

Supplementary materials

Tables 3–5 (full versions). Functional groups of genes of *B. emersonii* increasing the expression by 1.5 or more times, the expression level and homology of *B. emersonii* and *P. tribonematis* genes.

Blue color of the font – the presence of homologs in the entire Opisthokonta group; green color of the font – the presence of homologs only in the Holomycota (usually in Fungi group only).

The expression level is determined relative to the expression level in the vegetative growth phase, taken as 1 (Vieira and Gomes, 2013).

Cell fillings mark the functional groups:












	Actin cytoskeleton construction
	Chitin metabolism
	Metabolic activity
	Protein breakdown
	Protein synthesis and maturation
	Reactions of nucleic acids
	Redox reactions
	Regulation and signaling
	Transmembrane transport
	Tubulin cytoskeleton construction
	Vesicular transport

Table 3. The genes selected from genes with a maximum expression at 60 minutes of zoospore production.

ID of sequence	Annotation	Function of found homologs	Expression level	ID of <i>P. tribonemae</i> homologous sequence
BeE30N14B02	Q7S903 Proteasome subunit alpha type	Protein breakdown	2,95	Partr_v1_DN23897_C0_g1_i4_m63907
BeG90N22C02	Q9PTW9 Proteasome subunit alpha type 7	Protein breakdown	2,45	Partr_v1_DN23739_C0_g1_i1_m52965
BeE60N15C03	similar to RIKEN CDNA 5530601I19 [Rattus norvegicus]	Suppress the enzymatic activity	2,31	Partr_v1_DN28121_C0_g1_i1_m55411
BeE60H26C08	Q9P3A7 cell division cycle protein 48 homolog	Protein breakdown	2,27	Partr_v1_DN28702_c2_g2_i1_m62185
BeE60N14C07	O14413 Proteinase A GO:0004194	Protein breakdown	2,19	Partr_v1_DN26201_C1_g1_i2_m48315
BeE60N02F11	Q13200 26S proteasome non-ATPase regulatory subunit	Protein breakdown,	2,1	Partr_v1_DN27838_C0_g1_i1_m22683
BeE120N38C06	No match (putative 26S Proteasome non-ATPase regulatory subunit)	Protein breakdown,	2,06	Partr_v1_DN26287_C0_g1_i1_m48304
BeE30N15E12	Q9VUJ1 Proteasome subunit beta type	Protein breakdown	1,93	Partr_v1_DN24219_C0_g1_i3_m36916
BeE60H30E02	O60953 Proteasome subunit	Protein breakdown	1,82	Partr_v1_DN25068_c0_g1_i4_m50925
BeE60N10D10	Q7S2D6 Proteasome subunit alpha type	Protein breakdown	1,63	Partr_v1_DN26529_C2_g1_i1_m4044
BeE60H17C06	P52495 Ubiquitin-activating enzyme E1 1 (Fragment)	Protein breakdown	1,49	Partr_v1_DN27935_c0_g1_i1_m11059
BeE60N02A06	Q9P3F0 Related to ubiquitin-activating enzyme homolog	Protein breakdown	1,49	Partr_v1_DN27759_C3_g1_i5_m67301
BeE60N05B04	Q7SI81 Carboxypeptidase	Protein maturation	1,88	Partr_v1_DN22075_C0_g1_i1_m44393
BeG90N03D07	O94501 T-Complex protein 1, alpha subunit	Protein folding, including actin and tubulin assembly	1,68	Partr_v1_DN25589_C0_g1_i1_m20470
BeG120N25A08	Prefoldin?	Actin assembly, protein transport	1,7	--
BeE30N11G06	Q962X9 G10 protein	Mrna processing	1,55	Partr_v1_DN22811_C0_g2_i1_m77279
BeE60H29D03	Q7XZG6 Putative RNA binding protein	Mrna processing	1,45	Partr_v1_DN27187_c0_g1_i1_m16076
BeG60N07F05	Q9C6K5 Sm-like protein	Mrna processing	1,79	Partr_v1_DN27138_C0_g1_i3_m15699
BeE30N04B04	Q9UVH9 Fox2 protein	Redox balance, redox reactions	2,83	Partr_v1_DN21799_C0_g1_i1_m7783
BeE120N01E04	Q80W96 HesB	Redox balance, redox reactions	2,58	Partr_v1_DN28319_C0_g1_i1_m78869
BeE90D16C06	P91252 Probable glutathione S-transferase 6	Redox balance, redox reactions	1,94	Partr_v1_DN4745_c0_g1_i1_m5145
BeE60C31E12	Q94GY8 Putative glutathione S-transferase	Redox balance, redox reactions	1,92	Partr_v1_DN23918_c0_g1_i2_m48942
BeE30N17E08	P91252 Probable glutathione S-transferase 6	Redox balance, redox reactions	1,51	Partr_v1_DN4745_C0_g1_i1_m5145
BeE30N16B09	O77622 T-complex protein 1, zeta subunit	Telomerase activity regulation	1,51	Partr_v1_DN26168_C0_g1_i1_m10705
BeE60N18H09	hypothetical protein (putative PIF1 5'-to-3' DNA	Dna copying, genome stability	2,97	Partr_v1_DN26582_C1_g1_i1_m3558

	helicase homolog (<i>S. cerevisiae</i>))			
BeNSVP07B10	proton glutamate symport protein [<i>Bradyrhizobium</i>]	Transport of aspartate, glutamate and dicarboxylic acids	4,69	--
BeE120N03E08	No match (V-type proton ATPase)	Proton transport, creating an acidic environment	1,54	Partr_v1_DN27211_C0_g1_i2_m38478
BeE60N04H05	Q9BPW0 Serine/threonine protein phosphatase	Regulation of cell differentiation (in metazoa), protein serine / threonine kinase activity	1,58	Partr_v1_DN26742_C1_g1_i1_m8489
BeE60N03G10	Q7SBV0 Hypothetical protein (putative cyclopropane-fatty-acyl-phospholipid synthase)	Lipid biosynthesis	6,59	Partr_v1_DN23743_C0_g1_i1_m52921
BeG120N09B09	Q04767 Golgi apparatus membrane protein TVP18	Vesicular transport	1,61	
BeE60H14B07	P41887 Heat shock protein 90 homolog	Heat shock protein	1,69	Partr_v1_DN28132_c0_g1_i1_m56119
BeE60N14B10	No match	Unknown	5,74	
BeNSVP06B04	hypothetical protein [<i>Plasmodium yoelii yoelii</i>]	Unknown	4,53	
BeE90N12A05	No match	Unknown	2,35	
BeE30N11D01	No match	Unknown	2,28	
BeE60N01G04	No match	Unknown	1,71	

Table 4. The genes selected from genes with a maximum expression at 120 minutes of zoospore production.

ID of sequence	Annotation	Function of found homologs	Expression level	ID of <i>P. tribonemae</i> homologous sequence
BeG90N20H10	Threonyl-tRNA synthetase, Cytoplasmic (Threonine-1,00)	protein synthesis	4,99	Partr_v1_DN28019_C1_g1_i1_m57513
BeE60N09A10	Q96WN5 Dolichyl-phosphate-mannose: protein mannosyl	EPR protein transport, protein folding	1,46	Partr_v1_DN27509_C0_g1_i3_m30858
BeE120N38G07	No match (Stomatin)	actin assembly	7,36	Partr_v1_DN27917_C3_g1_i2_m11528
BeE60N07E05	P24032 Myosin regulatory light Chain 2, smooth musculature	myosin	4,2	Partr_v1_DN28637_C0_g1_i1_m50484
BeE120N30D02	Q8R384 Myh11 protein (motor activity)	cell contraction	3,29	Partr_v1_DN28942_C0_g1_i1_m25835
BeE60H28B01	P10989 Actin	actin	2,71	Partr_v1_DN25805_c0_g1_i1_m2964
BeE60N12E01	Q09196 Myosin regulatory light Chain Cdc4	myosin	2,66	Partr_v1_DN21838_C0_g2_i1_m70273
BeE60N16A06	Q873H2 Related to stomatin	actin assembly	2,28	Partr_v1_DN27917_C3_g1_i2_m11528
BeE90D04C07	Q96VU9 Cofilin	cell contraction	2,27	Partr_v1_DN22354_c0_g2_i1_m9247
BeE60N10E10	P19984 Profilin II	cell contraction	2,1	Partr_v1_DN28501_C0_g1_i15_m73444
BeE90D13B04	P05216 Tubulin alpha-6 chain	tubulin	4,89	Partr_v1_DN24548_c0_g1_i1_m19937
BeE90N18A12	No match (putative Dynein, axonemal heavy chain)	axonemal dynein	4,59	Partr_v1_DN29014_C0_g1_i1_m58781
BeE30N08A11	Q86ZW6 Alpha-tubulin (Fragment)	tubulin	4,14	Partr_v1_DN24548_C0_g1_i1_m19937
BeE90N11D07	Q8TD57 Axonemal heavy Chain dynein type 3	axonemal dynein	2,69	Partr_v1_DN29032_C0_g1_i1_m58576
BeE90N23C08	No match (dynein heavy chalk)	axonemal dynein	2,58	Partr_v1_DN29032_C0_g1_i1_m58576
BeE90N15E03	Q9DcM4 Dynein light polypeptide 4, axonemal	axonemal dynein	2,58	Partr_v1_DN21813_C0_g1_i1_m70213
BeE120N07A12	roadblock-related dynein light Chain [Ciona	axonemal dynein	2,46	Partr_v1_DN23034_C0_g2_i1_m27141
BeE90N17C06	Q9SMH3 Dynein 1-alpha heavy Chain, flagellar inner	axonemal dynein	2,23	Partr_v1_DN29037_C1_g1_i2_m58634
BeE120N38D06	RIKEN CDNA 4930506L13 [Mus musculus]	flagellum	2,13	Partr_v1_DN27517_C1_g1_i1_m30847
BeE60N12G09	P07436 Tubulin beta-1 Chain	tubulin	2,01	Partr_v1_DN27098_C0_g1_i2_m29329
BeG120N22C04	Q9D0M5 Dynein light Chain 2, Cytoplasmic	axonemal dynein	1,93	Partr_v1_DN21813_C0_g1_i1_m70213
BeE60N09H03	Q9R0L0 Mitogen-activated protein kinase-binding protein 1	Negative regulation in NF-kappab signaling (control of the genes for immune response, apoptosis and cell cycle in Metazoa). Negative regulation of interleukin-8 production (in Metazoa)	4,35	Partr_v1_DN27208_C0_g1_i2_m38843
BeE30N10H03	P31320 CAMP-dependent	CAMP-dependent	2,95	Partr_v1_DN24090_C0_g1_i1_m34665

	protein kinase regulatory Chain	regulation of enzyme activity		
BeE60H25C12	Q86HU8 NAD-dependent epimerase/dehydratase family protein	Coenzyme-dependent catalytic activity	2,77	Partr_v1_DN28528_c1_g1_i2_m73813
BeE120N25H03	Q9LKK9 14-3-3 protein	Broad spectrum regulatory protein (cell cycle, cell growth, differentiation, survival, apoptosis, migration and spreading)	2,48	Partr_v1_DN24195_C0_g1_i1_m70919
BeE120N32A12	Ankyrin repeat domain-containing protein 54 [Choanephora cucurbitarum]	Cellular response to influences, regulation of intracellular processes, signal transduction by p53 class mediator, protein kinase C signaling.	2,43	
BeE90N13A10	Q96VU5 UDP-glucose dehydrogenase Uxs2p	Biosynthesis of components of the extracellular matrix; likely play roles in signal transduction, cell migration, and cancer growth and metastasis	2,41	Partr_v1_DN27873_C1_g1_i2_m22458
BeE120N06B11	Q8CEE6 PAS domain Containing serine/threonine	Regulation of energy and metabolic processes	2,35	Partr_v1_DN27156_C0_g1_i2_m15570
BeE60N13H06	hypothetical protein UM03727,1 [Ustilago maydis 52	Protein folding, cell cycle regulator (yeast, Swi6 / Cdc10), Notch-signaling (Drosophila),	2,3	Partr_v1_DN27713_C2_g1_i2_m67234
BeE60N03A04	Q8K2P9 Rab12a protein (small GTPase mediated signal transduction)	Small gtpase mediated signal transduction	2,27	Partr_v1_DN24872_C0_g1_i1_m29831
BeG120N09D05	Q9LKK9 14-3-3 protein	Broad spectrum regulatory protein (cell cycle, cell growth, differentiation, survival, apoptosis, migration and spreading)	2,08	Partr_v1_DN24195_C0_g1_i1_m70919
BeE60N12F10	Translin domain-containing protein [Rozella allomycis CSF55]	Binding of RNA and DNA. Impact on transcription and translation.	1,62	
BeE30N07B02	Q9HFY6 Calmodulin	Enzyme activator	1,58	Partr_v1_DN23034_C0_g2_i1_m27141
BeE90N18E01	Q9C271 Probable cell division control protein CDc1	Hydrolase, participates in cell division	1,47	Partr_v1_DN25411_C0_g1_i3_m53616
BeE120N35H01	Q7SAQ1 AP-2 Complex subunit sigma (vesicle-mediated transport)	vesicular transport	4,26	Partr_v1_DN26963_C0_g1_i1_m6876
BeE60N08E08	O62547 Sec1-like protein	vesicular transport	2,93	Partr_v1_DN28591_C1_g1_i2_m73046
BeE120N28H02	O48920 ADP-ribosylation factor	vesicular transport	2,79	Partr_v1_DN23148_C0_g1_i1_m44017

BeE60N08B06	Q872J2 Probable Clathrin-associated adaptor	vesicular transport	2,73	Partr_v1_DN24926_C0_g1_i1_m45205
BeE60N09D06	Q9FRD2 Putative vesicle soluble NSF attachment pro	vesicular transport	2,73	Partr_v1_DN24409_C0_g1_i2_m66640
BeE90N18B06	No match (putative Adaptor-related protein complex)	vesicular transport	2,66	Partr_v1_DN26347_C1_g1_i1_m43463
BeE60H27A03	O74559 Surfeit locus protein 4 homolog	vesicular transport	1,89	Partr_v1_DN24815_c0_g1_i1_m29829
BeE30N10H08	P33723 GTP-binding protein ypt1	vesicular transport regulator	1,69	Partr_v1_DN25460_C0_g1_i1_m53725
BeE60N07F01	O13726 Putative sodium/hydrogen exchanger	H ⁺ and Na ⁺ balance	2,71	Partr_v1_DN26892_C0_g1_i1_m40512
BeE30N06A03	Q9U5N0 Vacuolar ATP synthase subunit H	creation of an acidic medium in vacuoles	2,6	Partr_v1_DN25385_C0_g1_i2_m21645
BeE120N26G05	P31413 Vacuolar ATP synthase 16 kDa proteolipid	creation of an acidic medium in vacuoles	2,51	Partr_v1_DN23964_C0_g1_i1_m49054
BeE60N10B03	Q7SEH8 Vacuolar ATP synthase 20 kDa proteolipid subunit	creation of an acidic medium in vacuoles	1,94	Partr_v1_DN23688_C0_g1_i2_m18889
BeE60N18C09	Q90ZF4 V-ATPase subunit A	transmembrane ion transport	1,85	Partr_v1_DN27211_C0_g1_i2_m38478
BeG30N03G06	Q9C0R0 Mitoch import inner membr translocase subunit tim23	protein transport to mitochondria	2,35	Partr_v1_DN23439_C0_g1_i2_m52658
BeE120N07F05	No match (Immature colon carcinoma transcript 1)	mitochondrial protein	2,69	Partr_v1_DN25096_C0_g1_i1_m51006
BeE60H27E10	P41764 Glucose-6-phosphate 1-dehydrogenase	carbohydrate and H ₂ O ₂ metabolism	2,45	Partr_v1_DN26620_c0_g1_i1_m69386
BeE60N16B11	Q7RVR8 Mannose-1-phosphate guanyltransferase	carbohydrate metabolism	2,03	Partr_v1_DN24856_C0_g1_i1_m29922
BeE60H22A08	Similar to tissue specific transplantation antigen	coenzyme binding	1,92	Partr_v1_DN25318_c2_g1_i2_m21631
BeE60N08H03	Q7PGR3 ENSANGP00000023984 (Fragment) (putative 26S protease regulatory subunit)	protein breakdown	2,35	Partr_v1_DN25528_C0_g1_i2_m20616
BeE60C01E02	Q7S2J5 Hypothetical protein (putative 26S protease regulatory subunit)	protein breakdown	2,73	Partr_v1_DN24210_c1_g1_i1_m36939
BeE120N08A01	Zgc:101786 [Danio rerio] (putative PARK2 co-regulated)	protein breakdown	2,48	Partr_v1_DN25066_C0_g1_i1_m50998
BeE120N37H01	Q9MZG9 Polyprotein (serine-type endopeptidase activity) (ubiquitin-40S ribosomal protein S27a)	protein breakdown	1,56	Partr_v1_DN33794_C0_g1_i1_m27932
BeE120N22B08	0	DNA polymerase	4,03	Partr_v1_DN26249_C0_g1_i1_m48730
BeE60N07E08	P40581 Glutathione peroxidase 3	cell antioxidant	2,33	Partr_v1_DN28822_C1_g1_i2_m33016
BeE30N14B04	No match	Unknown	4	
BeE60N06C01	No match	Unknown	3,84	Partr_v1_DN28443_C1_g1_i3_m42252
BeE60N07G07	No match	Unknown	3,18	
BeE120N02A03	No match	Unknown	3,1	
BeE120N31H05	No match	Unknown	2,5	
BeE60N05D04	No match	Unknown	2,19	Partr_v1_DN25113_C0_g1_i2_m76941

BeE90N04E09	Q9BZE7 Hypothetical protein EVG1	Unknown	2,19	
BeE90N16C12	No match	Unknown	2,08	
BeE120N03E07	No match	Unknown	2,01	
BeE60N09H02	No match	Unknown	1,97	
BeE90N21E01	No match	Unknown	1,93	Partr_v1_DN24250_C0_g1_i1_m36648
BeE60N05D09	No match	Unknown	1,83	Partr_v1_DN26918_C4_g1_i3_m7318

Table 5. The genes selected from genes with a maximum expression at 150 minutes of zoospore production.

ID of sequence	Annotation	Function of found homologs	Expression level	ID of <i>P. tribonemae</i> homologous sequence
BeE60N10H07	Q9BQH6 GTPase-activating Rap/Ran-GAP domain-like protein 3	Small gtpase signaling.	9,38	Partr_v1_DN24146_C0_g1_i1_m71146
BeE60N16D02	P34046 Guanine nucleotide-binding protein alpha-8	Transmembrane signaling, including the positive regulation of sporulation.	7,41	Partr_v1_DN25143_C0_g1_i2_m76558
BeE120N02E04	Q7YXG1 Soluble guanylyl cyclase 2 beta (Fragment)	Cgmp signaling.	6,96	Partr_v1_DN28109_C2_g1_i2_m55054
BeE60N07H08	Q8T367 Small G protein	Signal transduction.	4	Partr_v1_DN23557_C0_g1_i1_m14220
BeE60H29D02	O50052 Hypothetical protein (putative MOB kinase activator)	Hippo signaling. Control over cell division.	3,92	Partr_v1_DN27434_c2_g1_i10_m71583
BeE120N36B05	Q7QK56 AgcP14714 (Serine/threonine-protein kinase)	Regulation of the cell proliferation, programmed cell death (apoptosis), cell differentiation and embryonic development.	3,58	Partr_v1_DN27497_C1_g1_i2_m72423
BeE60N03C06	Q9HDE1 calcineurin B regulatory subunit	Ca-dependent signal transduction.	3,51	Partr_v1_DN23421_C0_g1_i3_m52587
BeZSPN16D09	Q12741 cAMP-dependent protein kinase catalytic sub	Ca-dependent signal transduction.	3,36	Partr_v1_DN26858_C1_g2_i1_m40852
BeG60N08H03	Q8J0B8 G protein alpha subunit	Signal transduction.	3,27	Partr_v1_DN24850_C0_g1_i3_m29490
BeE60N18D05	Q7RVR4 Negative regulator of the PHO system	Regulation of intracellular transport.	3,03	Partr_v1_DN24332_C0_g1_i2_m31940
BeE120N25C02	Q7PUT0 ENSANGP00000020068 (Fragment) (putative member of RAS oncogene family)	Ras-proteins. Cellular signaling (cell growth and cell death).	2,81	Partr_v1_DN23705_C0_g1_i1_m53132
BeE60H23E05	P14318 Muscle-specific protein 20	Calponin homology domain-protein. Actin binding, cellular signaling.	2,75	Partr_v1_DN23241_c0_g1_i1_m35364
BeE120N18F01	Q86WN6 Phosphodiesterase PDE9A13	Signal transduction.	2,75	Partr_v1_DN28842_C4_g1_i5_m33964
BeE90N24F09	No match (putative adenylate cyclase)	Signal transduction.	2,71	Partr_v1_DN28367_C1_g1_i4_m79020
BeE120N04B04	Q95WR8 PXF isoform c (putative Son of sevenless homolog)	Cellular signaling. Associated with ras proteins.	2,62	Partr_v1_DN28751_C1_g1_i5_m63184
BeG120N10E08	Q9Y6V7 Probable ATP-dependent RNA helicase DDX49	Signal transduction (mapk / erk pathway).	2,58	Partr_v1_DN26018_C0_g1_i2_m194
BeE120N28E07	Q9HFN1 G protein alpha subunit (Fragment)	Cellular signaling. Membrane receptors.	2,51	Partr_v1_DN25876_C1_g1_i2_m2864
BeE30N01C07	Q14107 cell division cycle protein 123 homolog	Regulation of cell division.	2,38	Partr_v1_DN25976_C1_g1_i1_m68296
BeE60N04E11	Q62219 Transforming growth factor beta 1 induced t	Cell adhesion. Control of proliferation, cell	2,36	Partr_v1_DN28657_C0_g1_i2_m50361

		differentiation (tgfb signaling, wnt signaling).		
BeE60H27A04	No match (putative mitogen-activated protein kinase)	Mapk signaling, control of transcription, metabolism, cell proliferation and motility, apoptosis, etc.	2,31	Partr_v1_DN28569_c1_g2_i3_m72568
BeE120N30B12	P31320 cAMP-dependent protein kinase regulatory	Regulation of metabolism.	2,31	Partr_v1_DN23954_C1_g1_i1_m49099
BeE120N26G06	Q8VcX2 Solute carrier family 35 member c2	Negative regulation of gene expression, positive regulation of notch signaling (embryogenesis in metazoa).	2,13	Partr_v1_DN28749_C2_g1_i1_m62829
BeG30N13H07	Q13685 Angio-associated migratory cell protein	Regulation of cell differentiation, cell migration.	2,07	Partr_v1_DN26285_C0_g2_i1_m48036
BeE90N12F11	No match (putative Coiled-coil domain containing 147)	Regulatory protein (organization of the cytoskeleton of microtubules, negative regulation of phosphatase activity, post-translational protein modification, regulation of mitotic nuclear division).	2,01	Partr_v1_DN28346_C1_g1_i2_m79229
BeE60H26C05	Q7PY52 AgcP12010 (Fragment) (putative stromal cell-derived factor)	Regulation of cell proliferation and interaction.	2	Partr_v1_DN23463_c0_g2_i1_m52447
BeE120N28B11	No match (Tetraspannin-domain-containing protein [Rhizophagus irregularis])	Membrane protein. Regulate trafficking, signaling, cell proliferation, adhesion, spreading, migration, cell-cell fusion, pathogen entry, cancer.	9,65	
BeE120N06A04	No match (transmembrane protein 229A-like [Acipenser ruthenus])	Membrane protein. Proliferation, cell motility.	4,89	
BeE120N02A09	23K integral membrane protein - fluke (Schistosoma) (Tetraspannin-domain-containing protein [Rhizophagus irregularis])	Membrane protein. Regulate trafficking, signaling, cell proliferation, adhesion, spreading, migration, cell-cell fusion, pathogen entry, cancer.	4,29	
BeE60N05B05	No match (Protein chibby-like 1 [Acipenser ruthenus])	Negative regulation of transcription, negative regulation of wnt signaling, cell differentiation.	3,12	
BeE90N06H03	Q81cV0 Hydrolase (Haloacid dehalogenase-like hydrolase)	Metabolic processes	7,11	Partr_v1_DN26256_C0_g2_i3_m48251
BeE120N26B11	O60931 cystinosin	Maintaining lysosome	4,17	Partr_v1_DN26937_C2_g1_i1_m6716

		activity		
BeE60H28F02	O74936 Acyl-coA oxidase 3	Lipid metabolism, ppar signaling (lipid metabolism, cell division)	3,58	Partr_v1_DN28236_c0_g1_i4_m76000
BeE120N01D10	Q8S9c7 Flavonoid 3'-hydroxylase	Biosynthesis	2,46	Partr_v1_DN26867_C0_g1_i1_m40175
BeE30N02B01	O04974 2-isopropylmalate synthase B	Metabolic processes	2,39	Partr_v1_DN24871_C0_g1_i1_m29706
BeE120N36H09	Q8EXG1 hypothetical protein (carbohydrate metabolic process) (putative Cellulase (glycosyl hydrolase family 5))	Cellulase	2,35	Partr_v1_DN27943_C0_g1_i1_m11403
BeE60N05D05	Q8EBH2 Transaldolase	Carbohydrate metabolism (in metazoa + signaling)	1,49	Partr_v1_DN24039_C0_g1_i1_m34556
BeE60N12E11	Q9NY68 choline transporter-like protein 2	Synthesis of phospholipids (membrane construction)	10,2	Partr_v1_DN28724_C1_g1_i1_m61712
BeG60N07D09	Q9NPJ3 Thioesterase superfamily member 2 (HotDog domain-containing protein [Catenaria anguillulae PL171])	Fatty acid oxidation and control glucose utilization	2,62	
BeE90D07E02	Q9RSD4 NADH-dependent flavin oxidoreductase, putative (FMN-linked oxidoreductase [Serendipita vermifera 'subsp. biscuit'])	Oxidative metabolism	2,53	
BeE120N07D10	No match (putative 60S ribosomal protein L6)	Ribosomes	6,23	Partr_v1_DN28753_C0_g1_i14_m63162
BeE120N01E11	P58466 carboxy-terminal domain RNA polymerase II p	Mrna maturation	4,56	Partr_v1_DN28056_C4_g1_i2_m57647
BeE90D20G12	P52808 60S ribosomal protein L30-1	Ribosomes	2,85	Partr_v1_DN2042_c0_g1_i1_m14547
BeE60H30F11	O74341 T-complex protein 1, gamma subunit	Protein folding, including actin and tubulin	2,53	Partr_v1_DN24252_c0_g1_i1_m36972
BeE90N10F09	O08678 Serine/threonine kinase	Metabolic processes, post-translational modification	2,48	Partr_v1_DN27202_C0_g1_i3_m38485
BeE30N13H09	Q81EK9 Peptidoglycan N-acetylglucosamine deacetylase (putative chitin deacetylase)	Chitin metabolism	6,96	Partr_v1_DN25951_C0_g3_i1_m68819
BeZSPN14D10	O93787 chs3	Chitin synthase	5,24	Partr_v1_DN27712_C1_g1_i1_m67620
BeE120N28C07	Q8KU53 EF0108	Chitin metabolism	3,71	Partr_v1_DN25951_C0_g3_i2_m68820
BeE60H27E01	O93787 chs3	Chitin synthase	3,36	Partr_v1_DN28730_c0_g1_i1_m62801
BeE120N32H02	O93787 chs3	Chitin synthase	3,27	Partr_v1_DN28871_C0_g1_i1_m33284
BeE120N27C01	Q7TNJ2 ATP-binding cassette transporter sub-family	Transmembrane transport	4,69	Partr_v1_DN28721_C1_g1_i5_m62799
BeE60N04B11	P26587 Aquaporin TIP3,1	Membrane water transport	3,34	Partr_v1_DN26309_C0_g1_i2_m42936

BeE120N05H04	Q7PFP4 Putative GABA-B receptor 3 (putative Inherit from COG: phosphate abc transporter)	Abc transport, excretion	2,97	Partr_v1_DN28206_C1_g1_i2_m76354
BeE120N27G08	Q86AY4 Similar to Ralstonia solanacearum (putative Inherit from COG: phosphate abc transporter)	Abc transport, excretion	2,57	Partr_v1_DN28206_C1_g1_i2_m76354
BeE60N19E10	Q8T665 ABC transporter AbcH,1	Abc transport, excretion	2,16	Partr_v1_DN25135_C0_g1_i4_m76893
BeE90N01E04	P53871 cHS1-SRP1 (glutathione catabolic process)	Redox balance, redox reactions	2,57	Partr_v1_DN28159_C4_g1_i2_m56092
BeE120N28D07	P40581 Glutathione peroxidase 3 GO:0005622	Redox balance, redox reactions	2,41	Partr_v1_DN28822_C1_g1_i2_m33016
BeE60H30C05	NADH-quinone oxidoreductase [Gloeophyllum trabeum]	Redox balance, redox reactions	2,41	Partr_v1_DN11653_c0_g1_i1_m42863
BeE60N07D05	Q7UHD8 Probable D-alanine-D-alanine ligase (Select seq gb OAQ35997.1 (glutathione synthetase ATP-binding domain-like protein [Mortierella elongata AG-77])	Redox balance, redox reactions	2,38	
BeE90N02C04	No match (putative Synaptojanin)	Endocytosis, actin work	6,5	Partr_v1_DN27916_C3_g1_i1_m11702
BeE60H15H11	Q7SGN0 Hypothetical protein (actin binding)	Depolymerization of actin filaments	4,99	Partr_v1_DN23512_c0_g1_i2_m14455
BeE90N21E02	No match (sever	Actin-based motility control	3,61	Partr_v1_DN28745_C0_g1_i1_m61670
BeG120N07D05	No match (putative Actin)	Actin	1,61	Partr_v1_DN28082_C0_g1_i3_m57489
BeE120N20H04	likely protein kinase [candida albicans Sc5314] (Map microtubule affinity-regulating kinase	Microtubule organization, axonem elongation	23,59	Partr_v1_DN27202_C0_g2_i1_m38488
BeE90D18C07	Q8AWD6 Tubulin, alpha 2	Tubulin	4,11	Partr_v1_DN24548_c0_g1_i1_m19937
BeE120N28A06	KIAA0590 Intraflagellar transport protein 140 homolog	Flagella assembly	2,28	Partr_v1_DN28604_C0_g1_i2_m50223
BeG60N12B02	No match (putative IMP-specific 5'-nucleotidase involved in IMP (inositol monophosphate) degradation)	Nucleotide metabolism (purine)	3,01	Partr_v1_DN25973_C1_g1_i3_m68482
BeZSPN15B04	hypothetical protein [Neurospora crassa] (putative Ectonucleoside triphosphate diphosphohydrolase)	Nucleotide metabolism	5,13	Partr_v1_DN28171_C1_g1_i1_m55599
BeG90N17F03	Q9NQT4 Exosome complex exonuclease RRP46	Nucleic acid metabolism	2,38	Partr_v1_DN24020_C0_g1_i1_m34703
BeE90N07F09	Q7W512 DNA repair protein	DNA repair	2,01	
BeE60N05G06	O15127 Secretory carrier-associated membrane protein (scamp family-domain-containing protein [Catenaria	Membrane protein, vesicular transport	2,81	

	anguillulae PL171])			
BeE120N25B05	No match (related to SERF-like protein)	Дестабилизация белка, образование фибрилл. Образование амилоидных фибрилл (у Метазоа)	2,79	
BeE120N38C11	No match	Unknown	3,76	Partr_v1_DN25917_C0_g1_i1_m68777
BeE60N19C09	No match	Unknown	37,53	
BeE120N22C08	No match	Unknown	9,06	
BeE60C25D08	Q88P63 Conserved hypothetical protein	Unknown	8,82	
BeE120N25E05	0	Unknown	8,63	
BeE120N30G01	No match	Unknown	7,94	
BeNSVP09G10	No match	Unknown	7,26	
BeZSPN17D01	No match	Unknown	4,5	
BeE120N20C04	No match	Unknown	3,32	
BeG60N06E08	No match	Unknown	3,32	
BeG30N16C06	No match	Unknown	2,85	
BeE60N10D02	No match	Unknown	2,81	
BeE90N04D01	No match	Unknown	2,53	
BeG30N14D11	No match	Unknown	2,5	
BeE120N27G03	No match	Unknown	2,22	
BeE120N08G03	No match	Unknown	2,11	
BeE120N32E07	No match	Unknown	2,04	
BeE60N13A03	No match	Unknown	2,01	
BeG120N14G12	No match	Unknown	1,75	