



**Figure S2:** Ramachandran plots of backbone dihedral angles for the three-dimensional structural models of **(a)** the PfVIT protomer and **(b)** the isolated PfVIT cytoplasmic MBD. Individual amino acid residues are represented as black squares or triangles or (for residues in disallowed regions) as red squares. A, B and L represent the most favoured regions of the plot; a, b, l and p represent additionally allowed regions; ~a, ~b, ~l and ~p represent generously allowed regions. Disallowed regions are shaded in light yellow.