

Title

Analysis of expressed sequence tags (ESTs) from Lentinula edodes

Author(s)

Takumi Suizu, Guo-Lei Zhou, Yasuo Oowatari & Makoto Kawamukai

Journal

Applied Microbiology and Biotechnology volume 79, pages461–470(2008)

Published 01 June 2008

URL https://doi.org/10.1007/s00253-008-1441-2

> この論文は出版社版でありません。 引用の際には出版社版をご確認のうえご利用ください。

Short contribution

Analysis of expressed sequence tags (ESTs) from Lentinula edodes

Takumi Suizu, Zhou Guo-Lei, and Makoto Kawamukai*

Running title: Lentinula edodes EST

*Corresponding author

Department of Life Science and Biotechnology, Faculty of Life and Environmental Science, Shimane University,

1060 Nishikawatsu, Matsue, Shimane 690-8504, Japan

Phone & Fax: +81-852-32-6587,

E-mail: kawamuka@life.shimane-u.ac.jp

Abstract

The 1,031 expressed sequence tags (ESTs) from the basidiomycete *Lentinula edodes* were generated as a pilot experiment to see distribution of genes expressed in *L. edodes*. Among them, genes for hydrophobin, which are specifically found in filamentous fungi, were most frequently obtained (33 times), indicating they are highly expressed in *L. edodes*. In addition to known hydrophobin 1 and 2 types, our analysis revealed the existence of novel types of hydrophobin, which we named hydrophobin 3, 4, and 5. As secondly and thirdly expressed genes, genes for phosphatidylserine decarboxylase and formate dehydrogenase were obtained 8 times and 7 times, respectively. It should be noted that two important genes involved in the RNAi pathway were found, suggesting a future application for gene shut down. The 50 ESTs were identical with the sequences already reported in *L. edodes*. The 402 ESTs were found to show significant sequence similarity (E value $\leq 1 \times 10^{-5}$) with the proteins reported (or predicted) in other species. The 419 ESTs contained polyA. In total 387,952 bp sequences were obtained and registered in DDBJ/GenBank (accession number BJ998097-BJ999127).

Keywords Lentinula edodes, cDNA, EST

Introduction

Lentinula edodes belonging to Basidiomycota is the edible mushroom popularly known as Shiitake mushroom in Japan. There are 250 genomic DNA or cDNA sequence entries available in GenBank database (Jul, 2006 release). Analysis of about 60 different genes from *L. edodes* were reported in the literature including the CAP and 14-3-3 genes which we had analyzed (Kawamukai et al., 1992; Zhou et al., 1998; Zhou et al., 2000). Isolation of the genes that are specifically expressed in fruit body formation in *L. edodes* led to the isolation of the gene encoding a cytochrome P450 protein (Hirano et al., 2004). A representational difference analysis during fruiting body formation in *L. edodes* revealed 105 genes (Miyazaki et al., 2005). Up to now, genomes of several mushrooms have been determined, but the genome and cDNA sequences of *L. edodes* have not been thoroughly elucidated. Because knowledge of *L. edodes* chromosomes is very limited, even the genome size and the exact chromosome number sof *L. edodes* has eight chromosomes (Tanaka R. and Koga I, 1972).

Expressed Sequence Tags (ESTs) were useful to know how many different genes were roughly expressed in a certain species. It will also help to know the sites of intron(s) by comparing EST with the genomic DNA sequences. Thus, EST provides a cost-effective approach for gene discovery. A large scale EST analyses were conducted in *Aspergillus niger* (Semova et al., 2006), *Neurosphora crassa* (Zhu et al., 2001), *Paracoccidioides brasiliensis*, and *Ustilago maydis* (Sacadura and Saville, 2003) among fungi apart from yeasts. Genome sequences of the lignocellulose degrading *fungus* *Phanerochaete chrysosporium* (Martinez et al., 2004) human pathogenic basidiomycetous yeast *Cryptococcus neoformanswas* (Loftus et al., 2005), rice blast fungus *Magnaporthe grisea* (Dean et al., 2005) and *Aspergillus fumigatus* (Nierman et al., 2005) were completed. But, no such an approach was conducted in *L. edodes*.

In this study, we have determined 1,031 ESTs of *L. edodes* as a pilot experiment by random sequencing of the cDNA library.

Materials and Methods

Construction of L. edodes cDNA libraries

We adopted two strategies for constructing the cDNA libraries which was made in the two-hybrid vector for the other purpose. One strategy made use of a previously-constructed phage library. We amplified a phage population of around 1.2 x 10⁶ plaque-forming units from a previously-constructed λ gt 10 cDNA library and extracted the phage DNA from 1 liter of phage culture. The phage DNA was digested with *Eco* RI and inserts longer than 500 bp were recovered by sucrose-gradient centrifugation. These cDNAs were then inserted into *Eco* RI-digested, dephosphorylated pGAD GH (Clontech), introduced into *E. coli* and purified using Qiagen-500 tips (Qiagen). The library thus obtained consisted of plasmids prepared from about 2 x 10⁶ *E. coli* colonies. The other strategy we used was more conventional. Total RNA was extracted from vegetative mycelia of strain FMC12 by the AGPC (acid guanidinium-phenol-chloroform) method. Poly (A)+ mRNA was purified with oligotex-dT 30 (TaKaRa) and cDNA was synthesized from poly (A)+ mRNA using a cDNA synthesis kit from Amersham according to the manufacturer's instructions. The cDNA fragments were purified using a spin column (Pharmacia) and those longer than 400 bp were collected. The library thus obtained consisted of about 5 x 10^6 independent clones.

DNA sequencing and analysis

For sequencing three primers, namely, M13 forward primer GTTTTCCCAGTCACGACGTTGTA, M13 primer reverse AGCGGATAACAATTTCACACAGGA GAD and primer CCGTCGACGTAATACGACTCACTATAG, were used. To determine the long DNA in some clones, oligonucleotides were synthesized. DNA sequences were determined by the dideoxynucleotide chain termination method using an ABI377 DNA sequencer. Similarity searches were performed by BLASTx, BLASTp and BLASTn against DNA/protein/EST data bases in DDBJ/GenBank.

Results

Sequence analysis

Random sequencing of cDNA from *L. edodes* was done in the library constructed in the vector pGAD GH. The library was originally constructed to find the proteins that interact with the bait protein by two hybrid screening (Zhou et al., 2000). But it was here used as an EST analysis. Because the cDNA library was constructed in the vector pGAD GH at the *Eco* RI sites, the fragments of cDNA frequently contained *Eco* RI sites in both ends. By randomly sequencing, 1,031 ESTs was constructed. In total 387,952 bp sequences were obtained and registered in GenBank/DDBJ (accession number BJ998097-BJ999127). Average EST length was calculated to be 376bp.

The list of the ESTs found in L. edodes that retain the sequence similarity at the amino acids (or DNA) level (E value $\leq 1 \times 10^{-5}$) with the proteins (or genes) from other species was shown in Table 1. Only one EST were listed in Table 1 even though more than two ESTs were obtained. The sequences of the genes homologous to uncharacterized genes were 98 and those are omitted from the list of Table 1. EST was first compared with the sequence registered in the NCBI data base by tBLASTx or BLASTn. The annotated web sites based on the characterized genes from two yeasts S. [http://www.yeastgenome.org/] S. cerevisiae and pombe [http://www.sanger.ac.uk/Projects/S pombe/] gave us the most useful references for estimation of their functions. By classification, the genes for metabolic enzymes were most frequently obtained and then ones for transport, translation, and protein degradation followed (Table 1).

The number of the times in which the same clones were obtained was shown in Table 2. The 25 genes obtained two times were omitted from the list of Table2. Among 1,031 ESTs, hydrophobins were most frequently identified. They summed up to 33 times that means hydrophobins 1, 2, 3, 4, and 5 types are obtained 24, 2, 2, 2, 3 times, respectively. From the sequences we found the existence of hydrophobin 3, 4, and 5 types besides already known hydrophobin 1 and 2 (Ng et al., 2000; Nishizawa et al., 2002). Our result that hydrophobins are highly expressed in *L. edodes* support the results that

hydrophobins are expressed at high levels in many filamentous fungi (Linder et al., 2005). The next frequently obtained ESTs are the ones that encode phosphatidylserine decarboxylase (8 times) and then formate dehydrogenase (7 times). Sometimes, two or more paralogous genes were obtained in ESTs such as the genes for D-arabinono-1,4-lactone oxidase, DAHP synthase, flavin-containing monooxygenase, superoxide dismutase, calmodulin, and metalloprotease. 21 different ribosome encoding ESTs were obtained, but no systematic naming of ribosomal proteins were performed here. 5.8 S, 25S and 18S ribosomal RNA sequences and their internal spacer sequences were included in ESTs, where 5.8S and 18S ribosomal RNA sequence have not been reported in *L. edodes*.

Discussion

In this study, we have determined the 1,031 ESTs from *Lentinula edodes* (Shiitake mushroom). The 50 ESTs were identical with the sequences already reported in *L. edodes*. The 402 ESTs were found to show significant sequence similarity (E value ≤ 1 x 10⁻⁵) with the proteins reported (or predicted) in other species. Those ESTs include many interesting genes to study for application and basic microbiology.

Some ESTs for glycoside hydrolases including alfa-amylase, chitinase, alfa-galactosidase, beta-1,3-glucanase (Sakamoto et al., 2005), beta-glucosidase, mannase, alfa-mannosidase, and beta-mannosidase were obtained. Those genes are potentially useful as enzyme resources for searching new sugar hydrolytic way. The genes for P450 type and other oxygenases may contribute the understanding and

application for none-degradable compound, which *L. edodes* naturally can degrade. To support the knowledge that *L. edodes* produces the precursor of vitamin D, several sterol biosynthetic genes were found. In addition to *fad1* encoding delta 9-fatty acid desaturase and *fad2* encoding delta 12-fatty acid desaturase (Sakai and Kajiwara, 2005), the gene for delta 6-fatty acid desaturase was obtained in ESTs. The *priA* gene which has been known to be developmentally regulated was obtained (Kajiwara et al., 1992). The second *ras* gene, which we named *ras2*, similar to *ras1* (Hori et al., 1991) was obtained. Those genes will probably play roles in development of *L. edodes*. Most interestingly, there exist the genes similar to argonaute and RNA dependent RNA polymerase in ESTs, that is the part of evidence that the RNAi mechanism is operating in *L. edodes*. The RNAi method for gene shut down will be extremely useful if it become possible, because otherwise it is extremely difficult at present to make gene disruption in *L. edodes*.

Our EST analysis proved that it is very efficient approach to find distributions of the expressed genes and the novels genes, which retain the potential source of beneficial enzymes for biotechnology. Continuation of the EST analysis will give us more information on the distributions of the genes in *L. edodes* and further contribute in the field of applied microbiology as well.

Acknowledgements

This study was supported by a grant-in-aid from Hokuto Corp. We like to thank K. Yagi, and D. Yano for technical assistance.

References

- Dean R A, Talbot N J, Ebbole D J, Farman M L, Mitchell T K, Orbach M J, Thon M, Kulkarni R, Xu J R, Pan H, Read N D, Lee Y H, Carbone I, Brown D, Oh Y Y, Donofrio N, Jeong J S, Soanes D M, Djonovic S, Kolomiets E, Rehmeyer C, Li W, Harding M, Kim S, Lebrun M H, Bohnert H, Coughlan S, Butler J, Calvo S, Ma L J, Nicol R, Purcell S, Nusbaum C, Galagan J E, Birren B W (2005) The genome sequence of the rice blast fungus *Magnaporthe grisea*. Nature 434: 980-986
- Hirano T, Sato T, Enei H (2004) Isolation of genes specifically expressed in the fruit body of the edible basidiomycete *Lentinula edodes*. Biosci Biotechnol Biochem 68: 468-472
- Hori K, Kajiwara S, Saito T, Miyazawa H, Katayose Y, Shishido K (1991) Cloning, sequence analysis and transcriptional expression of a *ras* gene of the edible basidiomycete *Lentinus edodes*. Gene 105: 91-96
- Kajiwara S, Yamaoka K, Hori K, Miyazawa H, Saito T, Kanno T, Shishido K (1992)
 Isolation and sequence of a developmentally regulated putative novel gene, *priA*, from the basidiomycete *Lentinus edodes*. Gene 114: 173-178
- Kawamukai M, Gerst J, Field J, Riggs M, Rodgers L, Wigler M, Young D (1992)Genetic and biochemical analysis of the adenylyl cyclase-associated protein, cap, in *Schizosaccharomyces pombe*. Mol Biol Cell 3: 167-180
- Linder M B, Szilvay G R, Nakari-Setala T, Penttila M E (2005) Hydrophobins: the protein-amphiphiles of filamentous fungi. FEMS Microbiol Rev 29: 877-896
- Loftus B J, Fung E, Roncaglia P, Rowley D, Amedeo P, Bruno D, Vamathevan J, Miranda M, Anderson I J, Fraser J A, Allen J E, Bosdet I E, Brent M R, Chiu R, Doering T L, Donlin M J, D'Souza C A, Fox D S, Grinberg V, Fu J, Fukushima M, Haas B J, Huang J C, Janbon G, Jones S J, Koo H L, Krzywinski M I, Kwon-Chung J K, Lengeler K B, Maiti R, Marra M A, Marra R E, Mathewson C A, Mitchell T G, Pertea M, Riggs F R, Salzberg S L, Schein J E, Shvartsbeyn A, Shin H, Shumway M, Specht C A, Suh B B, Tenney A, Utterback T R, Wickes B L, Wortman J R, Wye N H, Kronstad J W, Lodge J K, Heitman J, Davis R W, Fraser C M, Hyman R W (2005) The genome of the basidiomycetous yeast and human pathogen *Cryptococcus neoformans*. Science 307: 1321-1324

- Martinez D, Larrondo L F, Putnam N, Gelpke M D, Huang K, Chapman J, Helfenbein K G, Ramaiya P, Detter J C, Larimer F, Coutinho P M, Henrissat B, Berka R, Cullen D, Rokhsar D (2004) Genome sequence of the lignocellulose degrading fungus *Phanerochaete chrysosporium* strain RP78. Nat Biotechnol 22: 695-700
- Miyazaki Y, Nakamura M, Babasaki K (2005) Molecular cloning of developmentally specific genes by representational difference analysis during the fruiting body formation in the basidiomycete *Lentinula edodes*. Fungal Genet Biol 42: 493-505
- Ng W L, Ng T P, Kwan H S (2000) Cloning and characterization of two hydrophobin genes differentially expressed during fruit body development in *Lentinula edodes*. FEMS Microbiol Lett 185: 139-145
- Nierman W C, Pain A, Anderson M J, Wortman J R, Kim H S, Arroyo J, Berriman M, Abe K, Archer D B, Bermejo C, Bennett J, Bowyer P, Chen D, Collins M, Coulsen R, Davies R, Dyer P S, Farman M, Fedorova N, Feldblyum T V, Fischer R, Fosker N, Fraser A, Garcia J L, Garcia M J, Goble A, Goldman G H, Gomi K, Griffith-Jones S, Gwilliam R, Haas B, Haas H, Harris D, Horiuchi H, Huang J, Humphray S, Jimenez J, Keller N, Khouri H, Kitamoto K, Kobayashi T, Konzack S, Kulkarni R, Kumagai T, Lafon A, Latge J P, Li W, Lord A, Lu C, Majoros W H, May G S, Miller B L, Mohamoud Y, Molina M, Monod M, Mouyna I, Mulligan S, Murphy L, O'Neil S, Paulsen I, Penalva M A, Pertea M, Price C, Pritchard B L, Quail M A, Rabbinowitsch E, Rawlins N, Rajandream M A, Reichard U, Renauld H, Robson G D, Rodriguez de Cordoba S, Rodriguez-Pena J M, Ronning C M, Rutter S, Salzberg S L, Sanchez M, Sanchez-Ferrero J C, Saunders D, Seeger K, Squares R, Squares S, Takeuchi M, Tekaia F, Turner G, Vazquez de Aldana C R, Weidman J, White O, Woodward J, Yu J H, Fraser C, Galagan J E, Asai K, Machida M, Hall N, Barrell B, Denning D W (2005) Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus. Nature 438: 1151-6
- Nishizawa H, Miyazaki Y, Kaneko S, Shishido K (2002) Distribution of hydrophobin 1 gene transcript in developing fruiting bodies of *Lentinula edodes*. Biosci Biotechnol Biochem 66: 1951-1954
- Sacadura N T, Saville B J (2003) Gene expression and EST analyses of *Ustilago maydis* germinating teliospores. Fungal Genet Biol 40: 47-64
- Sakai H, Kajiwara S (2005) Cloning and functional characterization of a Delta12 fatty acid desaturase gene from the basidiomycete *Lentinula edodes*. Mol Genet

Genomics 273: 336-341

- Sakamoto Y, Irie T, Sato T (2005) Isolation and characterization of a fruiting body-specific exo-beta-1,3-glucanase-encoding gene, exg1, from *Lentinula edodes*. Curr Genet 47: 244-252
- Semova N, Storms R, John T, Gaudet P, Ulycznyj P, Min X J, Sun J, Butler G, Tsang A (2006) Generation, annotation, and analysis of an extensive Aspergillus niger EST collection. BMC Microbiol 6: 7
- Tanaka R, Koga I (1972) Karyological studies on *Lentinus edodes*, a basidiomycete. J Jpn Bot 7:289-296
- Zhou G L, Miyazaki Y, Nakagawa T, Tanaka K, Shishido K, Matsuda H, Kawamukai M (1998) Identification of a CAP (adenylyl-cyclase-associated protein) homologous gene in *Lentinus edodes* and its functional complementation of yeast CAP mutants. Microbiology 144 (Pt 4): 1085-1093
- Zhou G L, Yamamoto T, Ozoe F, Yano D, Tanaka K, Matsuda H, Kawamukai M (2000) Identification of a 14-3-3 protein from *Lentinus edodes* that interacts with CAP (adenylyl cyclase-associated protein), and conservation of this interaction in fission yeast. Biosci Biotechnol Biochem 64: 149-159
- Zhu H, Nowrousian M, Kupfer D, Colot H V, Berrocal-Tito G, Lai H, Bell-Pedersen D, Roe B A, Loros J J, Dunlap J C (2001) Analysis of expressed sequence tags from two starvation, time-of-day-specific libraries of *Neurospora crassa* reveals novel clock-controlled genes. Genetics 157: 1057-1065

Table 1. footnotes

^a The Accession number of DDBJ/GenBank

^bThe determined nucleotide base pair

^c Circle indicates the clone that contained polyA and hyphen did not.

^d The putative functions given by NCBI database are classified by a broad category.

^d The gene name in NCBI data base. Bold ones indicate the gene naming in *L. edodes*.

^f Abbreviations of organisms are followings:

Agaricus bisporus Agaricus xanthodermus Agrobacterium tumefaciens Amanita muscaria Antrodia camphorata Arabidopsis thaliana Arthroderma benhamiae Aspergillus flavus Aspergillus fumigatus Aspergillus nidulans Aspergillus niger Aspergillus oryzae Botryotinia fuckeliana Caenorhabditis elegans Candida albicans Chlamydomonas reinhardtii Chloroflexus aurantiacus Coprinus cinereus Cryptococcus neoformans Danio rerio Dictyostelium discoideum Emericella nidulans Ganoderma microsporum Homo sapiens Laccaria bicolor Lentinula edodes Mus musculus Neurospora crassa Nicotiana sylvestris Paracoccidioides brasiliensis Paxillus involutus Pleurotus djamor Pleurotus sapidus Rhizopus stolonifer Russula olivacea Saccharomyces cerevisiae Schizophyllum commune Schizosaccharomyces pombe Thermoascus aurantiacus Thermotoga maritima Ustilago maydis Xenopus tropicalis ⁸The E score corresponds to the tBLASTX expected value obtained from homology analysis, except scores donated by "* " where the BLASTn value was indicated.

Table 1 Putative functions of *L.edodes* ESTs

^a DDBJ/GenBank	^a bp	^c polyA	^d Category / Putative Function	egene	forganisms	gscore
	- r	r J	Metabolism	8	8	
BJ998177	557	-	17-beta-hydroxysteroid dehydrogenase type 4	mfp2	D. rerio	2.00E-21
BJ998991	497	-	2-methyl citrate dehydratase	PDH1	S. cerevisiae	5.00E-66
BJ998475	568	\bigcirc	2-nitropropanedioxygenase	Afu2g09850	A. fumigatus	1.00E-27
BJ998225	577	-	2.6-dihydroxybenzoic acid decarboxylase	rdc	A. tumefaciens	1.00E-23
BJ998281	552	\bigcirc	3'(2'),5'-bisphosphate nucleotidase	tol1	S. pombe	3.00E-29
BJ998531	507	Õ	6-phosphofructokinase	pfk1	S. pombe	6.00E-06
B1998600	226	-	6-phosphogluconate dehydrogenase	GND2	S. cerevisiae	3.00E-25
BJ998416	296	_	acetyl-CoA acetyltransferase	aat	L. bicolor	2.00E-21
BJ998465	614	_	acyl-Coenzyme A dehydrogenase, short/branched chain	ACADSB	H. sapiens	1.00E-53
BJ998238	569	_	alcohol dehvdrogenase	ADH1	S. pombe	3.00E-52
BJ999047	525	_	aldehvde dehvdrogenase 1	aldA	A. nidulans	3.00E-57
BJ998838	568	_	aldehyde dehydrogenase 2	ALD2	S. cerevisiae	2.00E-24
BJ998770	525	_	alpha-amylase	amvA	A. niger	3.00E-29
BJ998671	481	_	alpha-galactosidase	agl3	T. reesei	3.00E-41
BJ998955	369	-	alpha-glucan synthase	mok1	S. pombe	8.00E-08
BJ998453	632	-	alpha-mannosidase 1A class I	mns1A	E. nidulans	4.00E-24
BJ998729	444	-	alpha-mannosidase	MAN1B1	H. sapiens	3.00E-21
BJ998414	630	_	aminolevulinic acid synthetase	hem1	A. bisporus	2.00E-24
BJ998205	860	_	aminotransferase	YJL060w	S. cerevisiae	2.00E-44
BJ999076	638	_	beta-1,3-glucan binding protein	NCU04168.1	N. crassa	3.00E-32
BJ999109	333	_	beta-1,3-glucan synthase	bgs4	S. pombe	4.00E-17
BJ998774	448	\bigcirc	beta-1,3-glucanase	exg1	L. edodes	1.00E-71
BJ998278	400	-	beta-glucosidase	BGL2	T. aurantiacus	3.00E-13
BJ998470	676	_	beta-mannosidase	manB	T. maritima	7.00E-08
BJ998456	562	-	C-4 methyl sterol oxidase	erg25	S. pombe	5.00E-55
BJ998448	633	-	chitinase	chi	Aeromonas	4.00E-07
BJ998903	354	-	chitin deacetylase-like mannoprotein MP98	CND03490	C. neoformans	6.00E-06
BJ998551	473	-	citrate synthase	cit1	S. pombe	2.00E-33
BJ998189	194	_	cyclohexanone 1.2-monooxygenase	Afu8g00440	A. fumigatus	6.00E-05
BJ999008	487	_	DAHP-synthase 1	aro3	S. cerevisiae	6.00E-37
BJ998821	379	\bigcirc	DAHP-synthase 2	aro4	S. cerevisiae	1.00E-09
BJ998341	606	_	D-arabinitol dehydrogenase	arbD	E. nidulans	7.00E-15
BJ998665	266	\bigcirc	D-arabinono-1,4-lactone oxidase	CNN01640	C. neoformans	5.00E-07
BJ999025	167	-	delta 6 fatty acid desaturase	RnD6D	R. stolonifer	3.00E-08
BJ999042	535	-	delta 9-fatty acid desaturase	fad1	L. edodes	2.00E-117
BJ999088	291	\bigcirc	delta 12-fatty acid desaturase	fad2	L. edodes	2.00E-06
BJ998312	352	-	dolichyl-diphosphooligosaccharide protein glycotransferase	CNB05600	C. neoformans	4.00E-21
BJ998272	398	\bigcirc	dolichyl-diphosphooligosaccharide protein glycotransferase	CNJ01740	C. neoformans	3.00E-22
BJ998994	483	-	ectonucleotide pyrophosphatase	ENPP3	H. sapiens	9.00E-20
BJ998889	602	\bigcirc	endoglucanase	Afu7g06740	A. fumigatus	9.00E-05
BJ998998	522	-	flavin-containing monooxygenase 1	Afu5g00310	A. fumigatus	4.00E-21
BJ998331	566	\bigcirc	flavin-containing monooxygenase 2	Afu5g00310	A. fumigatus	1.00E-33
BJ998395	516	-	fructose 1,6-bisphosphate aldolase	FBA1	S. cerevisiae	2.00E-46
BJ999028	497	-	GDP-mannase 4,6-dehydratase	gmd	X. tropicalis	2.00E-63
BJ998656	514	-	GTP cyclohydrolase	SPAC1002.19	S. pombe	2.00E-54
BJ998323	529	-	glucose oxidase	god1	B. fuckeliana	6.00E-09
BJ998180	540	\bigcirc	glutamate decarboxylase	GAD1	S. cerevisiae	9.00E-49
BJ999111	378	\bigcirc	glutamine dependent NAD+ synthase	QNS1	S. cerevisiae	2.00E-17
BJ998863	581	-	glutaminyl cyclase	QPCT	H. sapiens	9.00E-12
BJ998839	614	\bigcirc	glycerol-1-phosphatase	CNM01280	C. neoformans	5.00E-20
BJ998383	697	\bigcirc	glyoxysomal citrate synthase	At3g58750	A. thaliana	2.00E-49
BJ999023	410	-	guanosine-diphosphatase	gda1	S. pombe	2.00E-14
BJ998420	446	\bigcirc	homoserine dehydrogenase	SPBC776.03	S. pombe	1.00E-15
BJ998680	450	\bigcirc	inorganic pyrophosphatase	ppa1	S. pombe	3.00E-27
BJ998918	348	-	isocitrate lyase I	ICL2	S. cerevisiae	4.00E-15
BJ998537	589	-	mannanase	man	A. bisporus	6.00E-27
BJ998354	503	-	monocarboxylate permease 1	MCH4	S. cerevisiae	5.00E-15
BJ998509	504	-	monocarboxylate permease 2	MCH5	S. cerevisiae	4.00E-13
BJ998618	568	-	N-acetylglucosamine-phosphate deacetylase	CaNAG2	C. albicans	2.00E-17
BJ998329	310	-	N-acetylglucosamine-phosphate mutase	SPAC13C5.05c	S. pombe	2.00E-20
BJ998999	517	-	NAD-dependent formate dehydrogenase 1	fdh1	S. cerevisiae	3.00E-44
BJ998387	317	-	NAD-dependent formate dehydrogenase 2	fdh2	C. boidinii	3.00E-23
BJ998661	499	-	NADH dehydrogenase Fe-S protein	NDUFS2	H. sapiens	3.00E-83
BJ998349	576	\bigcirc	N-oligosaccharyltransferase (gamma subunit)	SPAPB17E12.11	S. pombe	2.00E-22

BJ998696	481	-	OMST-oxidoreductase	ord1	A. flavus	2.00E-31	
BJ998337	266	-	oxalate decarboxylase	TOXDC	T. versicolor	2.00E-38	
BJ998428	708	-	oxysterol binding protein	SPBC646.08c	S. pombe	3.00E-35	
BJ999038	532	\bigcirc	para-aminobenzoic acid synthetase	pab1	C. cinereus	4.00E-46	
BJ998176	573	\bigcirc	phosphatidylserine decarboxylase	CNA08120	C. neoformans	5.00E-18	
BJ998676	411	-	phosphoglucomutase A	pgmA	D. discoideum	7.00E-24	
BJ998486	326	0	pyranose dehydrogenase	pdh1	A. xanthodermus	5.00E-15	
BJ998943	240	-	pyruvate decarboxylase	pdcA	A. fumigatus	6.00E-23	
BJ998228	788	\bigcirc	riboflavin aldehyde-forming enzyme	fbg16	L. edodes	2.00E-121	
BJ998683	449	\bigcirc	short chain dehydrogenase	SPAC4H3.08	S. pombe	1.00E-06	
BJ998472	642	-	sphinganine C4-hydroxylase	Sur2p	S. cerevisiae	1.00E-29	
BJ998487	486	-	sterol 14 alpha-demethylase	erg11	U. maydis	8.00E-40	
BJ998824	532	\bigcirc	succinate dehydrogenase	Sdh3	S. pombe	1.00E-28	
BJ998561	196	-	succinyl-CoA synthetase	LSC2	S. cerevisiae	7.00E-08	
BJ998651	127	-	succinyl-CoA:L-malate CoA transferase subunit A	SmtA	C. aurantiacus	2.00E-08	
BJ998978	499	0	sulfite reductase	cys-4	N. crassa	3.00E-27	
BJ998300	409	\bigcirc	thiazole biosynthetic enzyme	thi2	S. pombe	3.00E-13	
BJ998787	459	-	thiazole biosynthetic enzyme	nmt2	S. pombe	6.00E-45	
BJ998249	762	0	trehalose-6-phosphate synthase	tps1	P. ostreatus	3.00E-09	
BJ998108	738	-	UDP-glucose-glycoprotein glucosyltransferase	gpt1	S. pombe	2.00E-58	
BJ998284	222	0	uricase	AN9470.2	A. nidulans	1.00E-05	
BJ998879	528	\bigcirc	xylitol dehydrogenase	XYL2	S. cerevisiae	5.00E-05	
BJ998151	566	-	zinc-binding dehydrogenase	YML131W	S. cerevisiae	8.00E-09	
			Energy production				
BJ998479	654	-	ATP synthase subunit 4	ATP4	S. cerevisiae	7.00E-36	
BJ998650	505	0	ATP synthase subunit delta	ATP7	S. cerevisiae	6.00E-45	
BJ998170	397	-	ATP synthase subunit gamma	ATP3	S. pombe	5.00E-14	
BJ998165	409	0	cytochrome c oxidase subunit VIa	COX13	S. cerevisiae	2.00E-06	
BJ998565	570	-	cytochrome b5 reductase	CBR1	S. cerevisiae	3.00E-27	
BJ998741	424	-	mitochondrial ADP/ATP carrier protein	ANC1	S. pombe	2.00E-49	
BJ998330	602	-	NADH:ubiquinone dehydrogenase 51 kDa subunit	NDUFV1	H. sapiens	2.00E-77	
BJ998645	136	-	NADPH oxidase	Nox2	P. anserina	3.00E-07	
			Cell defence, Stress				
BJ998196	304	-	catalase	CTT1	S. pombe	8.00E-27	
BJ998815	508	\bigcirc	cyclophilin	cpal	P. ostreatus	4.00E-45	
BJ998959	146	-	cytochrome P450-1	cyp450	P. sapidus	5.00E-05	
BJ998306	606	-	cytochrome P450-2	cyp450	P. sapidus	3.00E-26	
BJ998385	683	-	cytochrome P450-3	cypA	A. bisporus	1.00E-24	
BJ998282	349	-	glutaredoxin	grx2	S. pombe	7.00E-12	
BJ998259	335	-	glutathione peroxidase	gpx1	S. pombe	2.00E-27	
BJ998800	102	-	glutathione S-transferase	ECM4	S. cerevisiae	5.00E-08	
BJ998355	256	\bigcirc	glyoxalase I	GLO1	H. sapiens	1.00E-11	
BJ998444	238	-	heat shock protein 104	HSP104	S. cerevisiae	2.00E-12	
BJ999007	413	\bigcirc	heat shock protein 12	CNG04220	C. neoformans	5.00E-17	
BJ998313	362	\bigcirc	heat shock protein 70-1	SSB1	S. cerevisiae	5.00E-12	
BJ998621	555	-	heat shock protein 70-2	SSC1	S. cerevisiae	5.00E-80	
BJ998702	561	-	heat shock protein 90	HSP90	C. neoformans	1.00E-60	
BJ998788	412	\bigcirc	heat shock protein 12	Afu6g12450	A. fumigatu	2.00E-06	
BJ998206	382	\bigcirc	manganese superoxide dismutase 1	sod1	A. bisporus	2.00E-46	
BJ998961	503	-	manganese-superoxide dismutase 2	sod2	G. microsporum	8.00E-66	
BJ998430	346	\bigcirc	metallothionein	MTI	P. involutus	6.00E-07	
BJ998930	448	\bigcirc	macrolide-binding protein FKBP12	frr I	C. neoformans	4.00E-30	
BJ998882	102	-	peroxisomal Omega-class glutathione transferase	GIOI	S. cerevisiae	6.00E-07	
D 1000 00 0		\sim	Cell growth			0.005.00	
BJ998795	593	0	calmodulin 1	cmd1	N. crassa	2.00E-69	
BJ998608	396	-	calmodulin 2	cmd2	N. crassa	2.00E-69	
BJ998634	592	-	developmentally regulated gene	priA	L. edodes	2.00E-112	
BJ999003	458	\cup	niament-specific protein	01057	U. maydis	4.00E-09	
BJ998762	160	-	nyarophobin I	nya1	L. edodes	3.00E-73	
B1998866	534	\cup	nyarophobin 2	nya2	L. edodes	/.00E-14	
B1999085	581	-	nyarophobin 3	nya3	L. edodes	2.00E-12	
BJ998875	515	\bigcirc	hydrophobin 4	nyd4	L. edodes	2.00E-09	
BJ998526	524	\bigcirc	hydrophobin 5	nyd5	L. edodes	4.00E-18	
BJ998436	465	\cup	highdosage growth inhibitor	HMF1	S. cerevisiae	2.00E-27	
BJ998418	528	-	opioid growth factor receptor-like 1	OGFRLI	H. sapiens	2.00E-31	
BJ999069	322	-	septin	aspA	A. nidulans	6.00E-16	
R1333113	462	-	zygote-specific class V copy B	AAB21907.1	C. reinhardtii	/.00E-14	
Cytoskeleton							

BJ998417	279	0	beta-tubulin	TUB2	S. cerevisiae	3.00E-07	
BJ999019	397	-	cofilin	adf1	S. pombe	3.00E-17	
D1008552	510		DNA, RNA, Chromatin	ahf5	C agraviaida	4 00E 88	
B1098540	510 601	-	DNA repair protein/DNA halicase	cojs rhn3	S. cerevisiae	4.00E-88	
B1000018	213	-	histone acetultransferase	μρ5 ΗΔΤ1	S. pombe S. cerevisiae	4.00E-91	
B1998909	213 474	_	histone H4	hhf	A hisporus	1.00E-05	
B1998785	459		histone methyltransferase	nnj svmd1	A. Disportus D. rerio	4.00E-40	
B1999086	559	_	RNA-binding protein	SPAC 328 05	S nombe	1.00E-12	
B1998694	554	_	RNA-binding protein	SND1	S. pombe	6.00E-00	
B1998922	322	_	glycine-rich RNA binding protein	ron2	N sylvestris	5.00E-13	
BI998591	471	_	ATP-dependent RNA helicase (DEAD)	RAD926191	H saniens	8.00E-06	
B1998906	323	\bigcirc	argonaute	alg_1	C elegans	3.00E-06	
BJ999065	605	-	RNA-dependent RNA polymerase	rrf-2	C. elegans	9.00E-18	
			Transcription, Splicing				
BJ998212	684	-	transcription factor	prr1	S. pombe	5.00E-14	
BJ999092	511	-	transcriptional coactivator	MBF1	S. cerevisiae	3.00E-33	
BJ998402	588	-	transformation/transcription domain-associated protein	TRA1	S. cerevisiae	8.00E-78	
BJ998751	223	-	prp5	prp5	S. pombe	3.00E-08	
BJ998914	273	-	U2 small nuclear RNA auxiliary factor 2	U2AF2	H. sapiens	4.00E-10	
D1000(05	1.5.5		Translation	GD4 G1020 07	G 1	2.005.07	
BJ998635	155	-	alanine racemase	SPAC1039.06	S. pombe	3.00E-07	
БJ998/9/ D1009977	578	-	EF 1 delte	elf 10 FFF1D	п. sapiens	1.00E-33	
BJ998877	574	-	EF-1 delta	EEF ID CAM1	H. sapiens	6.00E-20	
BJ999006	5/3 207	0	EF-1 gamma	CAM1	S. cerevisiae	3.00E-40	
BJ998220	397	-	elF4A	IIJI	S. pombe	4.00E-37 8.00E-42	
DJ998055 DJ008164	440 210	-	alaline-trive synthetases	MSD1	S. pombe S. pombe	8.00E-43	
BJ998104 BI008462	720	-	turosul tPNA synthetase	MSD1 MSV1	S. Cerevisiae	8.00E-19 8.00E-16	
B1008076	102	$\overline{\bigcirc}$	ribosomal protein (acidic) P2	m311 rnn203	S. cerevisiae	8.00E-10 8.00E-17	
BI998981	498	_	ribosomal protein [2	rp/205 rn/40?	S. pombe	1.00E-17	
BJ998807	425	\bigcirc	ribosomal protein L2B	RPL2B	S. cerevisiae	2.00E-49	
B1998992	517	$\tilde{\circ}$	ribosomal protein L2D	RPL3	S. cerevisiae S. cerevisiae	2.00E-30	
BJ998992	521	$\tilde{\circ}$	ribosomal protein L12	rn1201	S. pombe	8.00E-64	
BJ998126	459	-	ribosomal protein L16	RPL16A	S. cerevisiae	4.00E-53	
BJ998301	391	-	ribosomal protein L19	rp11902	S. pombe	9.00E-24	
BJ999050	502	\bigcirc	ribosomal protein L24	rpl24-2	S. pombe	5.00E-23	
BJ998283	282	0	ribosomal protein L34-like protein	RPL34B	S. cerevisiae	4.00E-15	
BJ998856	421	\bigcirc	ribosomal protein L37, mitochondrial precursor	yml37	C. neoformans	2.00E-06	
BJ998339	494	-	ribosomal protein L38	rpl38-1	S. pombe	2.00E-16	
BJ998478	361	\bigcirc	ribosomal protein L41	RPL41A	S. cerevisiae	4.00E-46	
BJ998494	242	\bigcirc	ribosomal protein S3a	cyc07	L. edodes	3.00E-46	
BJ998570	404	-	ribosomal protein S10	rps1002	S. pombe	1.00E-40	
BJ998646	332	\bigcirc	ribosomal protein S11	rps1102	S. pombe	2.00E-24	
BJ998363	392	\bigcirc	ribosomal protein S12	rps12	S. pombe	1.00E-13	
BJ998266	431	-	ribosomal protein S13	rps13	A. bisporus	9.00E-70	
BJ998728	306	\bigcirc	ribosomal protein S15	rps15-2	S. pombe	6.00E-12	
BJ998653	544	\bigcirc	ribosomal protein S22	rps2202	S. pombe	2.00E-60	
BJ998705	417	-	ribosomal protein S25	RPS25B	S. cerevisiae	7.00E-20	
BJ998956	349	\bigcirc	ribosomal protein S27	CNG02740	C. neoformans	1.00E-05	
DJ990902	304	-	1 St2 Protein degradation	1512	S. cereviside	2.00E-78	
Protein degradation							
B1008440	517		aspartyl proteinase	AAP37873 1	P hrasilionsis	8 00E-32	
B1998782	435	_	ATPase in proteasome	RPT1	S cerevisiae	7.00E-30	
B1998745	455	\cap	endopentidase 1	CNC04480	C. neoformans	3.00E-18	
B1998830	504	$\tilde{\circ}$	endopeptidase 2	CN.100730	C. neoformans	6.00E-05	
BJ998692	302	-	gamma glutamyl-transpeptidase	GGT2	S. pombe	9.00E-22	
BJ998831	214	-	metalloprotease 1	MEP2	A. benhamiae	1.00E-29	
BJ998254	291	-	metalloprotease 2	MEP4	A. benhamiae	8.00E-06	
BJ998245	572	\bigcirc	polyubiquitin	ubi4	S. cerevisiae	3.00E-87	
BJ998296	329	-	protease B precursor	PRB1	S. cerevisiae	1.00E-33	
BJ998910	665	-	protease	prot1	A. muscaria	7.00E-39	
BJ998899	499	\bigcirc	proteasome component beta 1 (20S)	DAPS-1	D. discoideum	8.00E-21	
BJ998754	219	-	proteasome component beta 7 (20S)	SPBC577.10	S. pombe	3.00E-05	
BJ998463	519	-	proteasome component beta 4 (20S)	PSMB4	H. sapiens	2.00E-57	
BJ998356	596	-	tripeptidyl aminopeptidase	TPAP1	A. oryzae	1.00E-23	
BJ998535	578	\bigcirc	tripeptidyl peptidase A	tppA	A. oryzae	7.00E-33	

$\begin{split} BJ99871 & 499 & - \ \ disputine conjugating enzyme E2 \\ BJ99805 & 238 & - \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \$	BJ998350	361	\bigcirc	ubiquitin carboxyl-terminal hydrolase5	CNH02890	C. neoformans	1.00E-15
BJ99881 606 - ubiquitin conjugating enzyme E2 Vabc14 X. Iaavis BJ095 BJ999052 430 - ubiquitin lingase K3 CUL1 H. sapiers ZJ00E-99 BJ9990163 430 - ubiquitin lingase K3 SODE-11 SODE-12 SODE-12 SODE-12 SODE-12 SODE-13 SODE-12 SODE-13 SODE-13 SODE-13 SODE-14 SODE-14 SODE-14 SODE-14 SODE-14 SODE-15 SODE-14 SODE-14 SODE-15 SODE-14 SODE-15 SODE-14 SODE-14 <t< td=""><td>BJ998971</td><td>499</td><td>-</td><td>ubiquitin conjugating enzyme E2</td><td>UBC4</td><td>S. pombe</td><td>9.00E-77</td></t<>	BJ998971	499	-	ubiquitin conjugating enzyme E2	UBC4	S. pombe	9.00E-77
BJ999085 228 Usbaptitic conjugating enzyme E2 UECS S. cerevisiae 200E-99 BJ999108 319 vacuolar activoty protesse PEP4 S. cerevisiae 7.00E-43 BJ999108 319 ABC transporter Mid2g00600 A. funiquatus 5.00E-11 BJ99829 337 ABC transporter Mid2g00600 A. funiquatus 6.00F-15 BJ99813 398 ABC transporter Mid2g00600 A. funiquatus 6.00F-15 BJ99813 336 Catter and transporter Mid2g00600 A. funiquatus 6.00F-15 BJ99813 336 Catter and transporter AAC1 S. cerevisiae 4.00E-12 BJ99813 Catter and transporter BAC4 Network and transporter AAC1 S. cerevisiae 4.00E-13 BJ99813 Catter and transporter BAC4/DF00 Consegremans 2.00E-16 BJ998143 Catter and transporter BAC4/DF00 Consegremans 2.00E-16 BJ99815 Catter and transporter-false protein CVC01500 Consegremans 2.00E-16 BJ99815 Fall Catter anapporter-false protein CVC0	BJ998891	606	-	ubiquitin conjugating enzyme E2	Xubc14	X. laevis	8.00E-28
B1999082 430 - ubiquitin figse E3 CUL1 H. sepiese 7.00E-43 B1999064 259 - vacuolar aperty protease PEP4 S. cerevisiae 5.00E-11 B1999805 337 O ABC transporter VDR1 S. cerevisiae 5.00E-11 B1998950 387 O ABC transporter YDR1 N. crasss 1.00E-25 B1999806 613 - chafthria associated adaptor complex AP-1 medium APM1 S. cerevisiae 4.00E-22 B19999103 613 - chafthria associated adaptor complex AP-1 medium APM1 S. cerevisiae 4.00E-27 B19998273 486 - contem zara subunit rec3 S. pombe 7.00E-43 B19998765 422 COP signaloxom estimatin 6 CW04/M90 C. neofyrmans 2.00E-17 B19998767 422 CE Ro Golgi transporter like protein GDF14 S. pombe 3.00E-06 B19998767 422 CE Ro Golgi transporter Huilding State GDF14 S. pombe 3.00E-06 B1999807 372 - introportin afpha submit	BJ999056	228	\bigcirc	ubiquitin conjugating enzyme E2	UBC5	S. cerevisiae	2.00E-09
BJ990103 319 \bigcirc vacuolar anyony professe PEPA S. cerevisiae 5.00E-17 BJ998204 259 - AlC transporter Ala (Jag00650 A. Junigatus 5.00E-12 BJ99831 388 \bigcirc ABC transporter YOR1 S. cerevisiae 6.00E-15 BJ99831 388 \bigcirc ABC transporter YOR1 S. cerevisiae 6.00E-15 BJ999301 651 \bigcirc ADP/ATP translocator AAC1 S. cerevisiae 4.00E-12 BJ9990103 651 \bigcirc hexose transporter HX11 S. cerevisiae 4.00E-12 BJ999103 651 \bigcirc hexose transporter HX11 S. cerevisiae 4.00E-15 BJ992104 478 $-$ COIP signalocouse subunit rci3 S. pombe 2.00E-16 BJ998268 241 $-$ golg inarris protein RAMAR Netrolocouse 2.00E-16 BJ998269 151 $-$ GDP fucese transporter Nationachandre protein CNU14700 C. neoformans 3.00E-06 BJ9982015 161 $-$ GDP fucese transp	BJ999082	430	-	ubiquitin ligase E3	CUL1	H. sapiens	7.00E-43
Bi99844229Cacuadir carboxy peptidase($SPACV2.08$ ($S, pombe2.00E-12Bi998929337OABC transporterMisg0x080A, functional3.00E-12Bi998930558-amino acid permeaseMAL71N, crassia1.00E-25Bi999830613-clathrin-associated daptor complex AP-1 mediumAPAH1N, crassia1.00E-25Bi999030613-clathrin-associated daptor complex AP-1 mediumAPAH1N, crassia2.00E-06Bi999030613-clathrin-associated daptor complex AP-1 mediumAPAH1N, crassia2.00E-06Bi998763125-catomer garma subunitscc21S, pombe7.00E-27Bi998763125-catomer garma subuniterd3S, pombe2.00E-16Bi998763422OFR to Golgi transport-related proteinCNOI500C. neoformans2.00F-14Bi998180614-Colf has subunitCNOI500C. neoformans3.00F-166Bi998199105-GTP nea activating protein of Rab-like GTPaseGYPIS, pombe1.00E-69Bi99810510-GDP choose transporternid_1d_2d_32320S, ecrevisiae4.00F-16Bi99810505-GTP has astunuitAI_1g0d500A, ingicatus2.00E-23Bi99810505-potassium chunnel beta subunitAI_1g0d502A, ingicatus2.00E-24Bi998120624-$	BJ999108	319	\bigcirc	vacuolar aspartyl protease	PEP4	S. cerevisiae	5.00E-11
Transport, SerretionBi998929337 \bigcirc ABC transporterAft3g00680A, funtigatusBi998240338 \bigcirc ABC transporterI/OR1S. cerevisiae6.00E.15Bi998318255-ADP/ATP translocatorAAC1S. cerevisiae2.00E.50Bi9990103651 \bigcirc bexose transporterHXT1S. cerevisiae4.00F.52Bi999103651 \bigcirc bexose transporterHXT1S. cerevisiae4.00F.52Bi999103651 \bigcirc bexose transporterC.MA04780C. neoformane2.00F.16Bi999276478-coatomer zta submiterc3S. pombe2.00F.16Bi999276478-COEP signalocone submit 6C.NE01500C. neoformane2.00F.16Bi999285161-Golf transporter-falsed proteinSPECU10.12S. pombe3.00F.06Bi998289727-mainchandig protein of Rab-like GTPaseCND04770C. neoformane2.00F.14Bi99827275-mainchandrail apport motorPAM18S. cerevisiae4.00E.16Bi998280624Omonscachard transportermainfill affill apport motorPAM18S. cerevisiae4.00E.16Bi998210656-values apportermainfill apport motorPAM18S. cerevisiae4.00E.16Bi998210656-values apportermainfill apport motorPAM18S. cerevisiae4.00E.16Bi998210656-values	BJ998644	259	-	vacuolar carboxy peptidase	SPAC24C9.08	S. pombe	2.00E-07
B1998929337 \bigcirc ABC transporter $Aftigg09600$ $Afting109600$ $Afting109600$ $Afting109600$ $Afting10800000000000000000000000000000000000$			-	Transport, Secretion			
BJ9998/1398 \bigcirc ABC transporterPOR1S. cerevisiae6.00E-15BJ9988.0255-ADP/ATP translocatorAAC/1K. cravisa1.00E-25BJ999010651-chintin-associated adaptor complex AP-1 mediumAAC/1S. crevisiae4.00E-52BJ990103651-hexose transporterHXT1S. crevisiae4.00E-52BJ990103651-hexose transporterHXT1S. crevisiae4.00E-52BJ998763215-coatiomer zta subunitret3S. pomhe2.00E-16BJ998763242C EK to Golgi transport-crelated proteinCNV01500C. neoformans2.00E-16BJ998763241-golgi matrix proteinSPD6/10-12S. pomhe3.00E-06BJ99858241-golgi matrix proteinGDD7PP. djamor2.00E-14BJ99867275-micchondrial import related proteinCND04770C. neoformans3.00E-06BJ998105161-GDP4-faces transportermicle GDP7P. djamor2.00E-12BJ99807273-micchondrial import motorPAM18S. crevisiae4.00E-16BJ998105704-potassium chamaelFAM1S. crevisiae4.00E-54BJ998105704-potassium chamaelFAM1A. faer3.00E-56BJ998105704-potassium chamaelFAM1A. faer3.00E-56BJ998105704-potassium chamaelFAM	BJ998929	337	\bigcirc	ABC transporter	Afu3g09680	A. fumigatus	3.00E-12
H9998340SNs- armuno acti permeaseNARPN. crewission 2.000-052.000-05B1999010613- chultrin-insociated adaptor complex AP-1 mediumAPM1S. cerevisiate4.000-52B1999010613- carnitine/aryl carnitine carrierCMA07300C. neoformaux2.000-06B1999203613- catomore gamma subunitrec3S. pombe2.000-106B199920477 cotomore zata subunitrec3S. pombe2.000-117B1998205446- cotomore zata subunitrec3S. pombe2.000-117B1998206422- COP signalcowne subunit 6C/VF01500C. neoformaux2.000-118B19998578422- COP signalcowne subunit 6C/VF01500C. neoformaux3.000-106B1998289649- GTPace activating protein of Rab-like GTPaseG/PFP. djamor3.000-106B1998230614- GDP fraces transporterIkpointike GDPFR. djamor3.000-120B1998373732- inportin alpha subunitC. Nc004770C. neoformaux3.000-120B19983707372- inportin alpha subunitAliger3.001-1263.002-126B1998370743- patasium channel beta subunitAliger3.002-1263.002-126B1998370744- patasium channel beta subunitAliger3.002-1263.002-126B1998370745- patasium channel beta subunitAliger3.002-1263.002-126B1998410 <t< td=""><td>BJ998931</td><td>398</td><td>\bigcirc</td><td>ABC transporter</td><td>YOR1</td><td>S. cerevisiae</td><td>6.00E-15</td></t<>	BJ998931	398	\bigcirc	ABC transporter	YOR1	S. cerevisiae	6.00E-15
BJ999818225-ADP/AP IransbicatorAAC/S. cerevistate2.001-06BJ9990103651-hexose transporterHXT/S. cerevistate4.00E-52BJ998137136-camiline/acyl camiline carrierCM.047917S. cerevistate4.00E-52BJ998763215-coatomer zeta submitpec21S. pombe7.00E-27BJ999126478-coatomer zeta submitpec3S. pombe2.00E-14BJ9988763220F. In Golyi transport-related proteinS. Pombe3.00E-06BJ998856241-polgi matrix proteinS. Pombe3.00E-06BJ998856161-GDP-fucese transporter-like proteinGDPFP. djamor2.00E-12BJ998105161-GDP-fucese transporterPM.18S. cerevisiae4.00E-52BJ998105161-GDP-fucese transportermitch-dondral inport motorPM.18S. cerevisiae4.00E-63BJ998105054-monocacdoxylate transportermitchAft/gid/201A. fumigans2.00E-23BJ998105055-potasium channel beta submitAft/gid/201A. fumigans2.00E-23BJ998105056-potasium channel beta submitAft/gid/201A. fumigans2.00E-23BJ998105055-potasium channel beta submitAft/gid/201A. fumigans2.00E-23BJ998105056-potasium channelKAB1A. fumigans3.00E-12BJ9	BJ998540	558	-	amino acid permease	NAAP1	N. crassa	1.00E-25
B)999000 613 - claffurn-associated adaptor complex AP-1 medium $APM1$ S. cerevistate 4.00E-32 B)990105 651 C hccose transporter ana submit $PAT1$ S. cerevistate 4.00E-32 B)998236 486 - coatomer gumma submit $PAT1$ S. cerevistate 4.00E-13 B)998239 486 - coatomer gumma submit $PAT1$ S. coreoformans 2.00E-14 B)998249 478 - COP3 signaloscome subunit 6 CXF01300 C. neoformans 2.00E-14 B)9982678 422 O FR to CoP3 signaloscome submit 6 CXF01300 C. neoformans 3.00E-06 B)998289 649 - GTPase activating protein of Rab-like GTPase GYP1 / S. pombe 1.00E-69 B)998289 649 - GTPase activating protein of Rab-like GTPase GYP1 / S. pombe 1.00E-69 B)99827 27 - imochandral import motor GP4 (M18) S. cerevisiate 4.00E-16 B)99827 27 - imochandral import motor RM18 S. cerevisiate 4.00E-16 B)998289 652 - mitochandral import motor RM18 S. cerevisiate 4.00E-16 B)99827 673 - mitochandral import motor RM18 S. cerevisiate 4.00E-16 B)998216 656 - sodium-changet ransporter Afrid_303220 A fungatus 2.00E-42 B)998105 704 - potasium channel beta submit Alg/04600 A. thaliana 3.00E-42 B)998320 656 - sodium-changet PSAC3AL206C S. pombe 1.00E-54 B)998320 657 - potasium channel beta submit Alg/04600 A. thaliana 3.00E-12 B)998320 656 - sodium-changet PSAC3AL206C S. cerevisiate 4.00E-14 B)998320 437 - winchandel KARE Stoff S. cerevisiate 1.00E-54 B)998320 439 - v.SNARE Stoff S. cerevisiate 1.00E-24 B)998320 437 - v.SNARE Stoff S. cerevisiate 1.00E-24 B)998320 437 - v.SNARE Stoff S. cerevisiate 1.00E-24 B)998320 437 - v.SNARE Stoff S. cerevisiate 1.00E-24 B)998820 433 - v.SNARE Stoff S. cerevisiate 1.00E-24 B)998820 433 - v.SNARE Stoff S. cerevisiate 1.00E-24 B)998820 434 - v.SNARE Stoff S. cerevisiate 1.00E-24 B)998820 434 - v.SNARE Stoff S. cerevisiate 1.00E-25 B)998900 377 - GDP dissociation inhibitor B)2A - cardivating 3.00E-16 B)998205 434 - v.SNARE Stoff S. cerevisiate 1.00E-25 B)998920 437 - cardivating protein kinase CK13 S. pombe 1.00E-05 B)998205 438 - Protein kinase CK13 S. pombe 1.00E-05 B)9989214 464 - immunocative protein kinase CK13 S. pombe	BJ998318	255	-	ADP/ATP translocator	AACI	S. cerevisiae	2.00E-06
BD990103651 \bigcirc hexose transporter <i>HAT11E. cerevisate</i> 4.00E-13R1998147136-cantimire/acyl carnitine carrier <i>CNA07891C.CN079100</i> 2.00E-07-27R1999126478-coatomer zeta subunitwc21 <i>S. pombre</i> 7.00E-27R1999126478-COP9 signalosome subunit 6 <i>CNC01300C. neoformans</i> 2.00E-14R1998578241-golg matrix proteinGAD-Ibit CTPase <i>CNC01300C. neoformans</i> 3.00E-06R1998586241-golg matrix proteinGAD-Ibit CTPase <i>CNC01300</i> 2.00E-11R19998576737-mitochondrial import protein of Rab-like CTPase <i>GDPFC. moformans</i> 3.00E-06R19988105161-GDP-faces cartening protein of Rab-like CTPase <i>CND01470</i> 2.00E-11R1999807273-mitochondrial import motor <i>BMI8S. cerevisiae</i> 4.00E-16R1998230624morosaccharde transporter <i>muBA. fumigatus</i> 2.00E-23R19984107659-potasium channel beta submit <i>Aligl3200A. fumigatus</i> 3.00E-24R1998810505-potasium channel beta submit <i>KAB1A. funitana</i> 7.00E-21R1998820650-potasium channel beta submit <i>KAB1A. funitana</i> 7.00E-21R1998820650-yotasium channel beta submit <i>KAB1A. funitana</i> 7.00E-21R1998820650-yotasium channel bet	BJ999080	613	-	clathrin-associated adaptor complex AP-1 medium	APMI	S. cerevisiae	4.00E-52
B)998751150-Cardinine acyl carine carineCVA0/4700C. Red/ormans2.00E-17B)998293486-coatomer gamma subunirel3S. pombe2.00E-14B)998293486-COP signalosone subuni 6CNF03400C. neeformans2.00E-14B)998267422CER to Golgi transport-related proteinCNF01400C. neeformans3.00E-06B)998289649-GTPase activating protein of Rab-like GTPaseGYP1P. gimoor2.00E-11B)998057372-mportin lapha submitCND04770C. neeformans3.00E-06B)99823943-mitochondral inporter the proteinCND04770C. neeformans3.00E-16B)99823043-mitochondral inportermitBA. inger3.00E-33B)998415704-potassium channelKABIA. Infaliana7.00E-21B)998105505-potassium channelKABIA. Infaliana7.00E-21B)998102656-sodium/calcium exchangerSPAC3A12.06C3.00E-126B)998216884-vacuolar H+Ca(2+) exchangerVCX1S. cerevisiae1.00E-24B)998810379CGDP dissociation inhibitorGDHS. cerevisiae1.00E-24B)998820423SNAREVTIS. cerevisiae1.00E-24B)998815316-Nac-2 proteininagerGDHS. cerevisiae1.00E-24B)998820423 <td>BJ999103</td> <td>651 126</td> <td>0</td> <td>hexose transporter</td> <td>HXII CNA04790</td> <td>S. cerevisiae</td> <td>4.00E-13</td>	BJ999103	651 126	0	hexose transporter	HXII CNA04790	S. cerevisiae	4.00E-13
BJ998705215-coalomer gamma subunitSec21S. pombe $2.00E-17$ BJ998126478-CCP signalosome subunit 6CNF034400C. neeformans $2.00E-17$ BJ998576241-golgi matrix proteinMab-like GTPassCNF034400C. neeformans $3.00E-08$ BJ998266241-golgi matrix proteinMab-like GTPassGVP11S. pombe $1.00E-69$ BJ998276372-GDP-fucese transporter-like proteinGDPFP. Jomobe $1.00E-69$ BJ998195161-GDP-fucese transporter-like proteinCND04770C. neeformans $3.00E-08$ BJ998275275-mitochondrial import motorP.M.18S. cerevisiae $4.00E-16$ BJ998276624-monocarboxylate transportermstBA. Indiana $3.00E-32$ BJ998105505-potassium channel beta subunitAlig/40600A. Indiana $3.00E-32$ BJ998105505-potassium channel beta subunitAlig/4060A. Indiana $3.00E-12$ BJ998105505-potassium channelKAD1A. Indiana $3.00E-12$ BJ998105505-potassium channelKAD1A. Indiana $3.00E-12$ BJ998105505-potassium channelKAD1A. Indiana $3.00E-12$ BJ998105504-vacuolar Hr/Ca(2+) exchangerVCX1S. cerevisiae $1.00E-24$ BJ998105504-vascolar Hr/Ca(2+) exchangerVCX1	BJ998347	136	-	carnitine/acyl carnitine carrier	CNA04780	C. neoformans	2.00E-06
Djpo223443-Colloues2000-11B1999124778-COP signalosone subunit 6CN-003400C. neoformans2000-14B1998567421-ER to Golgi transport-reliatel proteinCN-01500C. neoformans3.00E-06B1998289649-CTPase activating protein of Rab-like CTPaseGYP1S. pombe3.00E-06B1998195161-CDP-frose transporter-like proteinCDPFP. dimor2.00E-11B1998057372-mitochondrial import motorPAM18S. cerevisiae4.00E-16B1998239943-mitochondrial broosphate transportermultichondrial import motorPAM18S. cerevisiae4.00E-16B19982105704-potassium channel beta subunitA. ligligi320A. lindiana7.00E-21B1998105704potassium channelKAB1A. lindiana7.00E-21B1998105704-potassium channelKAB1A. lindiana7.00E-21B19982102656-sodium/calcium exchangerSPAC3A12.06cS. pombe3.00E-126B19982104Rad 2-vsauolar Ha/Cu(2+) exchangerVCX1S. cerevisiae1.00E-24B1998205622-Vpt intracting proteinradrad3.00E-1261.00E-24B1998205623SNAREVpt iS. cerevisiae1.00E-251.00E-25B1998205624SRPA1higer proteinradS. ce	BJ998703	213 496	-	coatomer gamma subunit	sec21	S. pombe	7.00E-27 2.00E-17
D99912047.6CUr 9 signatusouite southin 0CUr 001CUr 001200E 14B1998876241 <td>BJ998293</td> <td>480</td> <td>-</td> <td>CORD signal subunit 6</td> <td>reis CNE02400</td> <td>S. pombe</td> <td>2.00E-17</td>	BJ998293	480	-	CORD signal subunit 6	reis CNE02400	S. pombe	2.00E-17
BJ998807342.2CIR to Uoing it anisy proteinC/VCD/301C/VCD/301S.00E-06BJ998289649-GTPace activating protein of Rab-like GTPaceGYP1S. pombe3.00E-06BJ998195161-GDP-faces etransporter-like proteinGDPFP. diamor2.00E-11BJ998057372-iniportin alpha subunitCND04770C. neoformans3.00E-16BJ998239943-mitochondrial import motorPMH18S. cerevisiae4.00E-16BJ998308624-monosacchariot transportermitBA. finger3.00E-33BJ9984105704-potassium channel bet subunitKAB1A. findiana3.00E-42BJ9983105704-potassium channel bet subunitKAB1A. findiana3.00E-42BJ9983105704-potassium channelKAB1A. findiana3.00E-126BJ9983105704-potassium channelKAB1A. findiana3.00E-126BJ998310671C. Rab7rb7rb7rb7rb7BJ998320691-v.SNAREyM6S. cerevisiae1.00E-21BJ998323369-v.SNAREVT1S. cerevisiae1.00E-22BJ998205622-Ypt interacting proteinTP23S. commute6.00E-09BJ998235391-Ras2 proteinRA22RAP2AM. musculus3.00E-12BJ998235391-Ras2 proteinRas2S. ce	DJ999120	470	$\overline{\bigcirc}$	ED to Colgi transport related protoin	CNF03400	C. neoformans	2.00E-14
DJ990230 BJ990230211 ClificationClificationDotting StructureDotting StructureDotting StructureDotting StructureBJ990257 BJ990857 BJ990857 BJ990857 BJ990857 BJ990857 ClificationClification ClificationDotting ClificationDotting ClificationDotting ClificationDotting ClificationDotting ClificationBJ990850 BJ998106 BJ998106Clification ClificationDotting ClificationDotting ClificationDotting ClificationDotting ClificationDotting ClificationBJ998106 BJ998107 BJ998107Clification ClificationDotting ClificationDotting ClificationDotting ClificationDotting ClificationDotting ClificationBJ998107 BJ998107 BJ998107 BJ998106Clification ClificationDotting ClificationDotting ClificationDotting ClificationDotting ClificationDotting ClificationBJ998216 Clifica	BJ998078 B1008568	422 241	\bigcirc	algi matrix protain	SPRC 110 12	C. neojormans	3.00E-08
Dj998103Of 1 as a kit value protein of Kabine Of 11 as:Of 11 as:Of 11 as:Dj90111, pointer1, p	B1008280	241 640	-	GTPase activating protain of Pab like GTPase	GVP1	S. pombe	3.00E-00
DJ 2017ConstraintsConstraintsConstraintsConstraintsConstraintsBi99907275-mitochondrial import motorPAM18S. cerevisiae4.00E-16Bi99829943-mitochondrial phosphate transporterPAM18S. cerevisiae4.00E-16Bi998308624-monosaccharide transporterAniger3.00E-123.00E-12Bi998407669-monosaccharide transportermitBA. niger3.00E-23Bi998501505-potassium channel beta subunitAltg04690A. Italiana7.00E-21Bi998501505-potassium channelKAB1A. Italiana7.00E-21Bi998200505-sodium/cacine exchangerVCX1S. cerevisiae9.00E-09Bi998320369-v.SNAREVCX1S. cerevisiae9.00E-09Bi998320369-v.SNAREVTI1S. cerevisiae1.00E-21Bi998805423-v.SNAREVTI1S. cerevisiae1.00E-21Bi998875391-GDP dissociation inhibitorGDHS. cerevisiae1.00E-25Bi998799498ORas-2 protein Rap2ARAP2AM. macculus3.00E-15Bi998875391-GDP dissociation inhibitorGDHS. cerevisiae2.00E-33Bi998875391-GDP dissociation inhibitorGDUS. pombe4.00E-16Bi99896504-GDP dissociation inhibitorGDUS. pomb	DJ998289	161	-	CDD fugoes transporter like protoin		S. pombe P. diamor	1.00E-09
DJ998072751Important algorithm of the subunitC.R.D.F.M.R.B.S. C.R.C.F.M.R.B.S.J.O.D.F.12BJ998239943-mitochondrial phosphate translocator $micB$ $P. involatus$ 1.00E-54BJ998427689-monocachoxylate transporter Mid_3Q3203 $A. invigatus$ 2.00E-23BJ998105704-potassium channel beta subunit $Atlg04690$ $A. indiana3.00E-42BJ998105505-potassium channelKAB1A. indiana3.00E-142BJ998105505-potassium channelKAB1A. indiana3.00E-126BJ998206671C.Rab7rab7rab7C.Reversiae9.00E.09BJ998206622-VSNAREVCX1S. cerevisiae9.00E.09BJ998209622-Vp interacting proteinYIP3S. cerevisiae1.00E-24BJ9989709498-Ras-related protein Rap2ARAP2AM.musculus 3.00E-104BJ998235136MAP kinase kinase ByrlC.NC2350C.neoformans4.00E-104BJ998254435-protein kinasedsl.2S. pombe1.00E-25BJ998254150-molesulation factor subunitaC.NC2350C.neoformans4.00E-104BJ998255391-Ras-related protein kinaseCX13S. pombe1.00E-04BJ998254150-molesulation factor subunitaCST37S. pombe1.00E-05BJ998260$	BJ998195 B1000057	372	$\overline{\bigcirc}$	importin alpha subunit	ODTT CND04770	1. ajamor C. naoformans	2.00E-11 3.00E-12
DJ 2000 2.5 T Interconstant important translocator PAD TO D. C. D'Intall 1.0001-10 B1998208 624 O monocarboxylate transporter Afh320322 A. flumigatus 2.00E-23 B1998105 704 - potassium channel beta subunit Algel4600 A. flutiana 3.00E-33 B1998105 505 - potassium channel beta subunit Algel4600 A. flutiana 3.00E-42 B1998102 656 - sodium/calcium exchanger SPRC3A12.06c S. pombe 1.00E-14 B1998204 671 C Rab7 rab7 L edodes 3.00E-126 B1998205 662 - vscuolar H+Ca(2+) exchanger VCX1 S. cerevisiae 1.00E-24 B1998209 622 O Yp1 interacting protein YIP3 S. cerevisiae 1.00E-24 B1998209 379 GDP dissociation inhibitor GDH S. cerevisiae 1.00E-24 B1998251 136 - MAP kinase kinase Byr1 CNc02350 C. neoformans 4.00E-04 B1998262 111 - serine threnotin kinase </td <td>B1999057</td> <td>275</td> <td>\cup</td> <td>mitochondrial import motor</td> <td>PAM18</td> <td>C. neojormans S. cerevisiae</td> <td>3.00E-12 4.00E-16</td>	B1999057	275	\cup	mitochondrial import motor	PAM18	C. neojormans S. cerevisiae	3.00E-12 4.00E-16
B1998020624monocarboxylate transporterAlu3g03320AluagentalB1998102689monocarboxylate transportermstBA. ifger3.00E-32B1998105505-potassium channel beta subunitAll g04690A. thaliana3.00E-32B1998105605-sodium/calcium exchangerSPAC3AL2.06cS. pombe1.00E-14B1998102667-Rab7rab7L. edodes3.00E-126B1998206671-Rab7vacuolar H+(Ca(2+) exchangerVCX1S. cerevisiae9.00E-09B1998206423-v.SNAREyktóS. cerevisiae1.00E-24B1998209622-Yp interacting proteinYIP3S. cerevisiae4.00E-10B1998209622-Yp interacting proteinras2S. commune6.00E-09B1998209139-GDP dissociation inhibitorGDI1S. cerevisiae1.00E-24B1998209139-Ras2 proteinras2S. commune6.00E-09B1998231136-MAP kinase kinasegK13S. cerevisiae1.00E-15B1998235138-protein kinasegK13S. cerevisiae2.00E-13B1998243528-SRPK1-like protein kinasegK23S. cerevisiae2.00E-32B1998255438-protein kinasegK23S. cerevisiae2.00E-32B1998244157-armadillo repeat proteinGZ2S. cerevisiae2.00E-13 <td>B1998239</td> <td>943</td> <td></td> <td>mitochondrial phosphate translocator</td> <td>micR</td> <td>P involutus</td> <td>1.00E-10</td>	B1998239	943		mitochondrial phosphate translocator	micR	P involutus	1.00E-10
DrobotoConstruction interporterProf. SystemProf.	B1998308	624	\cap	monocarboxylate transporter	$\Delta f u 3 a 0 3 3 2 0$	Δ fumigatus	2.00E-34
B1998105 B1998105Total potassium channel beta subunit biolassium channel beta subunit biolassium channel beta subunit B1998105An thailiana Alt g04600A. thailiana A. thailiana3.00E-42 3.00E-42B1998105 B1998216656 S B1998216sodium/calcium exchanger vacuolar H+/Ca(2+) exchangerSPAC3A12.0cc VCX1S. correvisiae S. cerevisiae9.00E-09 3.00E-126B1998206 B1998206369 C2 C2v.SNARE v.SNAREVK1S. cerevisiae 4.00E-109.00E-09 3.0E-126B1998209 B1998209379 C2 C2GDP dissociation inhibitor Rasz proteinGD11 VIP3S. cerevisiae s. cerevisiae1.00E-24B19989209 B1998739498 S B1998739Rasz protein 	B1998427	689	$\tilde{\mathbf{O}}$	monosaccharide transporter	nstR	A. juniguius A niger	2.00E-23
Bi99850505.potassium channel $KABI$ $KABI$ $L. dulataaT.OOE-21Bi998102656-sodium/calcium exchangerSPAC3AI2.0ccS. pombe1.00E-14Bi998320671ORab7rab7L. edodes3.00E-126Bi998216884Ovacuolar H+/Ca(2+) exchangerVCXIS. cerevisiae9.00E-09Bi998320369-v-SNAREytt6S. cerevisiae1.00E-11Bi998209622OYpt interacting proteinYIP3S. cerevisiae1.00E-25Bi998799498QRas-related protein Rap2ARAP2AM.musculus3.00E-05Bi998750319-Ras-related protein Rap2ARAP2AM.musculus3.00E-05Bi998751136-MAP kinase kinase ByrlC.NC02350C. neoformast4.00E-04Bi998682111-serine/threonine protein kinasedsklS. cerevisiae2.00E-32Bi998250627-GTP binding proteinVPSIS. cerevisiae2.00E-32Bi998950528-SRPK1-like protein kinasesky2C. albicans3.00E-16Bi998905524GTP binding proteinVac8S. pombe1.00E-52Bi998905528-SRPK1-like protein kinasesky2C. albicans3.00E-16Bi998905528-SRPK1-like proteinCare4S. pombe1.00E-52$	BI998105	704	-	nonosacenariae transporter	At1004690	A thaliana	3.00E-33
B1998102656B1998120656sodium/calcium exchanger <td< td=""><td>BI998501</td><td>505</td><td>-</td><td>potassium channel</td><td>KAB1</td><td>A thaliana</td><td>7.00E-21</td></td<>	BI998501	505	-	potassium channel	KAB1	A thaliana	7.00E-21
BJ998389671Rab7 <i>L</i> edodes3.00E-126BJ998380671 \bigcirc vacuolar H+/Ca(2+) exchanger $VCXI$ <i>S. cerevisiae</i> 9.00E-09BJ998320369- \lor SNARE $yk66$ <i>S. cerevisiae</i> 1.00E-21BJ998209622 \bigcirc Vpt interacting protein $VIII$ <i>S. cerevisiae</i> 1.00E-21BJ998209622 \bigcirc Ypt interacting protein $VIIP3$ <i>S. cerevisiae</i> 1.00E-24BJ998790379 \bigcirc GDP dissociation inhibitor <i>GD11S. cerevisiae</i> 1.00E-24BJ998790379 \bigcirc Ras2 protein <i>ras2S. commune</i> 6.00E-09BJ998755391-Ras-related protein Rap2A <i>RAP2AM. musculus</i> 3.00E-05BJ998652111-serine/threonine protein kinase dkl <i>S. pombe</i> 4.00E-15BJ998235438-protein kinase dkl <i>S. pombe</i> 1.00E-24BJ998266627-GTP binding protein $VPSI$ <i>S. cerevisiae</i> 2.00E-32BJ99895528-SRPK1-like protein kinase $sky2$ <i>C. abicans</i> 3.00E-16BJ998454157-armadillo repeat protein <i>GIS2S. cerevisiae</i> 2.00E-32BJ999872451-chaperonin-containing T-complex <i>cct4S. pombe</i> 3.00E-16BJ998872450-clavarga grimulatoria factor subunit3CSTF3H. sapiens1.00E-52BJ999124464-immunoractive manoprotein MP88 <t< td=""><td>BI998102</td><td>656</td><td>-</td><td>sodium/calcium exchanger</td><td>SPAC3A12.06c</td><td>S nombe</td><td>1.00E-14</td></t<>	BI998102	656	-	sodium/calcium exchanger	SPAC3A12.06c	S nombe	1.00E-14
BJ998216884 \bigcirc vacuolar H+/Ca(2+) exchangerVCX1S. cerevisiae9.00E-09BJ998320369-v-SNAREykf6S. cerevisiae1.00E-21BJ998009622 \bigcirc Ypt interacting proteinYIP3S. cerevisiae1.00E-24Image: SignalingBJ99809622 \bigcirc Ypt interacting proteinYIP3S. cerevisiae1.00E-24Image: SignalingBJ998909379 \bigcirc GDP dissociation inhibitorGDI1S. cerevisiae1.00E-25BJ998755391-Ras-related protein Rap2ARAP2AM. musculus3.00E-05BJ998513136-MAP kinase kinase Byr1CNC02350C. neeformans4.00E-05BJ998253438-protein kinasedsk1S. pombe4.00E-15BJ998263504-izn finger proteinVPS1S. cerevisiae2.00E-32UnclassifiedUnclassifiedUnclassifiedUnclassifiedSpanbe3.00E-16BJ99805528-SRPK1-like protein infor subunit3CSTF3H. sapiens1.00E-52BJ99905524-ichaperonin-containing T-complexcCt4S. pombe3.00E-16BJ99805504-clasarge stimulation factor subunit3CSTF3H. sapiens1.00E-52BJ999012464-immunomodulatory proteinPAC6F6.12S.	B1998389	671	\bigcirc	Rab7	rah7	L. edodes	3.00E-126
BJ998320369-v-SNAREythS. cerevisiae1.00E-21BJ99805423-v-SNAREYTTIS. cerevisiae4.00E-10BJ998209622OYpt interacting proteinYP3S. cerevisiae1.00E-24SignalingBJ998900379OGDP dissociation inhibitorGDI1S. cerevisiae1.00E-25BJ998799498ORas-related protein Rap2ARAP2AM. musculus3.00E-05BJ998755391-Ras-related protein Rap2ARAP2AM. musculus3.00E-05BJ998851136-MAP kinase kinase ByrlCNC02350C. neoformans4.00E-04BJ99862111-serine/threonine protein kinase $CKI3$ S. pombe4.00E-04BJ99855528-SRPK1-like protein kinase $dskl$ S. pombe1.00E-04BJ998515504-in finge proteinVPS1S. cerevisiae2.00E-32UnclassifiedUnclassifiedUnclassifiedUnclassifiedBJ998454157-armadillo repeat protein $Aca1$ A. camphorata1.00E-05BJ9998454157-armadillo repeat protein $Aca1$ A. camphorata1.00E-52BJ999124464immunoreactive manoprotein MP88CNA07540C. neoformans2.00E-09BJ998382450-phosphatidylinositol 3-phosphate binding prote	BJ998216	884	$\tilde{\circ}$	vacuolar H+/Ca(2+) exchanger	VCX1	S. cerevisiae	9.00E-09
BJ998805423 BJ998200- CV-SNARE Ypt interacting proteinVTII 	BJ998320	369	-	v-SNARE	vkt6	S. cerevisiae	1.00E-21
BJ998209622 \bigcirc Ypt interacting proteinYIP3S. cerevisiae1.00E-24SignalingBJ998900379 \bigcirc GDP dissociation inhibitorGDI1S. cerevisiae1.00E-25BJ998755391-Ras-related protein Rap2ARAP2AM. musculus3.00E-05BJ998351136-MAP kinase kinase Byr1CNC02350C. neoformans4.00E-04BJ998235438-protein kinaseCK13S. pombe4.00E-15BJ998206627-GTP binding proteindsk1S. pombe1.00E-04BJ998613504-zinc finger protein kinasedsk1S. cerevisiae2.00E-32UnclassifiedUnclassifiedUnclassifiedUnclassifiedVac8S. pombe3.00E-16BJ998454157-armadillo repeat proteinGIS2S. cerevisiae2.00E-32UnclassifiedUnclassifiedVac8S. pombe1.00E-16BJ998454157-armadillo repeat proteinAcalA. camphorata1.00E-17BJ998906406immunoreactive manoproteinSPAC6F6.12S. pombe5.00E-09BJ998115503-nucleosid diphosphate kinase IndkAP. involutus6.00E-69BJ99812446-immunoreactive manoproteinSPAC6F6.12S. pombe6.00E-09BJ	BJ998805	423	-	v-SNARE	VTI1	S. cerevisiae	4.00E-10
SignalingBJ998900379 \bigcirc GDP dissociation inhibitorGDI1S. cerevisiae1.00E-25BJ998799498 \bigcirc Ras2 proteinras2S. commune6.00E-09BJ998755391-Ras-related protein Rap2ARAP2ARAP2AM. musculus3.00E-05BJ998351136-MAP kinase kinase Byr1 $CNC02350$ $C. neoformans$ 4.00E-04BJ998255438-protein kinase dsl $S. pombe$ 4.00E-04BJ998260627-GTP binding protein $VPS1$ $S. cerevisiae$ 2.00E-32BJ998955528-SRPK1-like protein kinase dsl $S. cerevisiae$ 2.00E-32BJ998051504-zinc finger protein $VPS1$ $S. cerevisiae$ 2.00E-23BJ998454157-armadillo repeat protein $GS2$ $S. cerevisiae$ 2.00E-16BJ998772451-chaperonin-containing T-complex $cct4$ $S. pombe$ 1.00E-05BJ999096360-cleavage stimulation factor subunit3 $CSTF3$ $H. sapiens$ 1.00E-17BJ998800406-immunoreduitory protein $Aca1$ $A. camphorata$ 1.00E-16BJ998124454-photshidtylinositol 3-photsphate binding protein $SPAC6F6.12$ $S. pombe$ 5.00E-06BJ998125503-nucleoside diphotsphate kinase I $SPAC6F6.12$ $S. pombe$ 5.00E-07BJ998124454photsphate	BJ998209	622	\bigcirc	Ypt interacting protein	YIP3	S. cerevisiae	1.00E-24
BJ998990379 \bigcirc GDP dissociation inhibitorGDI1S. cerevisiae1.00E-25BJ998795391-Ras2 proteinras2S. commune6.00E-09BJ998751136-MAP kinase kinase Byr1CNC02350C. neaformans4.00E-04BJ998682111-serine/threonine protein kinasedsk1S. pombe4.00E-04BJ998235438-protein kinasedsk1S. pombe1.00E-04BJ998260627-GTP binding proteinVPS1S. cerevisiae2.00E-32BJ99895528-SRPK1-like protein kinasesky2C. albicans3.00E-11BJ99813504-zinc finger proteinVPS1S. cerevisiae2.00E-32BJ998454157-armadillo repeat proteinGLasS. pombe1.00E-05BJ998454157-armadillo repeat proteinvac8S. pombe1.00E-05BJ999906360-cleavage stimulation factor subunit3CSTF3H. sapiens1.00E-05BJ999124464-immunoredativy proteinAcalA. camphorata1.00E-16BJ99815503-nucleoside diphosphate kinase IndkAP. involutus6.00E-09BJ998125503-phosphate kinase IndkAP. involutus6.00E-08BJ998126630-phosphate kinase IndkAP. involutus6.00E-08BJ998125503-nucleoside diphosphate binding protein <td></td> <td></td> <td></td> <td>Signaling</td> <td></td> <td></td> <td></td>				Signaling			
BJ998799498 \bigcirc Ras2 proteinras2S. commune6.00E-09BJ998755391-Ras-related protein Rap2ARAP2AM. musculuss3.00E-05BJ998351136-MAP kinase kinase ByrlCNC02350C. neoformans4.00E-04BJ998652111-serine/threonine protein kinaseCK13S. pombe4.00E-15BJ998255438-protein kinasedsk1S. pombe1.00E-04BJ998260627-GTP binding proteinVPS1S. cerevisiae2.00E-32BJ998955528-SRPK1-like protein kinasesky2C. albicans3.00E-11BJ998454157-armadillo repeat proteinGIS2S. cerevisiae2.00E-32UnclassifiedBJ998454157-armadillo repeat proteinvac8S. pombe3.00E-16BJ99872451-chaepronin-containing T-complexcct4S. pombe3.00E-17BJ99806406-immunoreactive manoprotein MP88CNA07540C. neoformans2.00E-05BJ998124464-immunoreactive manoprotein MP88CNA07540C. neoformans2.00E-06BJ998125503-nucleoside diphosphate kinase IndkAP. involutus6.00E-06BJ998126676-plasma membrane proteinSPAC6F6.12S. pombe5.00E-07BJ99812676-plasma membrane proteinSPAC6F6.12S. pombe6.00E-06	BJ998990	379	\bigcirc	GDP dissociation inhibitor	GDI1	S. cerevisiae	1.00E-25
BJ998755391-Ras-related protein Rap2ARAP2AM. musculus3.00E-05BJ998351136-MAP kinase kinase Byrl $CNC02350$ $C.neoformans$ 4.00E-04BJ998682111-serine/threonine protein kinase $CKI3$ $S. pombe$ 4.00E-04BJ99853438-protein kinase $dskl$ $S. pombe$ 1.00E-04BJ998260627-GTP binding protein $VPSI$ $S. cerevisiae$ 2.00E-32BJ99895528-SRPK1-like protein kinase $sky2$ $C. albicans$ $3.00E-11$ BJ99813504-zinc finger protein $GIS2$ $S. cerevisiae$ $2.00E-23$ BJ998454157-armadillo repeat protein $GIS2$ $S. cerevisiae$ $2.00E-23$ BJ999063360-clavage stimulation factor subunit3 $CSTF3$ $H. sapiens$ $1.00E-05$ BJ999124464-immunoreactive mannoprotein MP88 $CNA07540$ $C.neoformans$ $2.00E-09$ BJ998115503-nucleoside diphosphate kinase I $ndkA$ $P. involutus$ $6.00E-06$ BJ99812676-plasma membrane protein $SFK1$ $S. cerevisiae$ $5.00E-08$ BJ99812676-plasma membrane protein $SFAC6F6.12$ $S. pombe$ $6.00E-06$ BJ99812676-plasma membrane protein $SFK1$ $S. cerevisiae$ $5.00E-08$ BJ99812676-plasma membrane protein $SFK1$ $S. cerevisiae$ </td <td>BJ998799</td> <td>498</td> <td>\bigcirc</td> <td>Ras2 protein</td> <td>ras2</td> <td>S. commune</td> <td>6.00E-09</td>	BJ998799	498	\bigcirc	Ras2 protein	ras2	S. commune	6.00E-09
BJ998351136-MAP kinase kinase Byrl $CNC02350$ $C. neoformans$ $4.00E-04$ BJ998682111-serine/threonine protein kinase $CKJ3$ $S. pombe$ $4.00E-04$ BJ998235438-protein kinase $dsk1$ $S. pombe$ $1.00E-04$ BJ998205627-GTP binding protein $dsk1$ $S. cerevisiae$ $2.00E-32$ BJ99895528-SRPK1-like protein kinase $sky2$ $C. albicans$ $3.00E-11$ BJ998613504-zinc finger protein $GIS2$ $S. cerevisiae$ $2.00E-23$ BJ998654157-armadillo repeat protein $dsk3$ $S. cerevisiae$ $2.00E-23$ BJ998654157-armadillo repeat protein $vac8$ $S. pombe$ $1.00E-05$ BJ998772451-chaperonin-containing T-complex $ct4$ $S. pombe$ $1.00E-05$ BJ999066360-cleavage stimulation factor subunit3 $CSTF3$ $H. sapiens$ $1.00E-05$ BJ999124464-immunoreactive manoprotein MP88 $CNA07540$ $C. neoformans$ $2.00E-09$ BJ998115503-nucleoside diphosphate kinase I $ndkA$ $P. involutus$ $6.00E-06$ BJ99822548-phosphatidylinositol 3-phosphate binding protein $SPAC6F6.12$ $S. pombe$ $6.00E-06$ BJ99812676-plasma membrane protein $SPAC22EI2.03c$ $S. pombe$ $6.00E-09$ BJ998124403-IBS ribosomal RNA<	BJ998755	391	-	Ras-related protein Rap2A	RAP2A	M. musculus	3.00E-05
BJ998682111-serine/threonine protein kinase $CKI3$ S. pombe4.00E-15BJ998205438-protein kinase $dsk1$ S. pombe1.00E-04BJ998206627-GTP binding protein $VPS1$ S. cerevisiae2.00E-32BJ99895528-SRPK1-like protein kinase $sky2$ C. albiccans3.00E-11BJ998613504-zinc finger protein $GIS2$ S. cerevisiae2.00E-23Unclassifiedunclassified	BJ998351	136	-	MAP kinase kinase Byr1	CNC02350	C. neoformans	4.00E-04
BJ998235438-protein kinase $dsk1$ S. pombe1.00E-04BJ998260627-GTP binding protein $VPS1$ S. cerevisiae2.00E-32BJ99805528-SRPK1-like protein kinase $sky2$ C. albicans3.00E-11BJ998613504-icn finger protein $GIS2$ S. cerevisiae2.00E-32BJ998614157-armadillo repeat protein $vac8$ S. pombe3.00E-16BJ998772451-chaperonin-containing T-complex $cct4$ S. pombe1.00E-05BJ99906360-cleavage stimulation factor subunit3 $CSTF3$ H. sapiens1.00E-05BJ999124464-immunomedulatory proteinAcalA. camphorata1.00E-17BJ99850503-nucleoside diphosphate kinase I $ndkA$ P. involutus6.00E-06BJ998115503-phosphatidylinositol 3-phosphate binding protein $SPAC6F6.12$ S. pombe5.00E-08BJ999026300-P-type ATPase $SPBC887.12$ S. pombe6.00E-09BJ99812548-HUJ/PFPI family protein $SPAC22E12.03c$ S. pombe1.00E-16BJ998759265018S rRNA internal transcribed spacer-A. lycoperdoides1E-51*BJ99888131-25S ribosomal RNAA. loddes9E-41*BJ9988709705.85 ribosomal RNABasidiomycete sp9E-37*BJ998123	BJ998682	111	-	serine/threonine protein kinase	CKI3	S. pombe	4.00E-15
BJ998260627 BJ99895-GTP binding proteinVPS1 sky2S. cerevisiae2.00E-32BJ998053504-SRPK1-like protein kinase $sky2$ C. albicans $3.00E-11$ BJ99813504-zinc finger protein $GIS2$ S. cerevisiae $2.00E-32$ UnclassifiedUnclassifiedarmadillo repeat protein $yac8$ S. pombe $3.00E-16$ BJ998772451-chaperonin-containing T-complex $cct4$ S. pombe $1.00E-52$ BJ999066 360 -cleavage stimulation factor subunit3 $CSTF3$ H. sapiens $1.00E-05$ BJ999124464-immunoreactive mannoprotein MP88 $Aca1$ A. camphorata $1.00E-17$ BJ998155503-nucleoside diphosphate kinase I $ndkA$ P. involutus $6.00E-06$ BJ99812676-plasma membrane protein $SPAC6F6.12$ S. pombe $5.00E-08$ BJ99912448OSnodProt1 precursor probable $NCU07787.1$ N. crassa $7.00E-10$ BJ99814103-I8S ribosomal RNA- $A. lycoperdoides$ $1E-51*$ BJ998759265OI8S ribosomal RNA- $A. locades$ $9E-41*$ BJ998888131-25S ribosomal RNA- $A. locades$ $9E-41*$ BJ99887097O5.8S ribosomal RNA- $Basidiomycetes presentes and transcribed spacerBJ99887097O5.8S ribosomal RNA$	BJ998235	438	-	protein kinase	dsk1	S. pombe	1.00E-04
BJ998995 BJ998613528 504-SRPK1-like protein kinase zinc finger proteinsky2 GIS2C. albicans S. cerevisiae3.00E-11 2.00E-23UnclassifiedBJ998454157 Loperonin-containing T-complexvac8 cct4S. pombe s. pombe3.00E-16BJ998772451 Loberonin-containing T-complexcct4 cct4S. pombe l.00E-521.00E-52BJ990906360 Loberonin-containing T-complexcSTF3 Loberonin-containing T-complexH. sapiens l.00E-051.00E-52BJ999124464 Loberonin-containing T-complexCNA07540 Immunomodulatory proteinAca1 A. camphorata1.00E-17BJ99860406 Loberonin-containing T-complexCNA07540 Immunomodulatory proteinCNA07540 SPAC6F6.12S. pombe S. pombe5.00E-09BJ998115503 S03 Immunomeactive mannoprotein MP88 BJ998122crevisiae S. corevisiae5.00E-08S. Source08BJ998112676 Immunomodulatory proteinSPAC6F6.12 S. pombeS. pombe S. corevisiae5.00E-07BJ999012448 H8 Impospo12SodProt1 precursor probableNCU0778.1 N. crassa S. pombeN. crassa S. pombe1.00E-16BJ998114103 Immunomodul RNA Immune-A. lycoperdoides S. pombe1E-51*BJ998759265 S05 Immune18S ribosomal RNA Immune-A. lycoperdoides S. commune1E-51*BJ99888131 Immune-25S ribosomal RNA S. commune-S. colvacea S. commune2.00E-13 <td>BJ998260</td> <td>627</td> <td>-</td> <td>GTP binding protein</td> <td>VPS1</td> <td>S. cerevisiae</td> <td>2.00E-32</td>	BJ998260	627	-	GTP binding protein	VPS1	S. cerevisiae	2.00E-32
BJ998613 504 -zinc finger protein $GIS2$ S. cerevisiae $2.00E-23$ UnclassifiedBJ998454157-armadillo repeat protein $vac8$ S. pombe $3.00E-16$ BJ998772451-chaperonin-containing T-complex $cct4$ S. pombe $1.00E-52$ BJ999096 360 -cleavage stimulation factor subunit3 $CSTF3$ $H.$ sapiens $1.00E-05$ BJ999124 464 -immunomodulatory protein $AcaI$ $A.$ camphorata $1.00E-17$ BJ99860 406 -immunoreactive manoprotein MP88 $CNA07540$ $C.$ neoformans $2.00E-09$ BJ998115 503 -nucleoside diphosphate kinase I $ndkA$ $P.$ involutus $6.00E-66$ BJ99812 676 -plasma membrane protein $SPAC6F6.12$ $S.$ pombe $5.00E-08$ BJ999026 300 -P-type ATPase $SPBC887.12$ $S.$ pombe $6.00E-09$ BJ999012 448 OSnodProt1 precursor probable $NCU07787.1$ $N.$ crassa $7.00E-10$ BJ998114 103 - $18S$ ribosomal RNA- $A.$ lycoperdoides $1E-51*$ BJ99888 131 - $25S$ ribosomal RNA- $A.$ doi/acea $3.00E-13$ BJ998870 97 O $5.8S$ ribosomal RNA- $A.$ doi/acea $3.00E-13$ BJ998123 521 - $5S$ ribosomal RNA- $A.$ doi/acea $3.00E-13$ BJ998123 521 - $5S$ ribosomal R	BJ998995	528	-	SRPK1-like protein kinase	sky2	C. albicans	3.00E-11
UnclassifiedBJ998454157-armadillo repeat protein $vac8$ S. pombe3.00E-16BJ998772451-chaperonin-containing T-complex $cct4$ S. pombe1.00E-52BJ99906360-cleavage stimulation factor subunit3 $CSTF3$ $H. sapiens$ 1.00E-05BJ999124464-immunomodulatory protein $Acal$ $A. camphorata$ 1.00E-07BJ998106406-immunoreactive mannoprotein MP88 $CNA07540$ $C. neoformans$ 2.00E-09BJ998115503-nucleoside diphosphate kinase I $ndkA$ $P. involutus$ $6.00E-66$ BJ998382450-phosphatidylinositol 3-phosphate binding protein $SFAC6F6.12$ $S. pombe$ $5.00E-08$ BJ998112676-plasma membrane protein $SFK1$ $S. cerevisiae$ $5.00E-07$ BJ999026300-P-type ATPase $SPBC887.12$ $S. pombe$ $6.00E-09$ BJ99912448 \bigcirc SnodProt1 precursor probable $NCU07787.1$ $N. crassa$ $7.00E-10$ BJ998114103-I8S ribosomal RNA- $A. lycoperdoides$ IE-51*BJ99888131-25S ribosomal RNA- $S. commune$ $2.00E-13$ BJ99887097 \bigcirc $5.8s$ ribosomal RNA- $S. commune$ $2.00E-13$ BJ99887097 \bigcirc $5.8s$ ribosomal RNA- $S. commune$ $2.00E-13$ BJ998123521- $5S rRNA internal tran$	BJ998613	504	-	zinc finger protein	GIS2	S. cerevisiae	2.00E-23
BJ998454157-armadillo repeat proteinvac8S. pombe3.00E-16BJ998772451-chaperonin-containing T-complexcct4S. pombe1.00E-52BJ999096360-cleavage stimulation factor subunit3CSTF3H. sapiens1.00E-05BJ999124464-immunomodulatory proteinAcalA. camphorata1.00E-17BJ998960406-immunoreactive manoprotein MP88CNA07540C. neoformans2.00E-09BJ998115503-nucleoside diphosphate kinase IndkAP. involutus6.00E-66BJ998382450-phosphatidylinositol 3-phosphate binding proteinSPAC6F6.12S. pombe5.00E-07BJ998112676-plasma membrane proteinSFK1S. cerevisiae5.00E-07BJ999026300-P-type ATPaseSPBC887.12S. pombe6.00E-09BJ998202548-THIJ/PFPI family proteinSPAC22E12.03cS. pombe1.00E-16rRNA, IGRBJ99875926518S rRNA internal transcribed spacer-A. lycoperdoides1E-51*BJ998781151-25S ribosomal RNAS. commune2.00E-13BJ99887097 \bigcirc 5.8S ribosomal RNA-S. commune2.00E-13BJ99887097 \bigcirc 5.8S ribosomal RNA-S. commune2.00E-13BJ998123521-5S rRNA IGR2S. coddesSindowar	Unclassified						
BJ998772451-chaperonin-containing T-complexcct4S. pombe1.00E-52BJ999096360-cleavage stimulation factor subunit3 $CSTF3$ $H.$ sapiens1.00E-05BJ999124464-immunomodulatory protein $Aca1$ $A.$ camphorata1.00E-17BJ998960406-immunoreactive mannoprotein MP88 $CNA07540$ $C.$ neoformans2.00E-09BJ998115503-nucleoside diphosphate kinase I $ndkA$ $P.$ involutus $6.00E-66$ BJ998382450-phosphatidylinositol 3-phosphate binding protein $SPAC6F6.12$ $S.$ pombe $5.00E-08$ BJ998112676-plasma membrane protein $SFK1$ $S.$ cerevisiae $5.00E-07$ BJ999026300-P-type ATPase $SPBC887.12$ $S.$ pombe $6.00E-09$ BJ999012448OSnodProt1 precursor probable $NCU07787.1$ $N.$ crassa $7.00E-10$ BJ998202548-THIJ/PFPI family protein $SPAC22E12.03c$ $S.$ pombe $1.00E-16$ BJ998731103-18S ribosomal RNA- $A.$ lycoperdoides $1E-51^*$ BJ998788131-25S ribosomal RNA- $A.$ cledes $9E-41^*$ BJ99887097O5.8 ribosomal RNA- $S.$ commune $2.00E-13$ BJ998873521- $S.$ ribosomal RNA- $S.$ commune $2.00E-13$ BJ99887097O 5.8 ribosomal RNA- $S.$ commune	BJ998454	157	-	armadillo repeat protein	vac8	S. pombe	3.00E-16
BJ999096 360 -cleavage stimulation factor subunit3 $CSTF3$ $H.$ sapiens $1.00E-05$ BJ999124 464 -immunomodulatory protein $Aca1$ $A.$ camphorata $1.00E-17$ BJ998960 406 -immunoreactive mannoprotein MP88 $CNA07540$ $C.$ neoformans $2.00E-09$ BJ998115 503 -nucleoside diphosphate kinase I $ndkA$ $P.$ involutus $6.00E-66$ BJ998382 450 -phosphatidylinositol 3-phosphate binding protein $SPAC6F6.12$ $S.$ pombe $5.00E-08$ BJ998112 676 -plasma membrane protein $SFK1$ $S.$ cerevisiae $5.00E-07$ BJ999026 300 -P-type ATPase $SPBC887.12$ $S.$ pombe $6.00E-09$ BJ999012 448 \bigcirc SnodProt1 precursor probable $NCU07787.1$ $N.$ crassa $7.00E-10$ BJ998202 548 -IRS ribosomal RNA- $A.$ lycoperdoides $1E-51*$ BJ998114 103 -18S ribosomal RNA- $A.$ lycoperdoides $9E-41*$ BJ998731151-25S ribosomal RNA- $A.$ lycoperdoides $9E-41*$ BJ998888131-25S ribosomal RNA- $A.$ loddes $9E-41*$ BJ99887097 \bigcirc $5.8S$ ribosomal RNA- $Basidiomycete sp$ $9E-37*$ BJ998123 521 - $5S$ rRNA IGR2- $L.$ edodes $5E-92*$	BJ998772	451	-	chaperonin-containing T-complex	cct4	S. pombe	1.00E-52
BJ999124464-immunomodulatory proteinAca1A. camphorata1.00E-17BJ998960406-immunoreactive mannoprotein MP88 $CNA07540$ $C.$ neoformans2.00E-09BJ998115503-nucleoside diphosphate kinase I $ndkA$ $P.$ involutus $6.00E-66$ BJ998382450-phosphatidylinositol 3-phosphate binding protein $SPAC6F6.12$ $S.$ pombe $5.00E-08$ BJ998112676-plasma membrane protein $SFK1$ $S.$ cerevisiae $5.00E-07$ BJ999026300-P-type ATPase $SPBC887.12$ $S.$ pombe $6.00E-09$ BJ99912448 \bigcirc SnodProt1 precursor probable $NCU07787.1$ $N.$ crassa $7.00E-10$ BJ998202548-THIJ/PFPI family protein $SPAC22E12.03c$ $S.$ pombe $1.00E-13$ BJ998114103-18S ribosomal RNA- $A.$ lycoperdoides $1E-51*$ BJ998759265 \bigcirc 18S rRNA internal transcribed spacer- $A.$ lycoperdoides $9E-41*$ BJ998781151-25S ribosomal RNA- $S.$ commune $2.00E-13$ BJ99887097 \bigcirc 5.8S ribosomal RNA- $S.$ commune $2.00E-13$ BJ998123521- $S.$ rRNA IGR2- $L.$ edodes $5E-92*$	BJ999096	360	-	cleavage stimulation factor subunit3	CSTF3	H. sapiens	1.00E-05
BJ998960406-immunoreactive mannoprotein MP88 $CNA07540$ $C.$ neoformans $2.00E-09$ BJ998115503-nucleoside diphosphate kinase I $ndkA$ $P.$ involutus $6.00E-66$ BJ998382450-phosphatidylinositol 3-phosphate binding protein $SPAC6F6.12$ $S.$ pombe $5.00E-08$ BJ998112676-plasma membrane protein $SFK1$ $S.$ cerevisiae $5.00E-07$ BJ999026300-P-type ATPase $SPBC887.12$ $S.$ pombe $6.00E-09$ BJ99912448 \bigcirc SnodProt1 precursor probable $NCU07787.1$ $N.$ crassa $7.00E-10$ BJ998202548-THIJ/PFPI family protein $SPAC22E12.03c$ $S.$ pombe $1.00E-16$ rRNA, IGRBJ998759265 \bigcirc 18S ribosomal RNA- $A.$ lycoperdoides $1E-51*$ BJ998731151-25S ribosomal RNA- $L.$ edodes $9E-41*$ BJ99888131-25S rRNA internal transcribed spacer- $S.$ commune $2.00E-13$ BJ99870997 \bigcirc $5.8S$ ribosomal RNA- $L.$ edodes $9E-37*$ BJ998123521- $5S$ rRNA IGR2- $L.$ edodes $5E-92*$	BJ999124	464	-	immunomodulatory protein	Acal	A. camphorata	1.00E-17
BJ998115 503 -nucleoside diphosphate kinase 1ndkAP. involutus $6.00E-66$ BJ998382 450 -phosphatidylinositol 3-phosphate binding protein $SPAC6F6.12$ $S. pombe$ $5.00E-08$ BJ998112 676 -plasma membrane protein $SFK1$ $S. cerevisiae$ $5.00E-07$ BJ999026 300 -P-type ATPase $SPBC887.12$ $S. pombe$ $6.00E-09$ BJ999012 448 \bigcirc SnodProt1 precursor probable $NCU07787.1$ $N. crassa$ $7.00E-10$ BJ998202 548 -THIJ/PFPI family protein $SPAC22E12.03c$ $S. pombe$ $1.00E-16$ rRNA, IGRBJ998114 103 -18S ribosomal RNA- $A. lycoperdoides$ $1E-51*$ BJ998759265 \bigcirc 18S rRNA internal transcribed spacer- $A. lycoperdoides$ $9E-41*$ BJ998731151-25S ribosomal RNA- $L. edodes$ $9E-41*$ BJ998788131-25S rRNA internal transcribed spacer- $S. commune$ $2.00E-13$ BJ9987097 \bigcirc $5.8S$ ribosomal RNA- $Basidiomycete sp$ $9E-37*$ BJ998123 521 - $5S$ rRNA IGR2- $L. edodes$ $5E-92*$	BJ998960	406	-	immunoreactive mannoprotein MP88	CNA07540	C. neoformans	2.00E-09
BJ998382450-phosphatidylinositol 3-phosphate binding proteinSPAC 6F 6.12S. pombeS.00E-08BJ998112676-plasma membrane proteinSFK1S. cerevisiae $5.00E-07$ BJ999026300-P-type ATPaseSPBC887.12S. pombe $6.00E-09$ BJ999012448 \bigcirc SnodProt1 precursor probableNCU07787.1N. crassa $7.00E-10$ BJ998202548-THIJ/PFPI family proteinSPAC22E12.03cS. pombe $1.00E-16$ BJ998114103-18S ribosomal RNA-A. lycoperdoides $1E-51^*$ BJ998759265 \bigcirc 18S rRNA internal transcribed spacer-R. olivacea $3.00E-13$ BJ998731151-25S ribosomal RNA-L. edodes9E-41*BJ998788131-25S rRNA internal transcribed spacer-S. commune $2.00E-13$ BJ9987097 \bigcirc 5.8S ribosomal RNA-Basidiomycete sp9E-37*BJ998123521-5S rRNA IGR2-L. edodes5E-92*	BJ998115	503	-	nucleoside diphosphate kinase l	ndkA	P. involutus	6.00E-66
BJ998112676-plasma membrane proteinSFK1S. cerevisiae $5.00E-07$ BJ999026 300 -P-type ATPase $SPBC887.12$ S. pombe $6.00E-09$ BJ999012448 \bigcirc SnodProt1 precursor probable $NCU07787.1$ N. crassa $7.00E-10$ BJ998202548-THIJ/PFPI family protein $SPAC22E12.03c$ S. pombe $1.00E-16$ BJ998114103-18S ribosomal RNA-A. lycoperdoides $1E-51^*$ BJ998759265 \bigcirc 18S rRNA internal transcribed spacer-R. olivacea $3.00E-13$ BJ998731151-25S ribosomal RNA-L. edodes $9E-41^*$ BJ998988131-25S rRNA internal transcribed spacer-S. commune $2.00E-13$ BJ9987097 \bigcirc 5.8S ribosomal RNA-Basidiomycete sp $9E-37^*$ BJ998123521-5S rRNA IGR2-L. edodes $5E-92^*$	BJ998382	450	-	phosphatidylinositol 3-phosphate binding protein	SPAC6F6.12	S. pombe	5.00E-08
BJ999020 500 -P-type AI PaseSPBC887.12S. pombe $6.00E-09$ BJ999012448 \bigcirc SnodProt1 precursor probable $NCU07787.1$ $N. crassa$ $7.00E-10$ BJ998202548-THIJ/PFPI family protein $SPAC22E12.03c$ $S. pombe$ $1.00E-16$ BJ998114103-18S ribosomal RNA- $A. lycoperdoides$ $1E-51^*$ BJ998759265 \bigcirc 18S rRNA internal transcribed spacer- $R. olivacea$ $3.00E-13$ BJ998731151-25S ribosomal RNA- $L. edodes$ $9E-41^*$ BJ998988131-25S rRNA internal transcribed spacer- $S. commune$ $2.00E-13$ BJ9987097 \bigcirc 5.8S ribosomal RNA- $Basidiomycete sp$ $9E-37^*$ BJ998123521- $5S rRNA IGR2$ - $L. edodes$ $5E-92^*$	BJ998112	676	-	plasma membrane protein	SFKI	S. cerevisiae	5.00E-07
BJ999012448 \bigcirc SnodProf1 precursor probable $NCU0/787.1$ $N. crassa$ $7.00E-10$ BJ998202548-THIJ/PFPI family protein $SPAC22E12.03c$ $S. pombe$ $1.00E-16$ rRNA, IGRBJ998114103-18S ribosomal RNA- $A. lycoperdoides$ $1E-51*$ BJ998759265 \bigcirc 18S rRNA internal transcribed spacer- $R. olivacea$ $3.00E-13$ BJ998731151-25S ribosomal RNA- $L. edodes$ $9E-41*$ BJ998988131-25S rRNA internal transcribed spacer- $S. commune$ $2.00E-13$ BJ9987097 \bigcirc 5.8S ribosomal RNA- $Basidiomycete sp$ $9E-37*$ BJ998123521-5S rRNA IGR2- $L. edodes$ $5E-92*$	BJ999026	300	-	P-type AI Pase	SPBC887.12	S. pombe	6.00E-09
BJ998102346-IFILI/FEFT family proteinSPAC22E12.05cS. pombe1.00E-16rRNA, IGRBJ998114103-18S ribosomal RNA-A. lycoperdoides1E-51*BJ998759265O18S rRNA internal transcribed spacer-R. olivacea3.00E-13BJ998731151-25S ribosomal RNA-L. edodes9E-41*BJ99888131-25S rRNA internal transcribed spacer-S. commune2.00E-13BJ99887097O5.8S ribosomal RNA-Basidiomycete sp9E-37*BJ998123521-5S rRNA IGR2-L. edodes5E-92*	BJ999012	448	\cup	SnodProt1 precursor probable	NCUU//8/.1	N. crassa S. pombo	/.00E-10
BI998114103-A. lycoperdoides1E-51*BJ998759265018S rRNA internal transcribed spacer-R. olivacea3.00E-13BJ998731151-25S ribosomal RNA-L. edodes9E-41*BJ998988131-25S rRNA internal transcribed spacer-S. commune2.00E-13BJ9988709705.8S ribosomal RNA-Basidiomycete sp9E-37*BJ998123521-5S rRNA IGR2-L. edodes5E-92*	DJ998202	348	-		SFACZZE12.03C	s. pombe	1.00E-10
BJ998759265 \bigcirc 18S rRNA internal transcribed spacer \neg A. tycoperaoides $1E-51^*$ BJ998759265 \bigcirc 18S rRNA internal transcribed spacer \neg R. olivacea $3.00E-13$ BJ998731151 $-$ 25S ribosomal RNA \neg L. edodes $9E-41^*$ BJ998988131 $-$ 25S rRNA internal transcribed spacer \neg S. commune $2.00E-13$ BJ99887097 \bigcirc 5.8S ribosomal RNA $-$ Basidiomycete sp $9E-37^*$ BJ998123521 $-$ 5S rRNA IGR2 $-$ L. edodes $5E-92^*$							
BJ998731151-25S ribosomal RNA- <i>R. olivacea</i> 5.00E-13BJ998988131-25S rRNA internal transcribed spacer- <i>L. edodes</i> 9E-41*BJ99887097O5.8S ribosomal RNA- <i>S. commune</i> 2.00E-13BJ998123521-5S rRNA IGR2- <i>L. edodes</i> 5E-92*	DJ770114 B1008750	103	$\overline{\bigcirc}$	105 HUUSOIIIal KINA	-	A. tycoperaoides	1E-31" 3 00E 12
BJ998988131-25S rRNA internal transcribed spacer-L. eadaes $9E-41^{\circ}$ BJ99887097 \bigcirc 5.8S ribosomal RNA-S. commune2.00E-13BJ998123521- $5S$ rRNA IGR2-L. edodes $5E-92^*$	B1008731	205	\cup	258 ribosomal RNA	-	K. Ulivacea Ledodes	3.00E-13 QE /1*
BJ99887097 \bigcirc 5.8S ribosomal RNA-Basidiomycete sp9E-37*BJ998123521-5S rRNA IGR2-L. edodes5E-92*	B1008088	131	-	250 H0050IIIal NNA 258 rBNA internal transcribed spacer	-	L. eubles	2 00F 13
BJ998123 521 - 5S rRNA IGR2 - L. edodes 5E-92*	B1998870	97	\cap	5.8S ribosomal RNA	_	B. commune Rasidiomverte sr	2.00E-13 9F_37*
	BJ998123	521	-	5S rRNA IGR2	-	L. edodes	5E-92*

Name	Times	
Hydrophobin 1	24	
Phosphatidylserine decarboxylase	8	
Aldehyde dehydrogenase	6	
NAD-dependent formate dehydrogenase 1	4	
Metallothionein	4	
Riboflavin aldehyde-forming enzyme	4	
NAD-dependent formate dehydrogenase 2	3	
Manganese superoxide dismutase 1	3	
Polyubiquitin	3	
Catalase	3	
C-4 methyl sterol oxidase	3	
Hydrophobin 5	3	
Ras2	3	
Succinate dehydrogenase	3	
Ubiqutin conjugating enzyme Ubc4	3	

Table 2. Numbers of times ESTs were obtained