



Figure S1: Alignment of the protein sequences of TbALPH1, TbALPH2 and TbALPH3

For Tb927.6.640 (ALPH1), only the catalytic domain is shown, Tb927.4.4330 (ALPH2) and Tb927.8.8040 (ALPH3) are shown in full length. The three signature motifs that are characteristic for all PPPs are framed. The GDXGRD motif that is modified in a way that is characteristic for Alphas is shown in blue text, with the changes marked in red. The three Alphas are likely products of a recent gene duplication, as they are more similar to each other than to Alphas of non-Kinetoplastida. A structure is available for ALPH3 (PDB ID: 2QJC) (Almo et al., 2007).

Almo SC, Bonanno JB, Sauder JM, Emtage S, Diloranzo TP, Malashkevich V, Wasserman SR, Swaminathan S, Eswaramoorthy S, Agarwal R, Kumaran D, Madegowda M, Ragumani S, Patskovsky Y, Alvarado J, Ramagopal UA, Faber-Barata J, Chance MR, Sali A, Fiser A, et al (2007) Structural genomics of protein phosphatases. *J. Struct. Funct. Genomics* 8: 121–140