# Genome mining of SNARE proteins in *Trypanosoma brucei* and *Trypanosoma cruzi* and an investigation of their evolution

Edwin Murungi[1], Sumir Panji[1] and Alan Christoffels[1*]

[1]South African National Bioinformatics Institute, Faculty of Science, University of the Western Cape, Private Bag, X17, Bellville 7535, Cape Town, South Africa, edwin@sanbi.ac.za

The trypanosomatid parasites *Trypanosoma brucei* and *Trypanosoma cruzi* are pathogenic to humans and animals. These parasites largely depend on intracellular trafficking for both nutrient uptake and virulence. Among the factors characterized as essential for vesicle trafficking in eukaryotes are the soluble N-ethylmaleimide-sensitive factor activating protein receptors (SNAREs) that initiate membrane fusion by forming a *trans* complex via the SNARE motif. We have exhaustively mined the genomes of *T. brucei* and *T. cruzi* using sequence-based methods and hidden markov models and identified 22 and 26 SNAREs respectively. Further, phylogenetic analyses of the identified SNAREs clustered them into four groups. Within the R group, putative brevins have been identified in both *T. brucei* and *T. cruzi*. An investigation of selection using maximum likelihood codon substitution methods revealed that majority of the SNARE genes in the tritryps are under negative (purifying) selection.