

Supplementary File S5: BLAST results and Multiple sequence alignment of human Phafin2 with each of top hit protozoan sequence search.

BLAST result

<i>Description</i>	<i>Scientific Name</i>	<i>Taxid</i>	<i>Max Score</i>	<i>Total Score</i>	<i>Query Cover</i>	<i>E value</i>	<i>Per. Ident</i>	<i>Acc. Len</i>	<i>Accession</i>
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	140	140	71%	1e-38	43.09%	455	XP_655361.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	129	129	71%	6e-34	38.46%	555	XP_649382.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	124	124	89%	1e-32	36.13%	441	XP_651719.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	124	124	97%	7e-32	32.16%	631	XP_651964.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS-B]	Entamoeba histolytica HM-1:IMSS-B	885319	107	107	79%	2e-26	34.31%	460	EMH78141.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	107	107	79%	4e-26	34.31%	492	XP_655384.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	105	105	80%	1e-25	35.05%	495	XP_656365.1
Rho/RAC guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-3:IMSS]	Entamoeba histolytica HM-3:IMSS	885315	104	104	79%	5e-25	33.99%	876	EMS15045.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	104	104	79%	5e-25	33.99%	876	XP_651436.1
rho/RAC guanine nucleotide exchange factor, putative [Entamoeba histolytica KU27]	Entamoeba histolytica KU27	885311	104	104	79%	5e-25	33.99%	745	EMD43911.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	103	103	81%	1e-24	32.21%	730	XP_656765.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	101	101	88%	4e-24	29.61%	696	XP_654401.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	85.9	85.9	70%	7e-19	31.49%	452	XP_651674.1
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]	Entamoeba histolytica HM-1:IMSS	294381	79.0	79.0	71%	3e-16	30.05%	725	XP_651711.2
Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-3:IMSS]	Entamoeba histolytica HM-3:IMSS	885315	77.4	77.4	38%	7e-16	41.67%	487	EMS16071.1
High-resolution solution structure of the LM5-1 FYVE domain from Leishmania major [Leishmania major]	Leishmania major	5664	64.3	64.3	32%	3e-13	39.51%	84	1Z2Q_A
conserved hypothetical protein [Leishmania major strain Friedlin]	Leishmania major strain Friedlin	347515	56.2	56.2	26%	9e-09	42.65%	377	XP_003722823.1

FYVE_zinc_finger_containing_protein_putative [Leishmania major strain Friedlin]	<i>Leishmania major</i> strain Friedlin	347515	51.2	51.2	28%	1e-07	36.99%	172	CAG9576238.1
conserved hypothetical protein [Leishmania major strain Friedlin]	<i>Leishmania major</i> strain Friedlin	347515	49.3	49.3	28%	2e-06	32.61%	2420	XP_001684146.1
zinc finger protein, putative [Entamoeba histolytica HM-1:IMSS]	<i>Entamoeba histolytica</i> HM-1:IMSS	294381	48.1	48.1	26%	4e-06	36.36%	395	XP_656065.1
conserved hypothetical protein [Leishmania major strain Friedlin]	<i>Leishmania major</i> strain Friedlin	347515	48.1	48.1	24%	5e-06	42.62%	636	XP_001682467.1
putative ras-like small GTPases [Leishmania major strain Friedlin]	<i>Leishmania major</i> strain Friedlin	347515	47.4	47.4	18%	1e-05	40.82%	766	

Top aligned sequence of Entamoeba histolytica

>XP_655361.1 Rho guanine nucleotide exchange factor, putative [Entamoeba histolytica HM-1:IMSS]
MSKRLYVVNEIVSTEESYARALQTVVDLYITPLKGMDLISEEDMKGLFCNLEELLGDGANQLTKQLKDRLK
EFALNDNICDVFLLNKPLFNRFGPYIQNYEKASLLFDKLSKKKKFEEFCETQKENPLSNNGNLMSFLIFP
VQRIIPRYILLMKEYIKNTEKDHDAVIAEQVRRYLDSYAKAVNAIIANENNKQKMRDIIKMFTDLDPKTE
NDLKTLPRTLVRREGILRKQCRKAVKERYFYLFNDATVIYGEQQGKKIQFHQLLELTSVKDIEDSDISQNG
FQLKGLQKSVVYAETFDEKKEWMDLNKAFTGERKYEFEELSDNEAAPTWIPDDNVLDCMNCHSKFTL
LNRHHCKRKCGRVLC AECTKRRVVI PHISSKPVRVCENCATKFENKDFEGVDDNSEHVNANGVAPPSLPN
IPPPQRKQLIKISAMYPTLQPPSREPPPELPQYESY

Top aligned sequence of Leishmania major

>XP_003722823.1 conserved hypothetical protein [Leishmania major strain Friedlin]
MSSSLSSPRPPQAEALPAPRGTI RFEDLGEPVQRLRLSLKGDVSEEDMALLEYVSVKDMAKIYSEMATDR
HAEEIWQELRSALQARKEK IARREAE LAEKQRALEAEQEAEQRLRQQLEEEERERISAEEARQQRREER
RRRKA EKA AAAAAAAAAEAEQAAAAAAAAEAEAAAAAAAAEETERQRKA EKRRKRREARARELQEEQDALTA E
RARHETKKQKSLNQKDWSEFVQSHPLEY AQSETLDGAQQQLPAVIEQKELKHTLNAPPVSEQLLSRT
YSPACGACGTRFDRPPPEWNC PMCERRYKVKVQVQPDMMENCMCKEPIGRWSRHHCRNCGRLVCANC
SDKRAIIEDLGYDTPVRVCYDCFRLRS

There were no sequences found from Giardia lamblia

Multiple Protozoan Sequence Alignment with Human Phafin2

Homo_sapiens (Human)	-----LKSP LNDM-----SDDDDD-----D-----DSSD-----	249
XP_655361.1	-----APP SLPNIPPPQRKQLIKI-----S-----AMYPTL-----	439
XP_649382.1	ENSEMSEAKGCTKEEFKIE---NTNDIIRDNEEAKAESTTLEESKDTEENNVM-----S	493
XP_651719.1	LDSISMESTSP L LK-----	441
XP_651964.1	QQKILSGGDINDSE--QND---DWQEF-----EDIEFDKQPSPRSL	489
EMH78141.1	-----	460
XP_655384.1	-----	492
XP_656365.1	RSPRMSKSEKKDKQ--DK-----K--KDKKKGKKSDSDNDNSQQT--KVV	464
EMS15045.1	QDQQLTSSSNDN--KKI---DVQPILQEE--SSNEQSTSDVENMNNNEQP---LE	583
XP_651436.1	QDQQLTSSSNDN--KKI---DVQPILQEE--SSNEQSTSDVENMNNNEQP---LE	583
EMD43911.1	QDQQLTSSSNDN--KKI---DVQPILQEE--SSNEQSTSDVENMNNNEQP---LE	452
XP_656765.1	IRRDCKRSNSVGNPEEIFD---GLSVILNPDIQRT---QTANILNNVENS KSPLGRSIG	458
XP_654401.1	---KDTTSSPALPEQSKQ---FNNPIH-----S---TNNTLSQEQT PSTIK--	483
XP_651674.1	-----PLPSIPPPRRKTPFIQ-----N-----ATQFKKREPPR--	425
XP_651711.2	--TIRMKSSKEDEIVLRL-----EGVNLTRVRS	701
EMS16071.1	ENSEMSEAKGCTKEEFKIE---NTNDIIRDNEEAKAESTTLEESKDTEENNVM-----S	425
1Z2Q_A	-----	84
XP_003722823.1	-----	377
CAG9576238.1	---VLTTAGPGAPPVAAR---GQQDEGA-----GPTEPSTDDMNKPTSPLETP--	137
XP_001684146.1	---VMDTYGHALLPLAGI---AKEPLKG-----G---ASADMKEPEKPSAAQ--	1896
XP_656065.1	-----	395
XP_001682467.1	-----	636
XP_001687717.1	QGLDVSSASSSALLPGPLP---VCS---D-----GNGHPPSNALTAPSAVTALP--	182