

S2 Table. Mcmd1 and Pamd1 BLASTP searches

Query Protein	Group	Species	Top hit (ID)	BLASTP E-value*
Mcmd1	Multicellular animals	<i>Homo sapiens</i>	Mcm8 (sp Q9UJA3-4 MCM8_HUMAN)	0.024
		<i>Mus musculus</i>	Mcm8 (sp Q9CWV1 MCM8_MOUSE)	0.001
		<i>Danio rerio</i>	Mcm4 (ENSDARP00000097832)	2.64E-04
		<i>Drosophila melanogaster</i>	Rec (FBpp0306662)	1.98E-05
		<i>Caenorhabditis elegans</i>	Mcm4 (Y39G10AR.14a)	3.26E-06
	Land plants	<i>Aradidopsis thaliana</i>	Mcm8 (AT3G09660.1)	0.61
		<i>Saccharomyces cerevisiae</i>	Mcm4 (YPR019W)	2.22E-04
	Fungi	<i>Schizosaccharomyces pombe</i>	Sre2 (SPBC354.05c.1:pep)	1.7
	Protists	<i>Tetrahymena borealis</i>	EI9_20942.1	0
		<i>Tetrahymena ellioti</i>	EI7_15054.1	0
		<i>Tetrahymena malaccensis</i>	EIA_23651.1	0
		<i>Paramecium tetraurelia</i>	Mini-chromosome maintenance, DNA-dependent ATPase (GSPATP00012268001)	1.2
		<i>Ichthyophthirius multifilis</i>	mcm2-3-5 family protein, putative (IMG5_106700)	0.41
		<i>Oxytricha trifallax</i>	MCM8a (Contig7673.0.g5)	0.075
		<i>Styloynchia lemnae</i>	mcm family protein (Contig915.g1014)	0.054
		<i>Plasmodium falciparum</i>	Mcm5 (PF3D7_1211700)	2.9
		<i>Toxoplasma gondii</i>	Mcm5 (TGME49_243920)	0.003
		<i>Trypanosoma brucei</i>	MCM complex subunit, putative (Tbg972.11.13060)	0.14
		<i>Giardia lamblia</i>	Mcm5 (GL50581_282)	0.17
Pamd1	Multicellular animals	<i>Homo sapiens</i>	Cilia And Flagella Associated Protein 53 (sp Q96M91 CFA53_HUMAN)	0.064
		<i>Mus musculus</i>	N/A	N/A
		<i>Danio rerio</i>	Radial spoke head 3 homolog (ENSDARP00000017411)	1
		<i>Drosophila melanogaster</i>	Mei218 (FBpp0292855)	0.16
		<i>Caenorhabditis elegans</i>	T23F2.2b	4.8
	Land plants	<i>Aradidopsis thaliana</i>	N/A	N/A
		<i>Saccharomyces cerevisiae</i>	YAP5 (YIR018W)	1.4
	Fungi	<i>Schizosaccharomyces pombe</i>	Cell polarity protein alp21 (SPAC22H10.10.1:pep)	1.7
	Protists	<i>Tetrahymena borealis</i>	EI9_18594.1	0
		<i>Tetrahymena ellioti</i>	EI7_16247.1	0
		<i>Tetrahymena malaccensis</i>	EIA_22197.1	0
		<i>Paramecium tetraurelia</i>	Protein kinase-like domain (GSPATP00021108001)	5.6
		<i>Ichthyophthirius multifilis</i>	Hypothetical protein (IMG5_120920)	1.1
		<i>Oxytricha trifallax</i>	GCC2 and GCC3 (Contig473.1.g50)	0.057
		<i>Styloynchia lemnae</i>	Eukaryotic translation initiation factor 4e type 2 (Contig160.g191)	0.64
		<i>Plasmodium falciparum</i>	DEAD box ATP-dependent RNA helicase, putative (PF3D7_0411400)	0.86
		<i>Toxoplasma gondii</i>	Phospholipase, patatin family protein (TGME49_231370)	8.3
		<i>Trypanosoma brucei</i>	Hypothetical protein, conserved (Tbg972.8.460)	3.2
		<i>Giardia lamblia</i>	Hypothetical protein (GL50581_1233)	0.95

*BLASTP E-value threshold was set to 10 (default). Homologs with an E-value equal to or lower than 0.001 (1e-3) are colored in blue.