

Table S2. The 60 proteins significantly more or less present in conidia cultivated at 37°C. Positive values (green) in Log2 fold changes found significant ($p < 0.05$) show upregulation in conidia cultivated at 37°C, whereas negative values (red) show downregulation in conidia cultivated at 37°C. Descriptions are based on EuKaryotic Orthologous Groups (KOG) found as part of MycoCosm on the JGI website⁶⁸. All descriptions are putative and solely based on homology. The baseMean DESeq2 values represent the average of normalized counts and the LFQ intensities represent quantified proteome data based on peptides found (higher values = more protein present). Normalization, Log2FC and their significance were calculated with the DESeq2 package in R for the transcriptome data and the DEP package in R for the proteome data.

NRRL3-number	An-number	Description	Transcriptome			Proteome			
			baseMean DESeq2	Log ₂ FC_transcriptome	p-value	Average_LF Qintensity_2 8C	Average_LF Qintensity_37C	log ₂ FC_prot eome	p-value
NRRL3_10215	An18g00600	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)	12309	2.43	2.44E-44	5900	1178113	7.5	2.6E-13
NRRL3_04002	An15g05410	Molecular chaperone (small heat-shock protein Hsp26/Hsp42)	1759	4.60	1.14E-65	0	130312	7.01	2.2E-08
NRRL3_09378	An11g09460	Sorting nexin SNX11	606	0.17	0.593362	0	97338	5.94	4.9E-04
NRRL3_10516	An18g04270	Parvulin-like peptidyl-prolyl cis-trans isomerase	237	-0.13	0.762198	0	46732	5.85	1.6E-03
NRRL3_11626	An06g01530	Glucan 1,3-beta-glucosidase	33	-0.04	0.940552	2858	196177	5.64	1.3E-06
NRRL3_05700	An02g07130	Mitochondrial large subunit ribosomal protein (Img2)	499	0.94	5.76E-07	0	149847	5.63	3.2E-04
NRRL3_11083	An08g04410	NADH-ubiquinone oxidoreductase subunit	568	-0.50	0.147736	0	125943	5.3	2.7E-03
NRRL3_03693	An15g01410	Possible oxidoreductase	460	0.17	0.626468	0	66393	5.28	1.4E-06

NRRL3_00318	An09g03890	Glyoxylate/hydroxy pyruvate reductase	361	-0.37	0.213897	0	99540	5.27	2.5E-07
NRRL3_11707	An06g00650 An06g00660	Oxoprolinase	1303	0.14	0.652759	218194	349483	5.16	2.0E-07
NRRL3_06627	An16g09040	N-acetyl-glucosamine-6-phosphate deacetylase	1674	-0.13	0.61331	4435	115895	5.05	1.1E-03
NRRL3_08471	An03g04500	Nucleoside diphosphate-sugar hydrolase of the MutT (NUDIX) family	286	-0.24	0.5011	2028	66817	4.85	3.7E-03
NRRL3_07783	An04g05750	hypothetical protein with signal peptide for secretion	460	-0.46	0.089005	0	55409	4.62	1.2E-02
NRRL3_09219	An11g11260	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	3461	0.34	0.188724	11574	171360	4.57	3.6E-02
NRRL3_02034	An01g05040	dUTPase	85	-2.36	0.002346	0	30726	4.56	1.8E-02
NRRL3_07644	An04g07530	G protein-coupled receptor	1954	0.07	0.877749	58759	1304167	4.5	8.7E-03
NRRL3_05517	An02g09030	Nucleolar GTPase/ATPase p130	27504	-0.22	0.05141	0	58260	4.44	2.1E-02
NRRL3_00602	An14g00300	1-Acyl dihydroxyacetone phosphate reductase and related dehydrogenases	115	-0.08	0.857974	0	40197	4.38	2.7E-02
NRRL3_06470	An17g00880	Damage-control phosphatase ARMT1-like domain	284	0.14	0.575414	0	83084	4.23	8.9E-05

NRRL3_02586	An01g11680	cis-muconate cyclase	170	0.03	0.940182	5144	99614	4.23	3.2E-03
NRRL3_00413	An09g05140	Saccharopine dehydrogenase NADP binding domain	83	-2.28	2.29E-12	0	26898	4.17	7.3E-06
NRRL3_11096	An08g04540	Putative cyclase	83	-0.26	0.561376	4433	80027	4.05	1.5E-02
NRRL3_05056	An02g14900 An02g14910	Ubiquitin activating E1 enzyme-like protein	1866	-0.14	0.415603	#N/A	#N/A	3.56	3.8E-02
NRRL3_04347	An07g01530	GatB domain	63	-0.19	0.666369	26075	258020	3.32	1.1E-02
NRRL3_04490	An07g03340	Fungal hydrophobin <i>hyp1</i>	293	0.00	0.995224	539587	5093167	3.26	2.3E-02
NRRL3_09330	An11g09920	Apoptosis-related protein/predicted DNA-binding protein	439	-0.21	0.521993	50923	374457	2.86	4.1E-02
NRRL3_03532	An05g00140	Signal recognition particle receptor, beta subunit (small G protein superfamily)	682	-0.28	0.114883	243067	67113	-2.08	4.2E-02
NRRL3_02666	An01g12550	Mannosyl-oligosaccharide alpha-1,2-mannosidase and related glycosyl hydrolases	3984	-0.66	0.149562	380070	69265	-2.53	5.9E-03
NRRL3_00410	An09g05110	Acyl-CoA synthetase	23559	-1.57	8.83E-05	256357	43786	-2.73	9.1E-03
NRRL3_02657	An01g12450	Chitinase	2316	-2.40	2.9E-05	1256357	176317	-2.83	9.6E-03
NRRL3_06237	An02g00210	Non-ribosomal peptide synthetase/alpha-aminoadipate reductase and related enzymes	2397	-0.42	0.008291	101361	16332	-2.84	4.2E-02

NRRL3_03373	An12g04700	Dipeptidyl aminopeptidase	154	-0.79	0.069459	231517	34358	-3.04	5.2E-03
NRRL3_10599	An18g05500	Ceramidase	1652	-0.30	0.354418	166843	24713	-3.05	3.3E-02
NRRL3_04237	An07g00110	Beta-lactamase	406	-0.86	0.001611	905467	122393	-3.21	7.8E-03
NRRL3_00071	An09g00810	Zinc-binding oxidoreductase	303	-1.40	2.81E-08	176773	20027	-3.31	2.9E-03
NRRL3_00279	An09g03450	D-ribulose-5-phosphate 3-epimerase	922	-0.57	0.005181	16737	0	-3.49	9.2E-03
NRRL3_06024	An02g02930	ribose-5-phosphate isomerase	2280	-0.30	0.294115	701343	80009	-3.56	1.6E-02
NRRL3_10970	An08g03090	Calcium transporting ATPase	7420	0.15	0.457215	167843	19365	-3.67	4.6E-03
NRRL3_06352	An10g00800	Purine nucleoside permease (NUP)	32	-1.06	0.082256	325673	25999	-3.69	2.0E-04
NRRL3_02923	An12g10470	cyclin-dependent kinase	7273	-0.40	0.166186	1360567	119020	-3.84	3.4E-03
NRRL3_11047	An08g03960	Putative cargo transport protein ERV29	719	-0.39	0.142135	129678	7651	-4.15	2.1E-02
NRRL3_02139	An01g06310	hypothetical protein with DUF1793 domain	98	0.38	0.369748	52896	0	-4.36	3.7E-03
NRRL3_03251	An12g06060	hypothetical protein with YrdC-like domain	301	-1.87	6.26E-11	128167	6207	-4.41	2.2E-06
NRRL3_03449	An12g03850	ATP-dependent RNA helicase	1153	1.15	1.93E-12	42187	0	-4.42	9.7E-04
NRRL3_04236	An07g00100	Amidase	2983	-2.77	2.81E-50	50961	0	-4.5	4.8E-04
NRRL3_10468	An18g03780	Aminopeptidases of the M20 family	672	-0.13	0.662217	337473	14022	-4.58	8.0E-04

NRRL3_06750	An16g07450	Translation initiation factor 2C (eIF-2C) and related proteins	1599	-1.41	1.47E-10	239267	9344	-4.63	3.8E-08
NRRL3_03138	An12g07570	Synaptobrevin/VA MP-like protein	2175	0.97	1.39E-32	120507	2519	-4.73	1.7E-02
NRRL3_06942	An16g04640	Predicted membrane protein	318	0.00	0.998817	53285	0	-4.73	2.3E-02
NRRL3_02536	An01g11100	Predicted membrane protein	8115	0.33	0.011983	40871	0	-4.77	6.9E-03
NRRL3_03346	An12g04950	Mitochondrial F1F0-ATP synthase, subunit epsilon/ATP15	937	-0.04	0.940168	54565	0	-4.84	2.2E-02
NRRL3_08244	An04g00150	Glutaredoxin-related protein	502	-0.06	0.8883	85849	6223	-4.85	2.4E-02
NRRL3_07734	An04g06310	hypothetical protein with signal peptide for secretion	1476	-0.45	0.000469	61747	0	-5.06	4.3E-02
NRRL3_09480	An11g08250	Glutamate decarboxylase and related proteins	185	-0.90	0.016693	290377	6787	-5.46	1.5E-05
NRRL3_11110	An08g04690	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	141	-3.62	2.02E-09	192914	3916	-5.59	4.6E-04
NRRL3_04169	An15g07370	Chitinase	26	-0.35	0.414464	111428	0	-5.94	1.5E-06
NRRL3_03454	An12g03760	hypothetical protein	161	2.41	0.000117	1259540	21374	-6.04	2.3E-05

NRRL3_03951	An15g04790	Fungal specific transcription factor domain containing protein	372	0.35	0.135284	165789	0	-6.26	2.6E-03
NRRL3_10314	An18g01890	hypothetical protein	3670	-1.98	2.06E-12	1777000	23598	-6.44	2.6E-13
NRRL3_04228	An07g00020	alpha/beta hydrolase	206	0.35	0.394227	137507	0	-7.7	2.1E-02