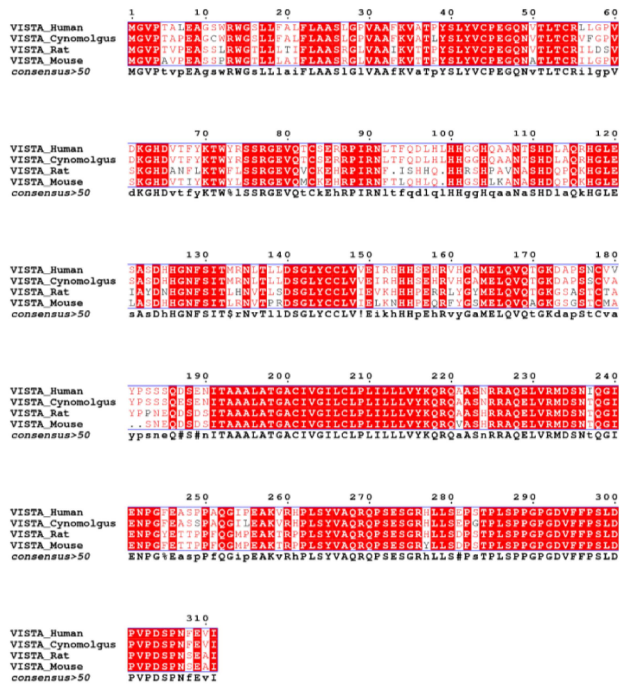


**A** VISTA ortholog sequence alignment



**B** VISTA homology model with highlighted residues involved in binding with putative partners

