A new 3D protein structure in your hand ?

**MED-SuMo** is a powerful software to compare 3D interaction surfaces into the PDB. Independent from the notion of protein sequence or backbone folding, **MED-SuMo** detects and compares biochemical functions on your protein surface such as HBond, Charges, Hydrophobic and Aromatic groups. From your new 3D protein structure of interest, **MED-SuMo** retrieves and ranks from the PDB all 3D protein-ligands matches. Those 3D patches starting from 3 to unlimited number of surface chemical feature could help you to (1) detect shared catalytic site (functional annotation), (2) detect allosteric binding site, (3) characterize your binding pocket regard to all proteins of the same family, (4) to discriminate structural chemical features belonging to your 3D query from those of the same protein family, (5) initiate target-based applications by exporting all co-crystallized ligands from hits superimposed by **MED-SuMo** in your binding site query.

Optionally, you may submit your protein binding site of interest to our **MED-Portions** database which encodes protein-fragment interactions (small molecules from Pubchem are crossmined on any co-crystallized ligands of the PDB to define **MED-Portions**). As an output, users are getting pool of protein-fragment complexes into the query 3D coordinates for drug design application.

**MED-SuMo 2010 promotions for academic users**

**MED-SuMo** in SaaS mode offer for only **1560€** instead of **6900€** (standard annual license for hosted server!)

With **MED-SuMo** in Software-as-a-Service mode, customers are getting:

- Search and Compare 3D interaction surfaces in the PDB;
- 2 month software license including the GUI (Graphical User Interface) to prepare query, analyze and classify hits;
- no Linux server to configure/install, all the PDB is ready to be mined.

**MED-SuMo/MED-Portions** in SaaS mode offer for only **1820€** instead of **7660€** (standard annual license for hosted server!)

With **MED-SuMo/MED-Portions** in Software-as-a-Service mode, customers are getting:

- Search and Compare 3D interaction surfaces in the PDB including all **MED-Portions** protein-fragment complexes;
- 2 month software license including the GUI (Graphical User Interface) to prepare query, analyze and classify hits;
- no Linux server to configure/install, all the PDB and **MED-Portions** are ready to be mined;
- pool of scored PDB-based fragments can be exported in SD files format (superposed into the binding site of the query).}

**Contact us**

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