

Supplemental Figures

Applied Microbiology and Biotechnology

Characterization of Tau95 led to the identification of a four-subunit TFIIC complex in trypanosomatid parasites

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Supplemental Figure S1

a

	Tb 647aa	Lm 700aa	Sp 456aa	Sc 649aa	Hs 519aa	Mm 520aa	Rn 515aa	At 554	Ce 433	Pf 916aa	Tg 637aa	Nf 731aa
Tb	100	34.92	17.09	14.37	15.47	14.33	13.97	16.85	14.24	14.92	17.53	11.70
Lm		100	16.78	14.40	14.87	15.41	14.45	16.38	15.59	15.24	19.77	14.25
Sp			100	24.05	26.58	27.00	27.00	19.15	24.44	22.74	19.65	22.82
Sc				100	17.86	17.86	18.21	21.07	19.33	21.26	20.65	16.18
Hs					100	85.36	83.88	25.51	27.51	20.92	21.98	27.01
Mm						100	95.15	24.55	27.99	20.68	20.99	27.63
Rn							100	23.68	28.23	20.68	20.99	27.63
At								100	20.16	20.45	20.22	21.98
Ce									100	21.95	19.30	23.66
Pf										100	21.48	20.16
Tg											100	21.40
Nf												100

b

	Tb 647 aa	Tev 647 aa	Tco 603 aa	Tc 597 aa	Tv 587 aa	Lmx 693 aa	Lbr 693 aa	Lin 698 aa	Lta 719 aa	Ld 697 aa	Lm 700 aa
Tb	100.00	99.54	54.85	47.95	48.23	34.72	34.33	34.39	32.69	34.44	33.83
Tev		100.00	55.02	48.12	48.23	35.06	34.67	34.72	33.01	34.78	34.00
Tco			100.00	46.06	45.94	34.31	34.36	33.45	33.96	33.50	32.71
Tc				100.00	50.09	36.78	36.95	36.52	35.66	36.59	35.94
Tv					100.00	34.29	34.72	33.87	32.14	33.93	33.15
Lmx						100.00	83.53	93.36	85.09	93.50	92.64
Lbr							100.00	84.49	80.15	84.33	81.77
Lin								100.00	84.13	99.57	92.84
Lta									100.00	84.26	83.14
Ld										100.00	92.97
Lm											100.00

Supplemental Fig. S1. Percent identities among amino acid sequences of Tau95 from different groups of organisms (a) and trypanosomatids (b). The species analyzed are: (a) *Trypanosoma brucei* (Tb, Tb927.10.980), *Leishmania major* (Lm, LmjF.21.1100), *Schizosaccharomyces pombe* (Sp, NP_593297), *Saccharomyces cerevisiae* (Sc, GFP66923), *Homo sapiens* (Hs, AAH11355), *Mus musculus* (Mm, NP_001277413), *Rattus norvegicus* (Rn, NP_001073410), *Arabidopsis thaliana* (At, NP_197833), *Caenorhabditis elegans* (Ce, CAA84675), *Plasmodium falciparum* (Pf, KNG75525.1), *Toxoplasma gondii* (Tg, ESS35509), and *Naegleria fowleri* (Nf, KAF0983925); (b) *T. brucei* (Tb, Tb927.10.980), *Trypanosoma evansi* (Tev, STIB805.10.1070), *Trypanosoma congolense* (Tco, TcIL3000_10_840), *Trypanosoma cruzi* (Tc, TcCLB.511131.20), *Trypanosoma vivax* (Tv, TvY486_1000950), *Leishmania mexicana* (Lmx, LmxM.21.1100), *Leishmania braziliensis* (Lbr, LbrM.30.3810), *Leishmania infantum* (Lin, LinJ.21.1340), *Leishmania tarentolae* (Lta, LtaP21.1280), *Leishmania donovani* (Ld, LdBPK_211340.1), and *L. major* (Lm, LmjF.21.1100).

Supplemental Figure S2

<i>T. brucei</i>	558	GWIGS-(48)	-ASSTSSVSP	ESYG	DDD	NED	SLE	SVSPV	DD	LSQHP	DD	G	647	
<i>L. major</i>	609	GWLSE-(46)	-ESSTSSLR	DEE	L	EDDE	EDD	SAMF	SVS	AGD	LSE	AA	DDDD	DE
<i>S. pombe</i>	349	GWYRS-(82)	-EHGFE	D	LEE	IDD	YDD	IF	G				456	
<i>S. cerevisiae</i>	468	GWFKS-(122)	-DDD	VDD	VDA	DEE	EEQ					-(40)-	649	
<i>H. sapiens</i>	437	GWCLP-(41)	-ESGE	DEE	DEE	DEE	DEE	DEE	DEE	DEE	DEE	DEE	DEE	
								FKPS	D	GS	E	NEMETE	I	
												ILD	YV	
													519	

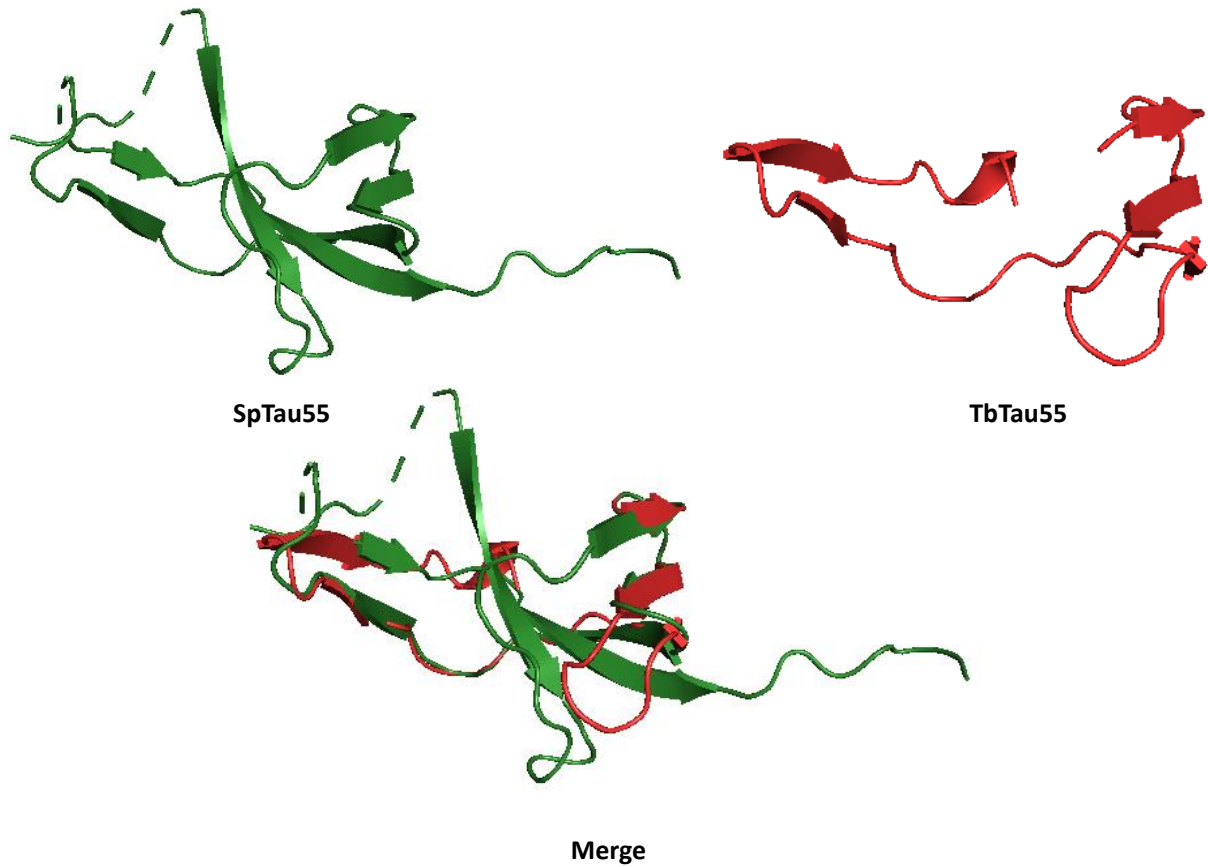
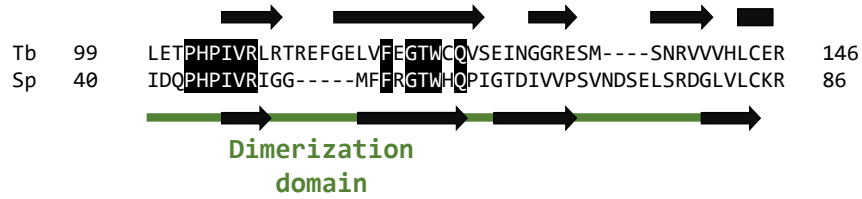
Supplemental Fig. S2. Sequence alignment of acidic tail residues of Tau95 from *T. brucei*, *L. major*, *S. pombe*, *S. cerevisiae* and *H. sapiens*. Acidic residues are shown in red.

Supplemental Figure S3

Tb927.11.1590

Annotated as: Hypothetical protein

Putative ortholog of *S. pombe* **Tau55 (Sfc7)**. Probability: 82.97%. E-value: 1.8



Putative ortholog of *S. pombe* **Tau55 (Sfc7)**. Probability: 84.25%. E-value: 1.5

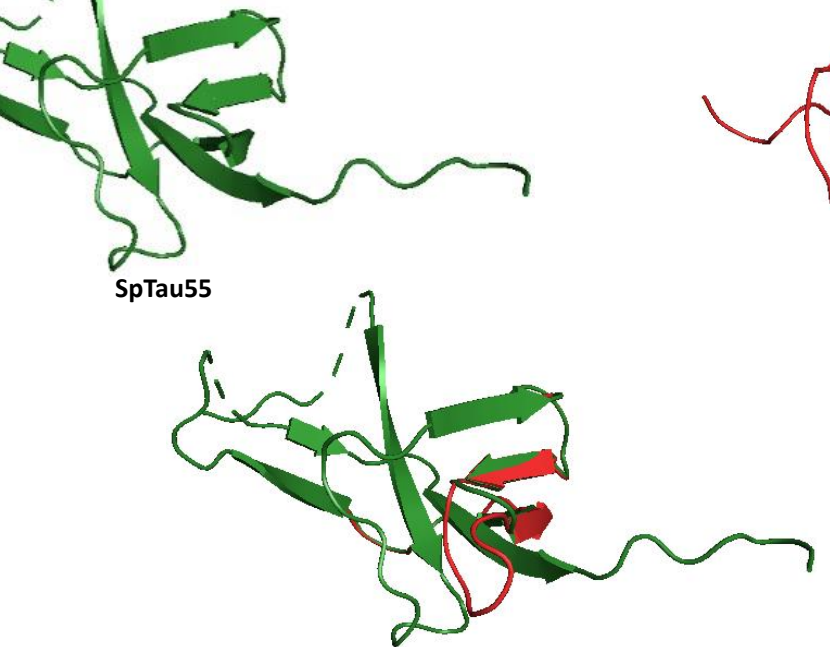
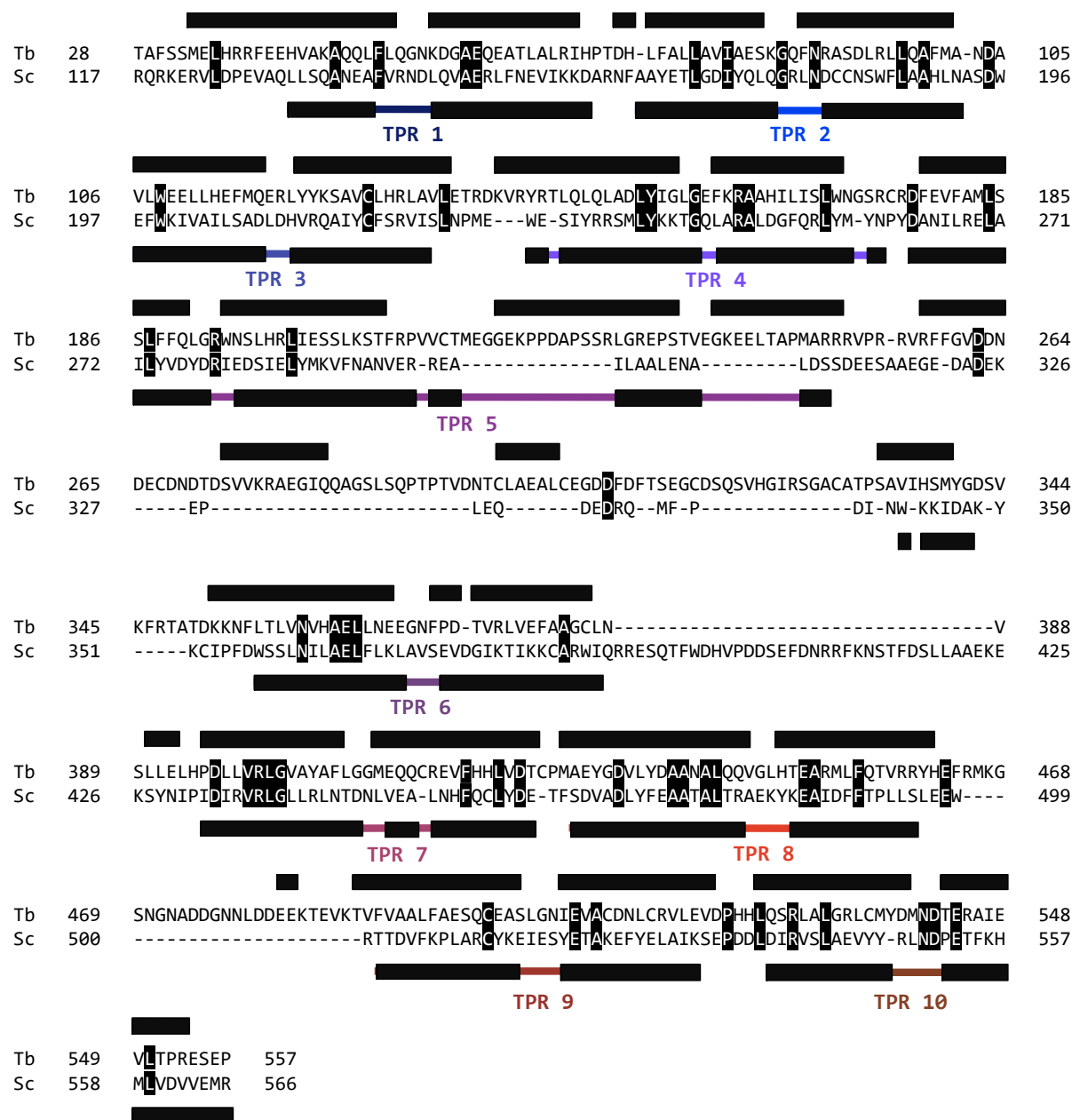
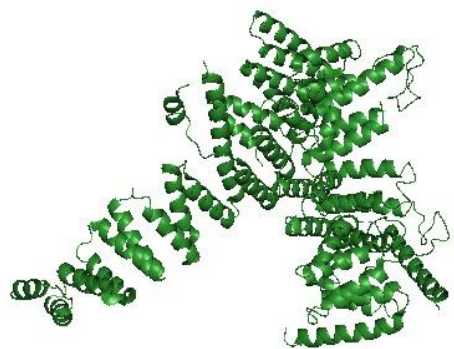


Figure 1 displays the structural alignment of SpTau55 (green) and LmTau55 (red). The top left panel shows SpTau55, the top right panel shows LmTau55, and the bottom panel shows the Merge of the two structures. The structures are shown as ribbon models, with the green ribbon representing SpTau55 and the red ribbon representing LmTau55. The merge panel shows the two structures overlaid, highlighting the differences in their folds.

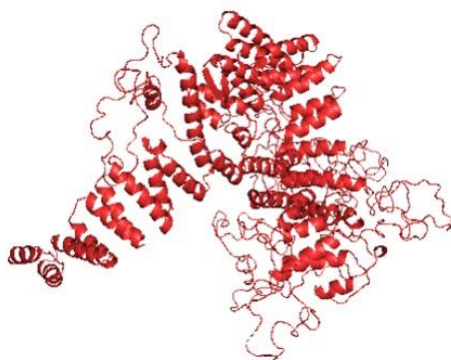
Tb927.1.3860

Annotated as: Hypothetical protein

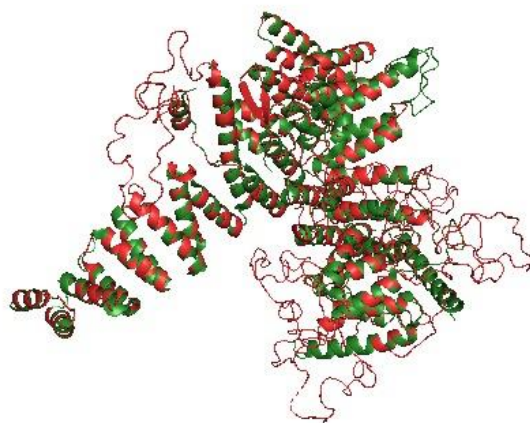
Putative ortholog of *S. cerevisiae* **Tau131**. Probability: 100%. E-value: 3.7e⁻⁵⁶



ScTau131



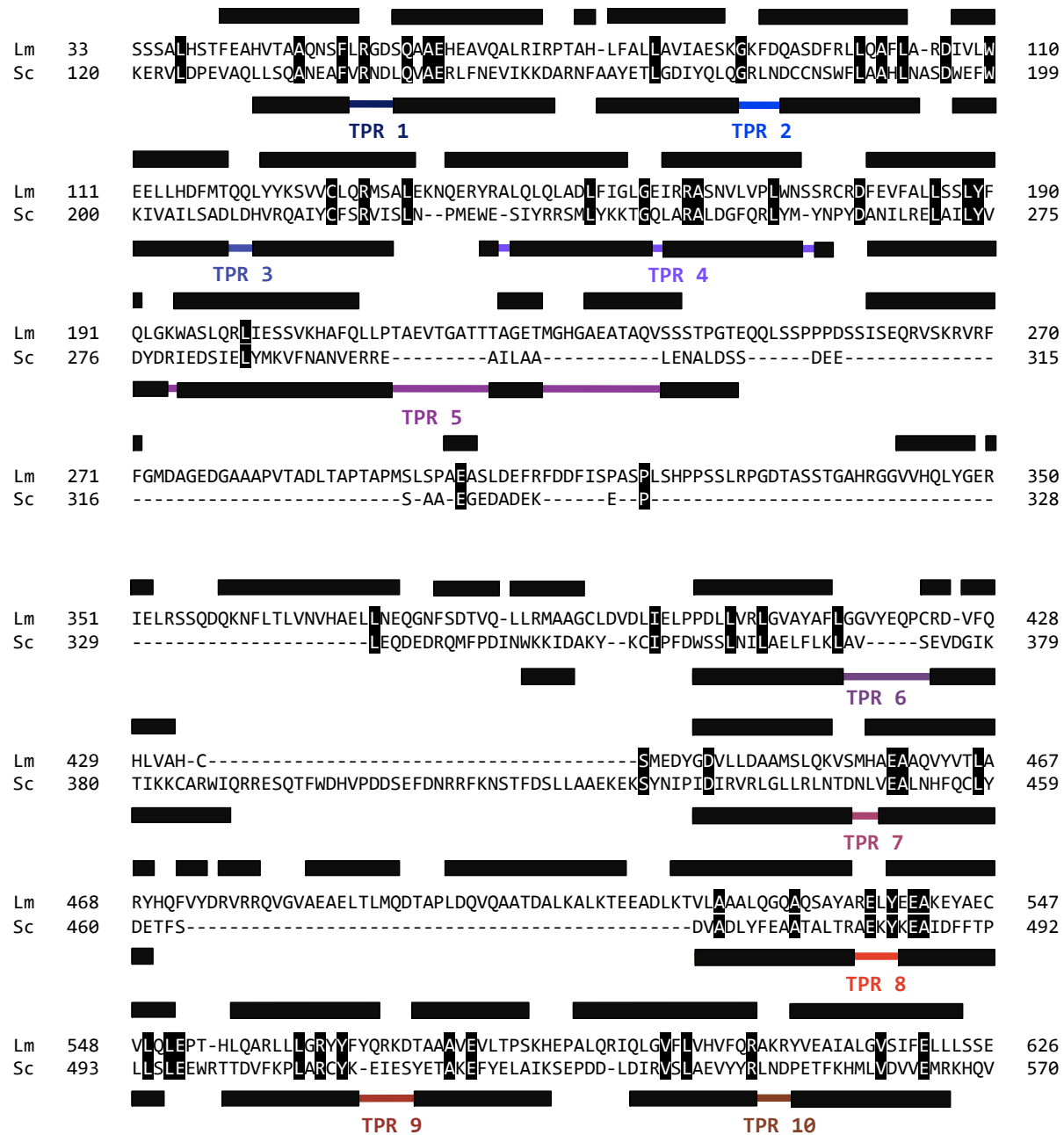
TbTau131

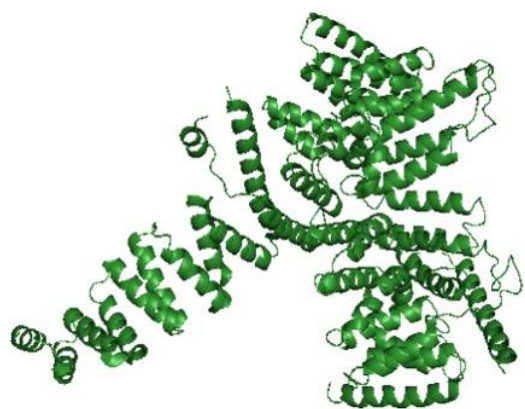


Merge

LmjF.12.0560

Annotated as: Hypothetical protein

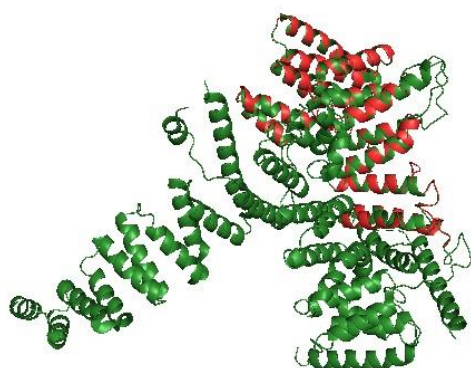
Putative ortholog of *S. cerevisiae* **Tau131**. Probability: 100%. E-value: 1.3e⁻³⁷



ScTau131



LmTau131

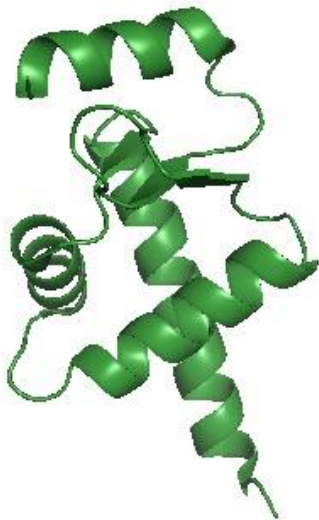


Merge

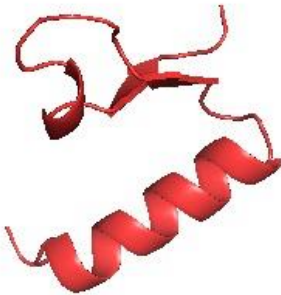
Tb927.11.4520

Annotated as: Hypothetical protein

Putative ortholog of *S. cerevisiae* **Tau138**. Probability: 78.91%. E-value: 13



ScTau138



TbTau138

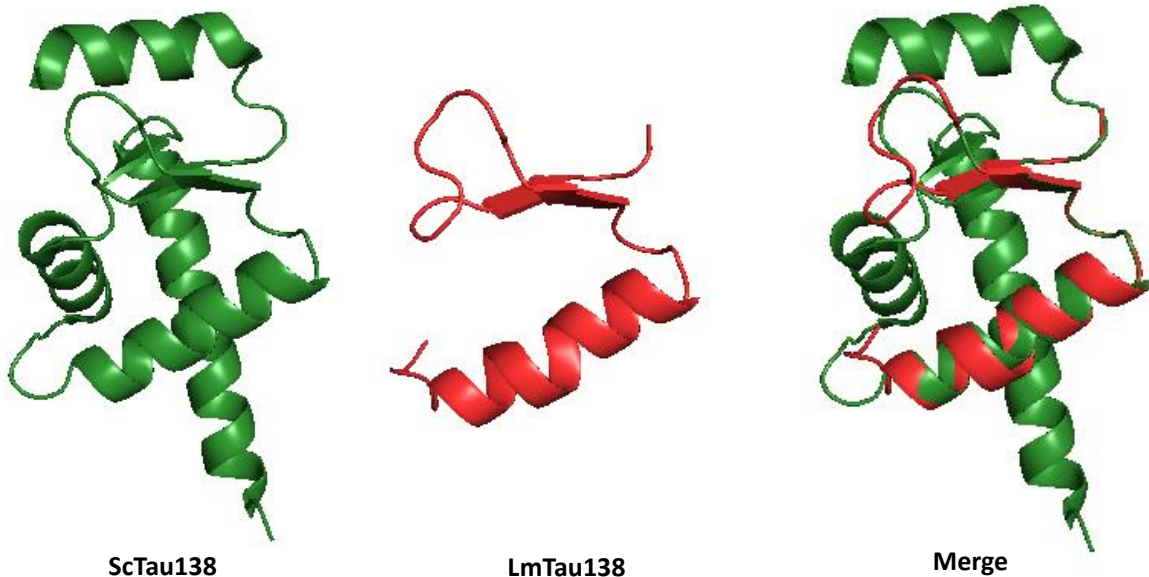


Merge

LmjF.13.0270

Annotated as: Hypothetical protein

Putative ortholog of *S. cerevisiae* **Tau138**. Probability: 30.23%. E-value: 240



Supplemental Fig. S3. Sequence and structure analyses of the presumed orthologs of Tau55, Tau131 and Tau138 in *T. brucei* and *L. major*. The HHpred (<https://toolkit.tuebingen.mpg.de/tools/hhpred>) and Swiss-Model (<http://swissmodel.expasy.org/interactive>) programs were used to analyze the sequence and predicted three-dimensional structure of the three proteins. Conserved domains are indicated in the sequence alignments. For Tau131, the alignment shown corresponds to the first 10 TPRs (in the N-terminal region of the protein); the C-terminal region is not presented.