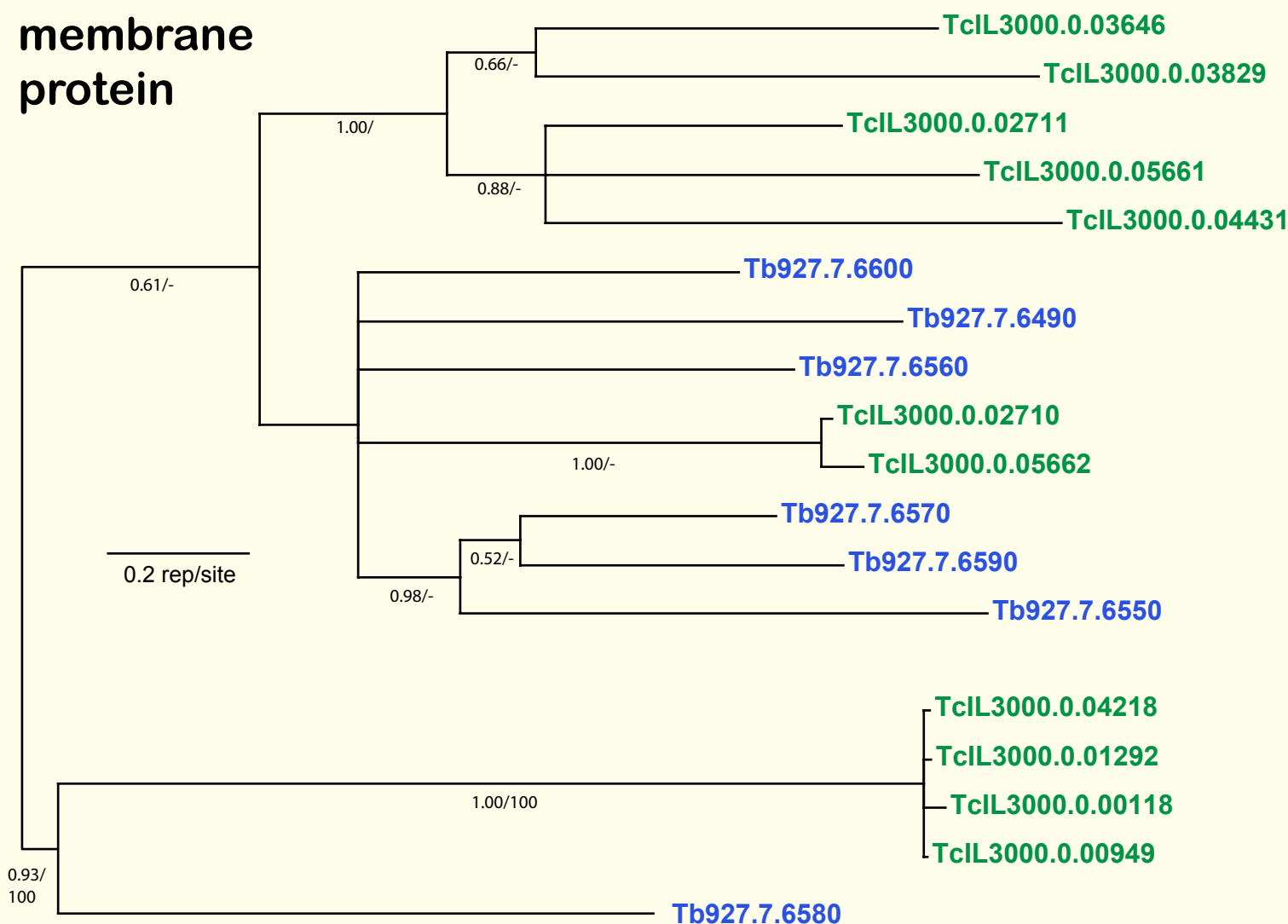


If you use these data, please cite:

Jackson, AP et al. 2012. A cell surface phylome for African Trypanosomes. *Manuscript submitted.*

## Fam10: Putative membrane protein



Key: Tb927.927.  
*T. brucei*  
TcIL3000.  
*T. congolense*

**NOTES:** Fam10 comprises six genes from a tandem gene array on chromosome 7 in *T. brucei* and a singleton gene just upstream, as well as unplaced homologs from *T. congolense*. The tandem gene array is located at a strand-switch region and the genes vary considerably in length, with two genes >3000 amino acids due to the presence of a hexameric repeat (Tb927.7.6580 and 7.6590), while other genes lacking the repeat are ~700 amino acids in length (*inset*). As the *T. congolense* copies are unassembled, the current alignment could contain sequence duplicates. All gene copies have predicted signal peptides.

The Bayesian phylogram was estimated from a multiple protein sequence alignment of 177 characters, corresponding to the non-repetitive N-terminal domain present in all cases, using MrBayes under default settings. The tree is rooted with orthologous, divergent sequences from both species. Selected nodes are supported by posterior probabilities and non-parametric bootstraps generated from a maximum likelihood analysis using an LG model with rate heterogeneity.