisopliae</i> ARSEF 23	97	3	73	3	140	4
gi 402078777	formate dehydrogenase		<i>Gaeumannomyces graminis</i> var. tritici R3-111a-1	127	4	266	16	221	11
gi 320591859	formate dehydrogenase		<i>Grosmannia clavigera</i> kw1407	202	5	240	15	199	5
gi 406863832	formate dehydrogenase		<i>Marssonina brunnea</i> f. sp. ~multigermtubi~ MB_m1	174	20	125	4	231	19
gi 378730528	formate dehydrogenase		<i>Exophiala dermatitidis</i> NIH/UT8656	65	3	67	2	124	6
gi 239613197	formate dehydrogenase-III		<i>Ajellomyces dermatitidis</i> ER-3	114	5	119	4	190	7
gi 58257473	formate dehydrogenase-like protein		<i>Magnaporthe grisea</i>	151	6	252	14	216	6
gi 46135911	GR78_NEUCR 78 KDA GLUCOSE-REGULATED PROTEIN HOMOLOG PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN HOMOLOGY) (BIP)		<i>Fusarium graminearum</i> PH-1	96	4	153	9	71	2
gi 171695468	hypothetical protein		<i>Podospira anserina</i> S mat+	87	3	103	8	65	2
gi 171694107	hypothetical protein	NAD-dependent Formate Dehydrogenase	<i>Podospira anserina</i> S mat+	97	3	183	10	159	9
gi 171684501	hypothetical protein	transaldolase	<i>Podospira anserina</i> S mat+	158	3	154	4	153	3
gi 68481811	hypothetical protein CaO19.4371	Transaldolase	<i>Candida albicans</i> SC5314	105	3	67	2	112	2
gi 46120358	hypothetical protein FG04826.1	mannitol dehydrogenase	<i>Fusarium graminearum</i> PH-1	85	3	82	2	67	2
gi 46128691	hypothetical protein FG08723.1	transaldolase	<i>Fusarium graminearum</i> PH-1	170	7	141	5	191	5
gi 342887440	hypothetical protein FOXB_02545	malate dehydrogenase	<i>Fusarium oxysporum</i> Fo5176	182	7	122	3	143	4
gi 406867531	hypothetical protein MBM_01251	malate dehydrogenase	<i>Marssonina brunnea</i> f. sp. ~multigermtubi~ MB_m1	219	6	163	5	195	5
gi 367046552	hypothetical protein THITE_66001	malate dehydrogenase	<i>Thielavia terrestris</i> NRRL 8126	198	4	210	4	221	5
gi 358380047	hypothetical protein TRIVIDRAFT_92614	malate dehydrogenase	<i>Trichoderma virens</i> Gv29-8	101	2	194	4	244	5
gi 169766066	malate dehydrogenase		<i>Aspergillus oryzae</i> R1B40	183	5	174	4	161	4
gi 322711869	malate dehydrogenase		<i>Metarhizium anisopliae</i> ARSEF 23	115	2	101	2	205	4
gi 58269764	malate dehydrogenase		<i>Cryptococcus neoformans</i> var. <i>neoformans</i> JEC21	71	2	53	2	63	2
gi 402083083	malate dehydrogenase		<i>Gaeumannomyces graminis</i> var. tritici R3-111a-1	215	7	206	5	209	5
gi 261187650	malate dehydrogenase		<i>Ajellomyces dermatitidis</i> SLH14081	101	2	118	4	139	3
gi 302407417	malate dehydrogenase		<i>Verticillium alfalfae</i> VaMs.102	198	4	210	4	221	5
gi 576981370	malate dehydrogenase		<i>Rhizoctonia solani</i> AG-3 Rh51AP	89	2	120	3	138	3
gi 115399894	malate dehydrogenase, mitochondrial precursor		<i>Aspergillus terreus</i> NIH2624	176	4	209	6	184	6
gi 331221307	malate dehydrogenase, NAD-dependent		<i>Puccinia graminis</i> f. sp. tritici CRL 75-36-700-3	101	2	79	3	97	2
gi 470317118	malate dehydrogenase, NAD-dependent		<i>Pneumocystis murina</i> B123	110	3	142	3	158	3
gi 358399186	malate dehydrogenase, NAD-dependent		<i>Trichoderma atroviride</i> IMI 206040	204	4	194	3	234	4

gi 85792474	mannitol dehydrogenase		<i>Botryotinia fuckeliana</i>	55	2	56	2	55	2
gi 378730548	NADP-dependent mannitol dehydrogenase		<i>Exophiala dermatitidis</i> NIH/UT8656	94	3	61	2	65	2
gi 500254375	putative enolase protein		<i>Togninia minima</i> UCRPA7	62	2	73	2	159	5
gi 500252859	putative formate dehydrogenase protein		<i>Togninia minima</i> UCRPA7	133	4	275	13	242	8
gi 500260161	putative malate dehydrogenase protein		<i>Togninia minima</i> UCRPA7	146	3	98	2	138	3
gi 361131607	putative Malate dehydrogenase, mitochondrial		<i>Glarea lozoyensis</i> 74030	212	6	201	5	221	5
gi 212536424	sorbitol/xylulose reductase SouI-like, putative		<i>Talaromyces marneffei</i> ATCC 18224	74	3	68	2	60	2
gi 28564133	TALI	Transaldolase	<i>Saccharomyces bayanus</i>	147	7	50	3	150	5
gi 145237640	transaldolase		<i>Aspergillus niger</i> CBS 513.88	200	8	192	6	215	6
gi 115400267	transaldolase		<i>Aspergillus terreus</i> NIH2624	200	8	134	5	180	6
gi 310800107	transaldolase		<i>Colletotrichum graminicola</i> M1.001	142	4	142	3	154	4
gi 406859442	transaldolase		<i>Marssonina brunnea</i> f. sp. ~multigermtubi~ MB_m1	226	8	209	6	278	7
gi 58758723	translation elongation factor EF1-alpha		<i>Climacodon septentrionalis</i>	70	2	94	3	52	2
gi 58618698	translation elongation factor EF1-alpha		<i>Marasmius alliaceus</i>	70	2	94	3	52	2
gi 584394834	unnamed protein product	malate dehydrogenase	<i>Kuraishia capsulata</i> CBS 1993	54	3	101	2	69	2
gi 254577865	ZYRO0A12914p	transaldolase	<i>Zygosaccharomyces rouxii</i>	126	6	50	3	190	6