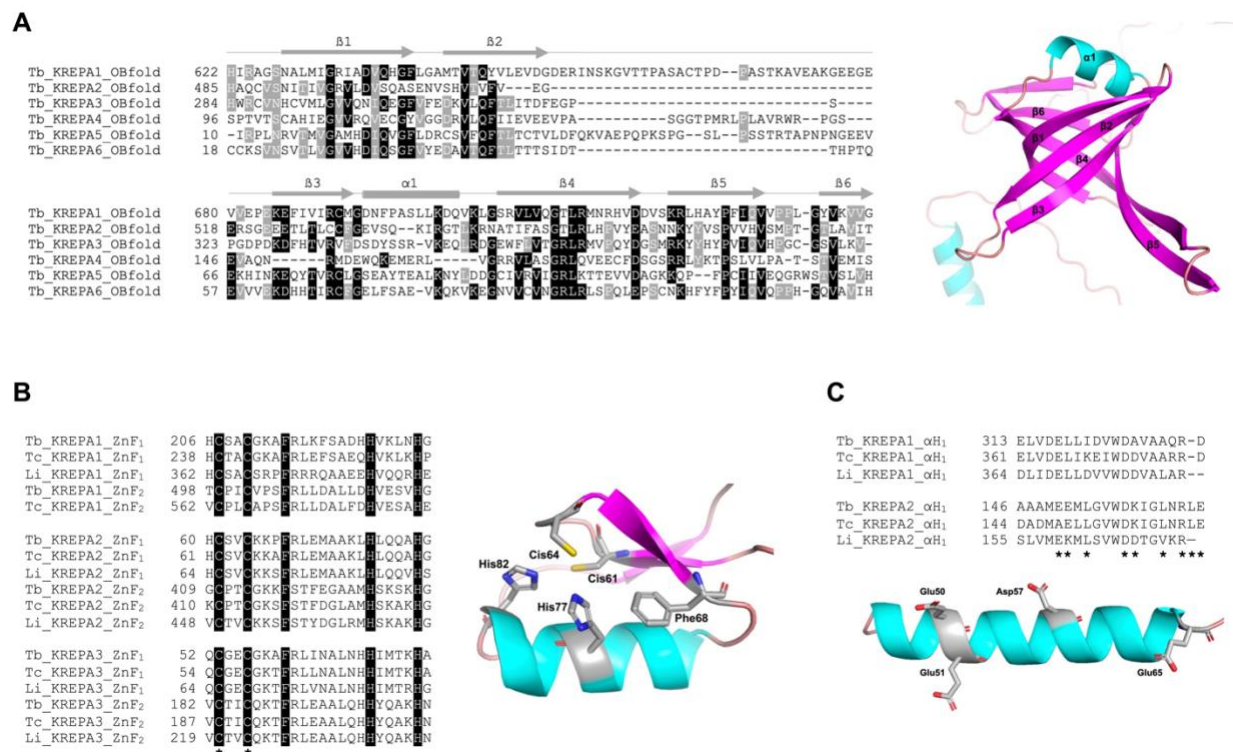




Supplemental Figure S3. Sequence alignment of KREPA2 structural domains. (A) Amino acid multiple sequence alignment of the oligonucleotide binding fold domain (OB fold) of KREPA1-6 of *Trypanosoma brucei* (Tb), with predicted alphafold structure beside it. (B) Amino acid multiple sequence alignment of the zinc finger domains (ZnF) of KREPA1-3 of *Trypanosoma brucei* (Tb), *Trypanosoma cruzi* (Tc) and *Leishmania infantum* (Li), with predicted alphafold structure beside it. The sequence alignment shades five conserved residues, C2FH2, which are specific to this ZnF domain family. (C) Amino acid sequence alignment of the αH1 of KREPA1 and KREPA2 of Tb, Tc and Li, with predicted alphafold structure below it. Each residue mutated for analysis is represented by a below asterisk.