

**S2 Table. Identification of potential RibJ transporters in trypanosomatids in totally assembled genomes.**

Parasite	Host	Accession number	MFS (e-value) <sup>a</sup>	Region <sup>b</sup>	TcRibJ similarity (%) <sup>c</sup>
<i>Trypanosoma cruzi</i>	<i>Homo sapiens</i> (Chagas disease)	TcCLB.509885.70	Yes (1.7 e-16)	19-288	100
<b>A</b> <i>Trypanosoma brucei</i>	<i>Homo sapiens</i> (African trypanosomiasis)	Tb927.5.470	Yes (3.2 e-27)	19-337	62.0
<i>Leishmania (Leishmania) mexicana</i>	<i>Homo sapiens</i> (cutaneous leishmaniasis)	LmxM.05.0480	Yes (7.2 e-19)	36-218	49.0
<i>Trypanosoma evansi</i>	<i>Bubalus bubalis</i> (water buffalo)	TevSTIB805.5.460	Yes (3.6 e-27)	19-377	62.5
<i>Trypanosoma congolense</i>	<i>Bos</i> spp. (African bovine trypanosomiasis)	TcIL3000_0_01740	Yes (7.6 e-29)	19-354	60.5
<b>B</b> <i>Trypanosoma grayi</i>	<i>Glossina palpalis</i> (tsetse fly)	Tgr.1850.1000	Yes (9.4 e-24)	19-295	76.1
<i>Trypanosoma rangeli</i>	<i>Homo sapiens</i> (asymptomatic)	TRSC58_01116	Yes (1.3 e-21)	19-288	83.3
<i>Trypanosoma vivax</i>	<i>Bos taurus</i>	TvY486_0500070	Yes (8.0 e-27)	20-291	67.6
<i>Leishmania (Leishmania) tropica</i>	<i>Homo sapiens</i> (cutaneous leishmaniasis)	LTRL590_050009300	Yes (1.1 e-19)	39-218	49.8
<i>Leishmania (Leishmania) aethiopica</i>	<i>Homo sapiens</i> (cutaneous leishmaniasis)	LAEL147_000064200	Yes (9.2 e-20)	39-218	49.8
<i>Leishmania (Viannia) braziliensis</i>	<i>Homo sapiens</i> (cutaneous leishmaniasis)	LBRM2903_050010000	Yes (2.0 e-22)	33-375	50.9
<i>Leishmania (Viannia) panamensis</i>	<i>Homo sapiens</i> (cutaneous leishmaniasis)	LPAL13_050009400	Yes (6.7 e-23)	33-373	50.8
<i>Leishmania</i> sp. MAR LEM2494	<i>Homo sapiens</i> (cutaneous leishmaniasis)	LMARLEM2494_050009900	Yes (2.3 e-15)	33-392	48.7
<i>Leishmania (Leishmania) major</i>	<i>Homo sapiens</i> (cutaneous leishmaniasis)	LmjF.05.0480	Yes (3.0 e-17)	39-393	49.8
<b>C</b> <i>Leishmania (Leishmania) donovani</i>	<i>Homo sapiens</i> (visceral leishmaniasis)	LdBPK_050480.1	Yes (8.7 e-16)	39-337	49.7
<i>Leishmania (Leishmania) infantum</i>	<i>Homo sapiens</i> (infantile visceral leishmaniasis)	LinJ.05.0480	Yes (7.4 e-16)	39-337	49.7
<i>Leishmania (Leishmania) gerbelli</i>	<i>Rhombomys opimus</i> (gerbil)	LGELEM452_050009800	Yes (1.2 e-16)	36-400	49.6
<i>Leishmania (Leishmania) turanica</i>	<i>Rhombomys opimus</i> (gerbil)	LTULEM423_050009600	Yes (9.5 e-17)	39-396	50.0
<i>Leishmania (Leishmania) arabica</i>	<i>Psammomys obesus</i> (rodent)	LARLEM1108_050009800	Yes (1.1 e-16)	36-396	49.5
<i>Leishmania (Sauroleishmania) tarentolae</i>	<i>Tarentola mauritanica</i> (lizard)	LtaP05.0490	Yes (4.1 e-16)	33-383	49.2
<i>Leishmania enriettii</i> complex	Rodents	ENLEM3045_050009900	Yes (1.2 e-20)	44-509	48.1
<b>D</b> <i>Endotrypanum monterogeii</i>	<i>Choloepus hoffmanni</i> (sloth)	EMOLV88_050009300	Yes (3.3 e-22)	37-495	50.5
<i>Crithidia fasciculata</i>	<i>Anopheles quadrimaculatus</i> (mosquito)	CFAC1_020011500	Yes (1.2 e-15)	36-374	51.9
<b>E</b> <i>Leptomonas pyrrhocoris</i>	<i>Pyrrhocoris apterus</i> (european bug)	LpyrH10_07_0560	Yes (1.9 e-23)	36-364	52.6
<i>Leptomonas seymouri</i>	<i>Dysdercus suturellus</i> (red bug)	Lsey_0441_0040	Yes (7.5 e-19)	33-480	52.4

Identification of putative riboflavin transporters using TcRibJ as query in Trityps database. <sup>a</sup>Predicted domains in Pfam server. <sup>b</sup>Regions included in the MFS domain. <sup>c</sup>Similarity with TcRibJ obtained by ClustalW.

A: human parasites used in this work.

B: other parasites from the *Trypanosoma* genus.

C: other parasites from the *Leishmania* genus

D: other mammalian parasites.

E: parasites exclusive from insects.