Supplemental Table 1

Comparison of Predicted OPB Proteins from Trypanosomatids

Species:	AA Identity:	Length (AA):	kDa:	Catalytic Triad:
L. donovani	100.0%	731	83.1	S577, D662, H697
L. infantum	99.7%	731	83.1	S577, D662, H697
L. major	95.5%	731	83.0	S577, D662, H697
L. amazonensis	90.3%	731	83.5	S577, D662, H697
L. braziliensis	86.5%	731	83.1	S577, D662, H697
T. cruzi	63.2%	714	81.0	S562, D647, H682
T. brucei brucei	62.1%	715	80.7	S563, D648, H683
T. evansi	61.8%	715	80.7	S563, D648, H683

Supplemental Table 1. Comparison of predicted OPB proteins from trypanosomatids. The homologous OPB proteins predicted in five *Leishmania* and three *Trypanosoma* species are compared. Amino acid identities were compared to the sequence of *L. donovani* OPB. All of the proteins were found to be between 714 and 731 amino acids in length, between 80.7 and 83.5 kDa in mass, and to contain the conserved canonical clan SC catalytic triad.