

**S3 Table. Identification of potential RibJ transporters in kinetoplastids with partially assembled genomes.**

Parasite	Host	Accession number (contig or scaffold)	MFS (e-value) <sup>a</sup>	Region <sup>b</sup>	TcRibJ similarity (%) <sup>c</sup>	Reference
<b>A</b> <i>Trypanosoma equiperdum</i>	Equines (venereal disease dourine)	CZPT01000402	Yes (3.2 e-27)	19-377	62.5	NP
<b>B</b> <i>Leishmania (Viannia) peruviana</i>	<i>Homo sapiens</i> (visceral leishmaniasis)	LN609254.1	Yes (5.2 e-23)	33-375	50.8	[1]
<i>Angomonas desouzai</i>	<i>Ornithia obesa</i> (fly)	AUXL01001118	Yes (6.9 e-20)	35-309	55.4	[2]
<i>Angomonas deanei</i>	<i>Zelus leucogrammus</i> (hemiptera)	AUXM01000876	Yes (1.3 e-24)	34-419	56.6	[2]
<i>Lotmaria passim</i>	<i>Apis mellifera</i> (honey bee)	AHIJ01002325	Yes (1.4 e-16)	35-371	50.2	[3]
<b>C</b> <i>Crithidia acanthocephali</i>	<i>Acanthocephala femorata</i> (fly)	AUXI01000737	Yes (6.6 e-18)	36-370	51.5	[2]
<i>Herpetomonas muscarum</i>	<i>Musca domestica</i> (fly)	AUXJ01001726	Yes (2.5 e-18)	38-355	49.8	[2]
<i>Strigomonas oncopelti</i>	<i>Zelus leucogrammus</i> (hemiptera)	AUXK01003753	Yes (9.1 e-25)	33-474	50.4	[2]
<i>Strigomonas galati</i>	-	AUXN01003492	Yes (7.6 e-18)	26-330	50.9	[2]
<i>Strigomonas culicis</i>	<i>Aedes vexans</i> (mosquito)	AUXH01000639	Yes (8.1 e-19)	38-332	52.6	[2]
<i>Phytomonas serpens</i> 9T	<i>Solanum lycopersicum</i> (isolate from tomato)	AIHY01002387	Yes (5.4 e-21)	74-412	38.1	[4]
<b>D</b> <i>Phytomonas</i> sp. isolate Hart1	phloem-restricted pathogenic isolate from a diseased coconut from Guiana	HF955203 CAVR020000000*	Yes (1.7 e-22)	55-370	37.7	[5]
<i>Phytomonas</i> sp. isolate EM1	asymptomatic latex isolate from <i>Euphorbia</i>	HF955064 CAVQ010000000*	Yes (3.2 e-28)	61-429	39.9	[5]
<i>Bodo saltans</i>	None (free-living kinetoplastid)	BS47350	Yes (5.6 e-14)	12-413	39.9	[6]
<b>E</b> <i>Trypanoplasma borreli</i>	Cyprinid fish	NODE_24555_length_ 1382_cov_9.405933	Yes (6.0 e-24)	35-307	28.2	NP

Identification of putative riboflavin transporters using TcRibJ as query in NCBI database. Currently, these genomes are partially assembled. <sup>a</sup>Predicted MSF domains by Pfam server. <sup>b</sup>Regions included in the MFS domain. <sup>c</sup>Similarity with TcRibJ obtained by ClustalW. NP: Not published.

A: other parasites from the *Trypanosoma* genus.

B: other parasites from the *Leishmania* genus.

C: parasite exclusive from insects.

D: phytoparasites.

E: parasite belonging to different order than Trypanosomatida.

### Supplementary References

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