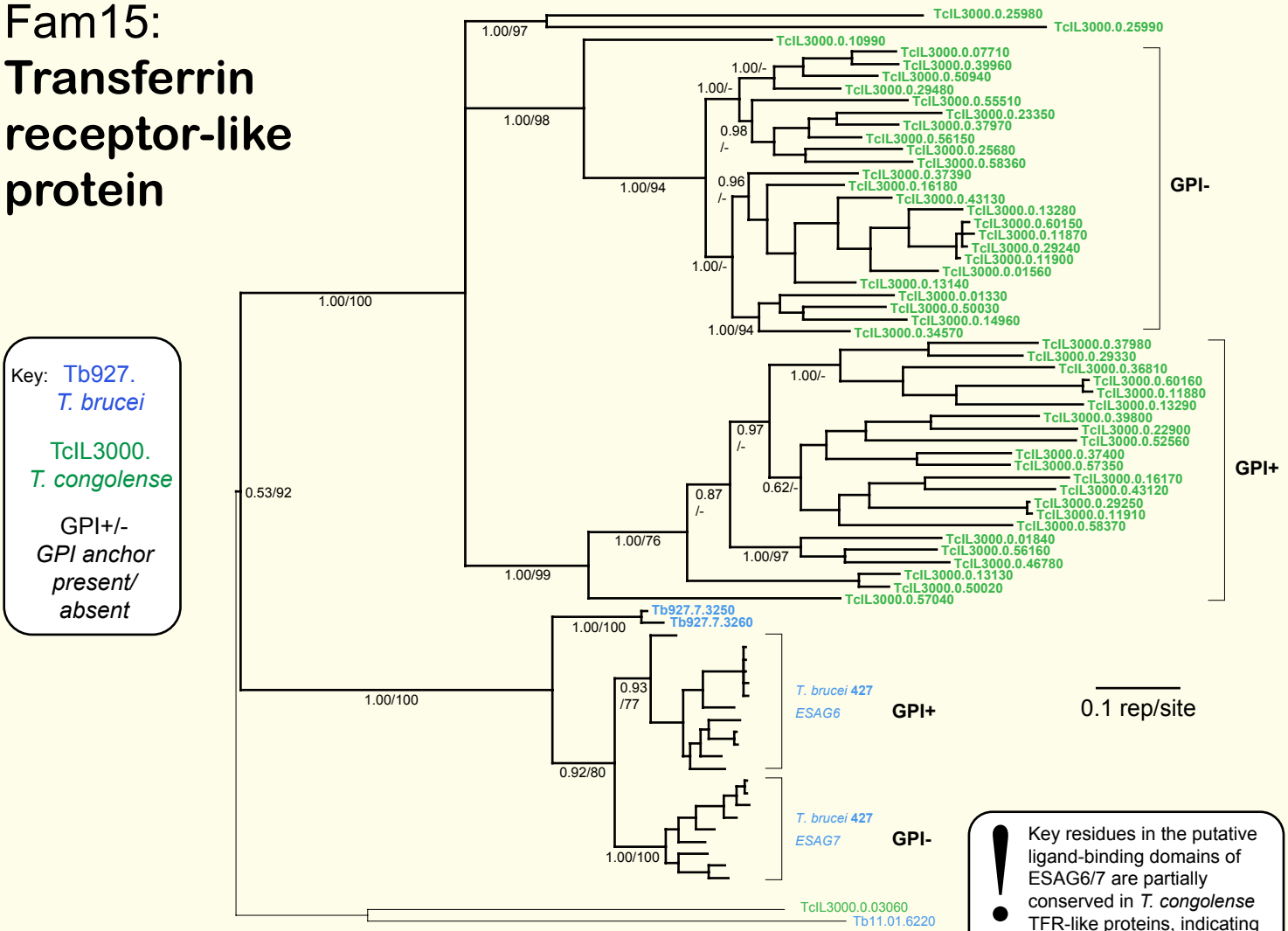
If you use these data, please cite:

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

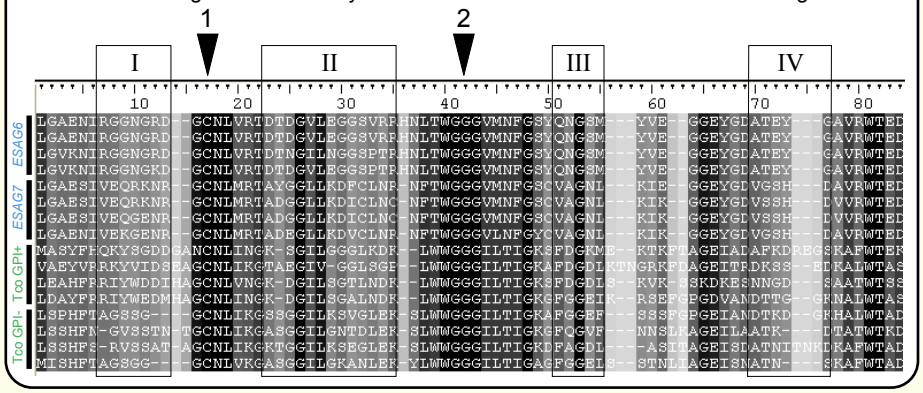
Fam15: **Transferrin receptor-like protein**



ESAG6 and *7* encode two halves of a heterodimeric TFR protein, which is attached to the membrane with a single GPI anchor (via ESAG6). The phylogeny indicates that this heterodimer is present in *T. congolense*. In both species there are two *TFR* clades that differ in the presence of a predicted GPI anchor.

In both cases the two *TFR* clades are sister lineages, i.e. *ESAG7* has evolved recently from *ESAG6* through loss of the C-terminal domain, and the separation of *T. congolense TFR* clades also seems to have occurred after speciation. So the TFR heterodimer may be convergent. Alternatively, concerted evolution might make *TFR* within a genome look more closely related artifactually.

The alignment shows the ligand-binding domain in which the most conserved residues are shaded darkest. The most darkest regions surround a conserved cysteine position (1) and the site of a conserved peptidic turn (2). Four variable regions (I-IV) that are required for transferrin binding are shown*. Glycine residues in II and III are conserved throughout.



Key residues in the putative ligand-binding domains of ESAG6/7 are partially conserved in *T. congolense* TFR-like proteins, indicating that they also bind transferrin.

NOTES: **Fam15** includes the recognized bloodstream expression site-associated transferrin-receptor genes in *T. brucei* 427 (ESAG6/7), two related sequences located on the core chromosome in *T. brucei* 927 (i.e. Tb927.7.3250/60), and all *T. congolense* homologs (but not those more closely related to the *PAG* genes (see Fam14)). GPI anchors were predicted using *Fraganchor*. The Bayesian phylogram was estimated from a multiple protein sequence alignment of 453 characters, using MrBayes under default settings. The tree is rooted with an outgroup of two *PAG* genes. Selected nodes are supported by posterior probabiliies and non-parametric bootstraps generated from a maximum likelihood analysis using an LG model with rate heterogeneity. * Salmon *et al.* (1997). *The EMBO Journal* **16**, 7272–7278.