

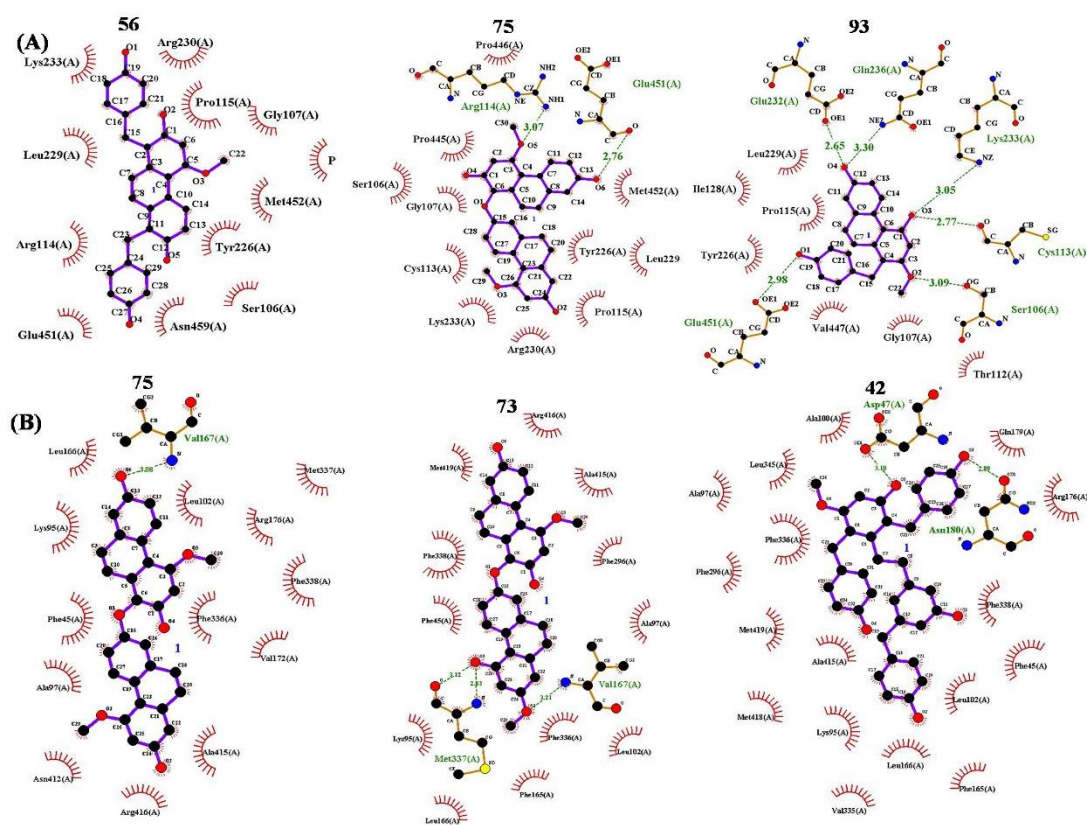


Fig. S1 Two-dimensional representation of interaction between studied ligands and amino acids inside binding pocket of homology model of (A) tyrosinase and (B) adenylyate cyclase.