



Amino acid residues I77 to R591 of OppA_{MTB} was modeled as described in Materials and Methods. The three domains are shown in different colors: domain I (green), domain II (red), and domain III (yellow). The peptide-binding pocket resides in the interface between domains I and III. The residues of OppA viz., G109, N110, N230, F496 and D494 that were mutated resulting in more than 50% loss of GSH and bradykinin activity have been highlighted.

