

Fig.1. A) Structures of catalytic domains of a) Acetylcholinesterase (2ack), b) malonyl-CoA ACP transacylase (1mla), c) Aspartyl dipeptidase PepE (1fye) and d) the conserved $\beta/\beta\alpha$ structural motif. The figures are generated using Pymol ; B) Schematic representation of the alignment relationships. The location of the structural motif in the full length catalytic domains is shown in dark gray.

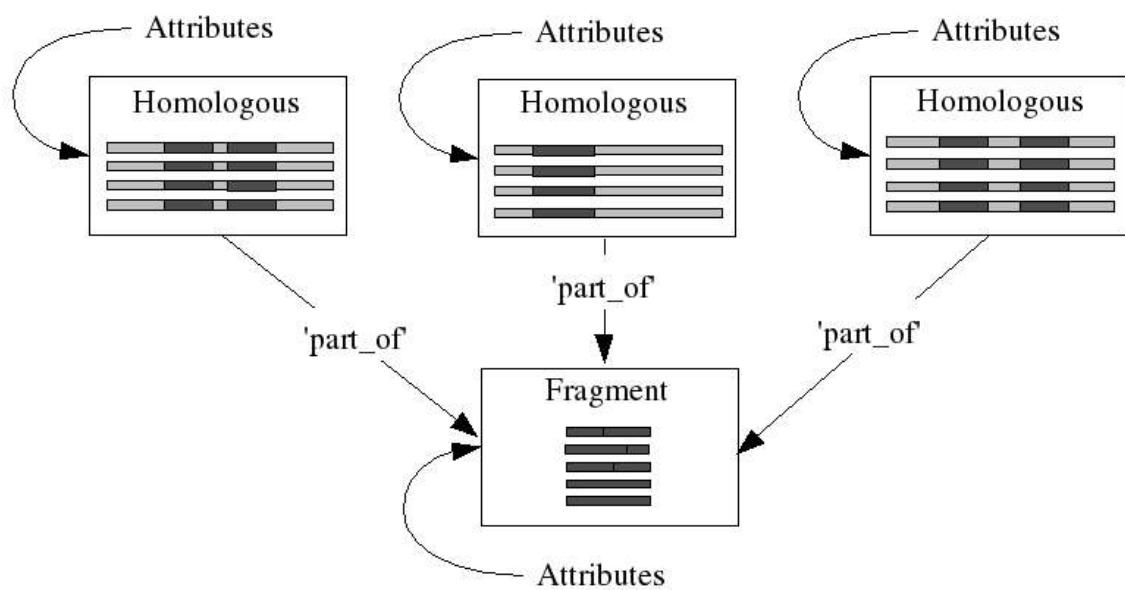
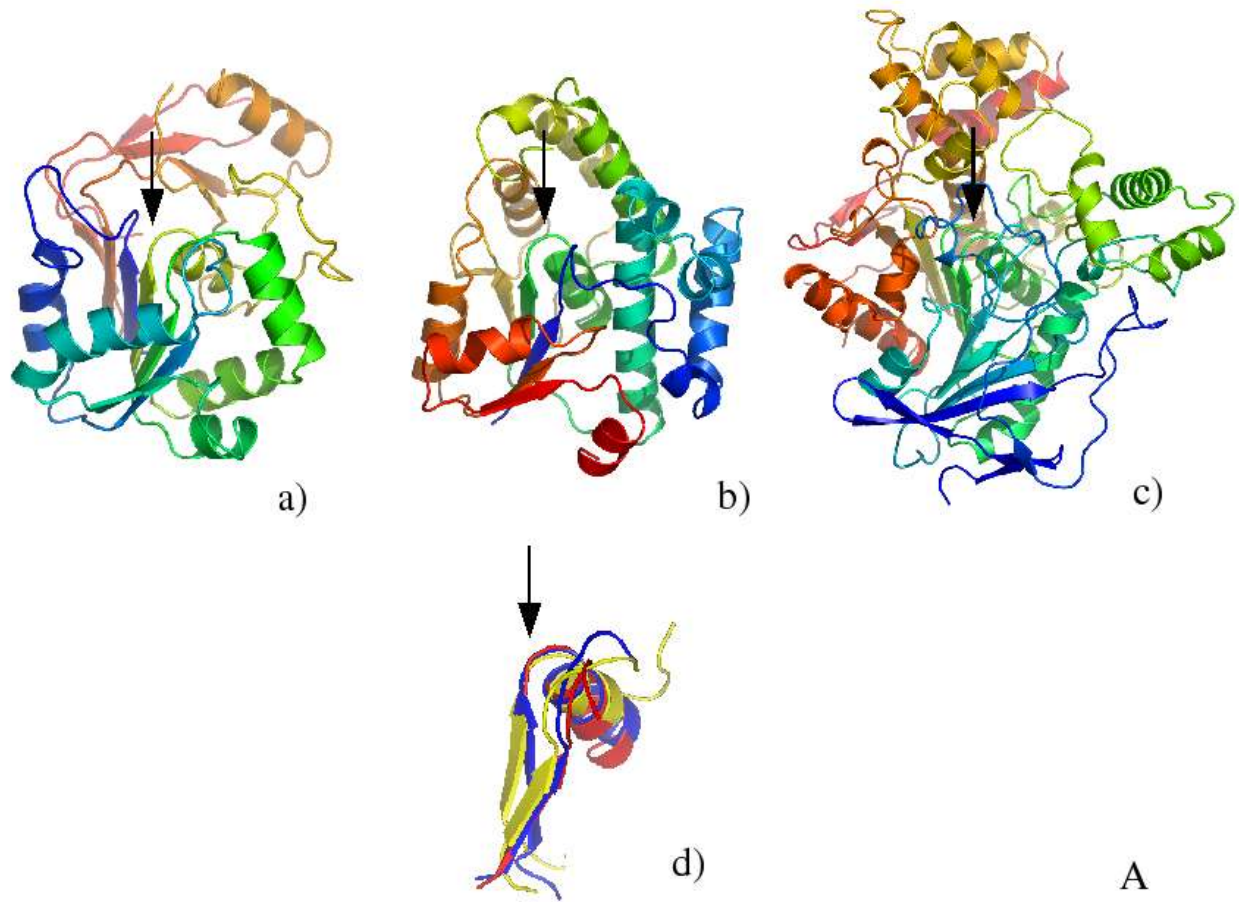


Fig.2. A) Structures of a) Antioxidant defense protein AhpD (1knc), the structural repeats are shown in light and dark blue; b) hypothetical protein TM1620 (1p8c), the individual subunits are shown in purpleblue and purple, the swapped segments are shown in dark purple; c) hypothetical protein TTHA0727 (2cwq), the individual subunits are shown in light and dark green; d) hypothetical protein Atu0492 (2gmy), the structural repeats are shown in light and dark yellow; e) the AhpD-like structural repeats. The figure is produced using Pymol; B) Schematic representation of the arrangement of equivalent segments in the alignment and alignment relationships.

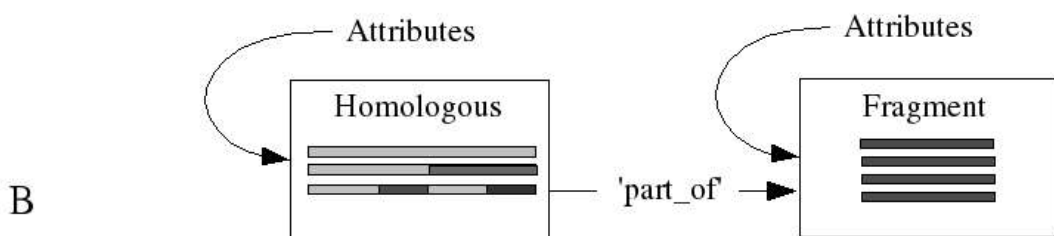
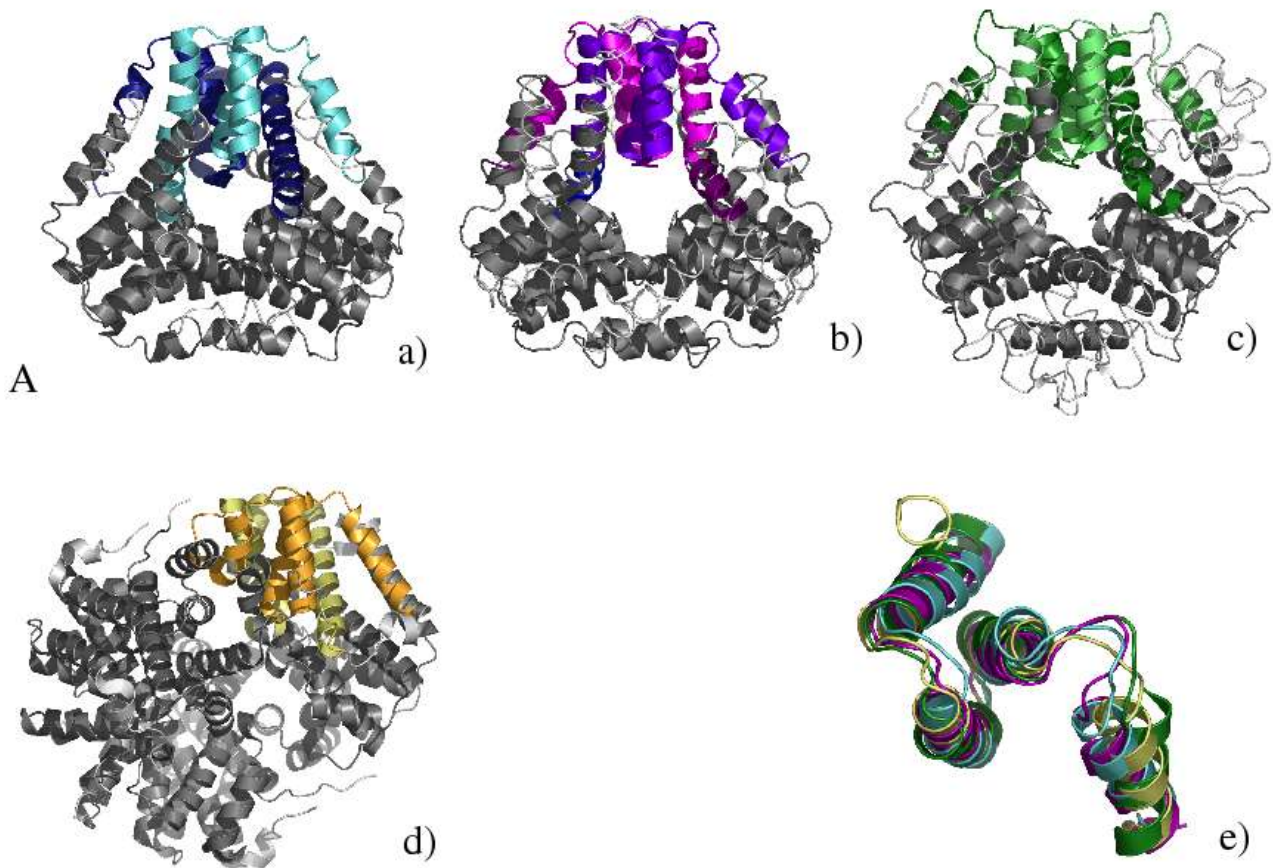


Fig.3. A) Structures of a) the third domain of hDIg (1pdr) and b) the PDZ domain of Photosystem II D1 C-terminal processing protease (1fc9). The circularly permuted strand is shown in blue and red corresponding to its sequential position (blue – N-terminal; red – C-terminal). This figure is created using Pymol; B) Schematic representation of the alignment relationships. The location of the sequentially rearranged strand is shown in dark gray.

