

**Table 1: Small GTPases represented in trypanosomatids, excluding the Rab and Arf families.** *T. brucei*, *T. cruzi* and *L. major* GTPases are listed by GeneDB accession number. The group loosely related to Ras, Gtr1-RagA and genes encoding products containing the Mmr-Hsr1 GTP-binding domain and having some members in common with prokaryotes are shown. A three letter systematic name, based on domain architecture, is given. Domain data from Pfam or CD-search at NCBI.

Class	Name	GTPase (+ other) domain	<i>T. brucei</i>	<i>L. major</i>	<i>T. cruzi</i>
Ras	TbRLJ	Ras	Tb11.52.0014	LmjF09.0850	Tc00.1047053511559.30
	TbRLP	Ras	Tb11.02.3850		Tc00.1047053504149.110
	TcRho	Ras			Tc00.1047053506649.40
	TbRHP	Miro/Rho	Tb10.70.0590	LmjF36.1820	Tc00.1047053507641.104
	TbRAN	Ras	Tb927.3.1120	LmjF25.1420	Tc00.1047053509455.80
	TbFRP	Ras (FYVE)	Tb927.7.3790	LmjF14.1170	Tc00.1047053506795.60
	TbRX1	Ras	Tb927.3.5550	LmjF29.0090	Tc00.1047053510647.60
	TbRX2	Ras	Tb927.4.4220	LmjF31.0860	Tc00.1047053507277.10
	TbRX3	Ras	Tb927.8.8140	LmjF31.0860	Tc00.1047053507277.10
	TbRABL	Rab-like	Tb11.01.8590	LmjF32.3210	Tc00.1047053511535.20
MMR-HSR1	TbEAR	EngA	Tb927.7.1640	LmjF26.0270	Tc00.1047053509509.60
	TbNST	Y1qF (nucleostemin)	Tb11.02.0240	LmjF33.2400	Tc00.1047053504153.300
	TbNGP	NGP-1	Tb927.7.7450	LmjF05.0460	Tc00.1047053510609.30
	TbNOG1	NOG	Tb11.02.0620	LmjF33.1870	Tc00.1047053510431.160
	TbYQE	YqeH	Tb09.211.0830	LmjF35.5170	Tc00.1047053504123.40
	TbOBG	OBG	Tb10.6k15.3230	LmjF36.2990	Tc00.1047053507769.40
	TbEBP1	EngB	Tb11.03.0660	LmjF25.0450	Tc00.1047053507093.184
	TbEBR2	EngB	Tb927.7.2630		Tc00.1047053511815.160
	TbMMR	MMR-HSR1	Tb927.7.580	LmjF26.1370	Tc00.1047053510647.60
Gtr1-RagA	TbGRP	Gtr1-RagA	Tb10.6k15.1520	LmjF36.5880	Tc00.1047053509791.170
	TbGTR	Gtr1-RagA	Tb11.02.0820	LmjF13.1560	Tc00.1047053503999.70

**Table 2: Small GTPase GAPs and GEFs from *T. brucei*.**

GEF (nucleotide exchange factor)	GAP (GTPase activating protein)
<i>rhoGEF</i> Tb11.01.4480	<i>rhoGAP</i> Tb09.160.4180 Tb11.03.0310 (very weak similarity)
<i>arfGEF (sec7)</i> Tb11.01.7610, Tb927.8.1840, Tb927.4.2200	<i>arfGAP</i> Tb11.01.6060, Tb09.244.2540, Tb11.01.1230, Tb927.3.5330, Tb11.01.0920
<i>rab3GEF (DENN)</i> Tb09.v1.0370, Tb10.70.0190 (weak similarity)	<i>RabGAP (TBC)</i> Tb10.6k15.2930, Tb10.6k15.1770, Tb10.6k15.1790, Tb927.2.4560, Tb927.6.2830, Tb927.7.2470, Tb11.02.3320, Tb927.5.2740, Tb927.6.4120, Tb927.6.1750, Tb10.6k15.0190, Tb09.160.3890, Tb927.1.3220, Tb09.160.2980
<i>rab5GEF (Vps9)</i> Tb10.6k15.0260, Tb927.3.2430	

**Note:** It is important to appreciate that the annotation here is based on domain architecture, and while this is a valid proxy for function, it is an approximation only. For example, some TBC domain proteins have no known RabGAP activity - this may be due to sequence changes or is artifactual as the substrate or relevant assay conditions have not been defined. Also, it is likely that additional domains contain GAP or GEF activity that remain to be discovered or characterized; for example, the tethering complexes HOPS and TRAPP are also Rab nucleotide exchange factors.