



Raptor
by DesertSci

Raptor

A superior tool for chemists, modelers, structural biology, and AI model builders for improved understanding of non-covalent interactions in protein-ligand and protein-protein complexes.

Advantages

DATA DRIVEN

Created by industry experts, Raptor is accurate and comprehensive in finding the many different types of hydrogen bonds, polar interactions, and lipophilic contacts in binding sites.

RULE BASED

Raptor ensures interactions are correctly identified by using an extensive range of rigorously tested rules. These rules form the basis of a superior algorithm, developed from the latest findings in structural biology, molecular modeling, molecular recognition and database mining studies.

VISUALISATION

Raptor creates scripts that allow fast and easy exploration of the key protein-ligand interactions determining binding affinity.

HANDLING WATER MOLECULES

Rank scores provide easy identification of bound water molecules for targeting in ligand design experiments.

IDENTIFIES UNFAVOURABLE INTERACTIONS

Raptor allows for the detection of desolvation penalties that negatively affect target binding.

EASE OF USE

Enables both experts and non-experts to make the best use of protein structure data in Structure Based Drug Design (SBDD).

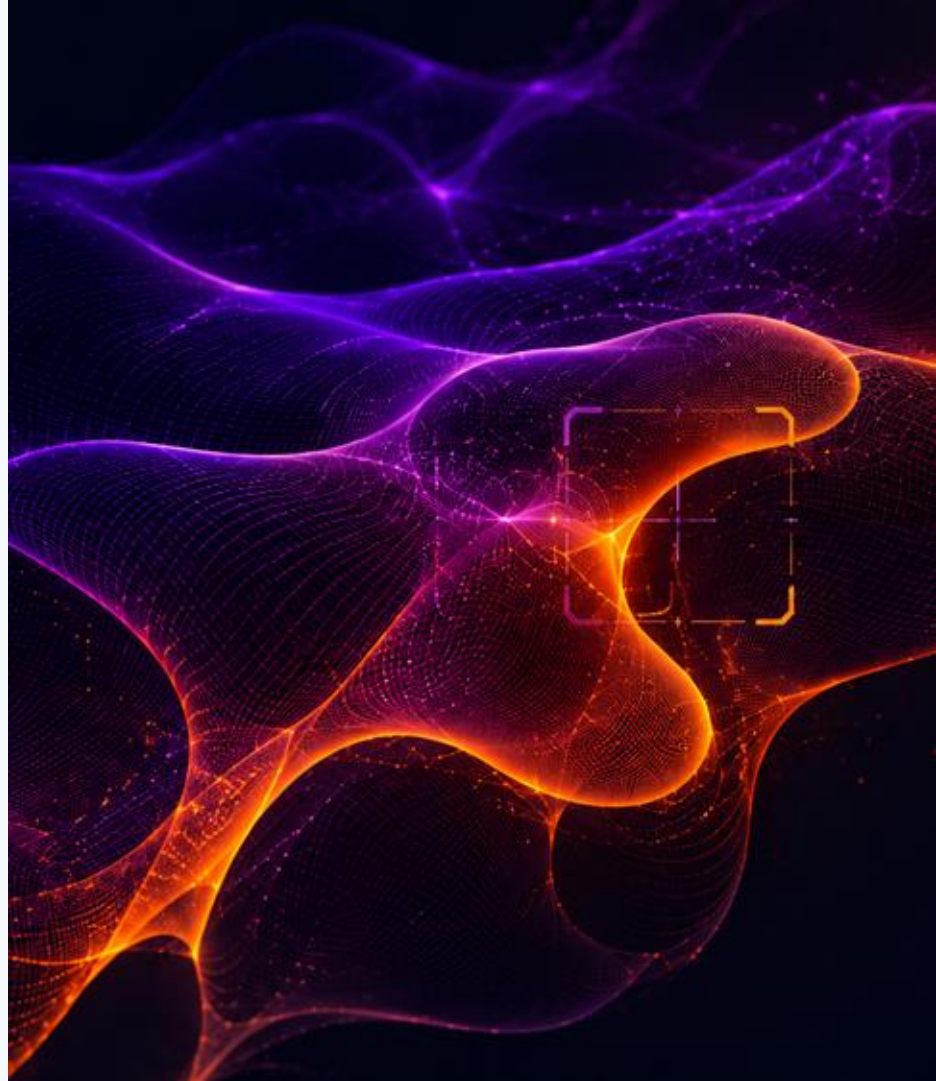
Overview of interaction types

Raptor identifies commonly occurring interactions types:

- hydrogen bonding
- ionic pairs
- van der Waals contacts

Raptor identifies many, less well understood interactions types:

- cation-pi
- hydrogen bonding to pi-systems
- halogen bonding
- orthogonal dipolar alignment
- dipolar antiperiplaner interactions
- pi-stacking
- pi edge-to-face contact
- hydrogen bonding involving CH groups

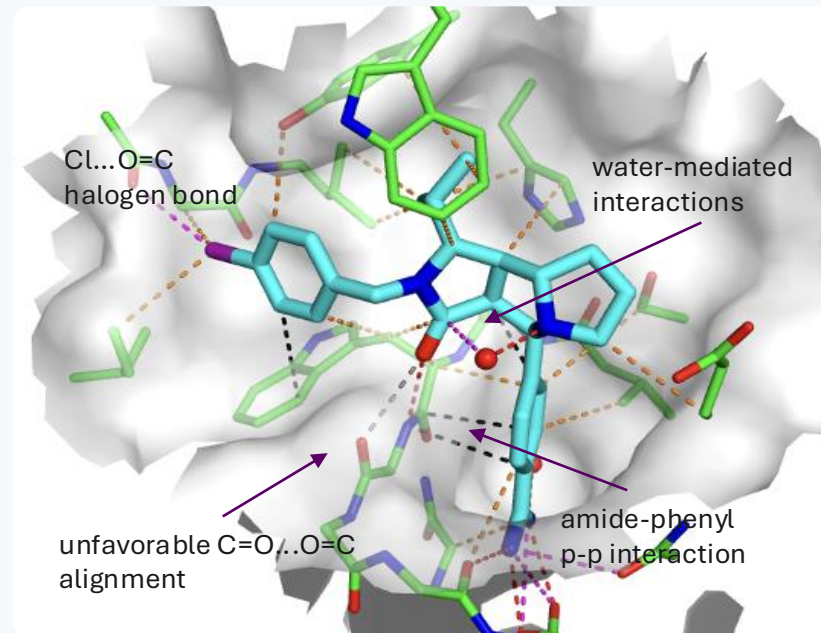


Pair interaction definitions

Automatic assignment of SMARTS-based atom types and detection of different types of favourable and unfavourable interactions (with distance & angle constraints, pruning of excess contacts.)

Classification of interaction types:

- | | |
|------------------------|--------------------------------|
| 1. Hydrogen bond | 8. H donor-pi |
| 2. Metal | 9. Pi-pi |
| 3. Ionic | 10. vdW |
| 4. Cation-dipole | 11. Unfavourable of 1, 2, 3, 6 |
| 5. Cation-pi | 12. Polar and nonpolar clashes |
| 6. Dipolar | 13. Polar-nonpolar mis-matches |
| 7. σ -hole bond | |



EX. 2CF8 (THROMBIN)

Raptor creates table data and also PyMol scripts allowing for fast and easy visual exploration of the key protein-ligand and protein-protein interactions determining affinity.

Handling of water molecules

Scoring of water replacement potential based on deviation from ideal tetrahedral coordination of protein-bound water molecules.

$$Rank = \sum_n \left\{ (2.80 A / r_n) + \left[\sum_m \cos(\Theta_{Td} - \Theta_{ym}) \right] / 6 \right\}$$

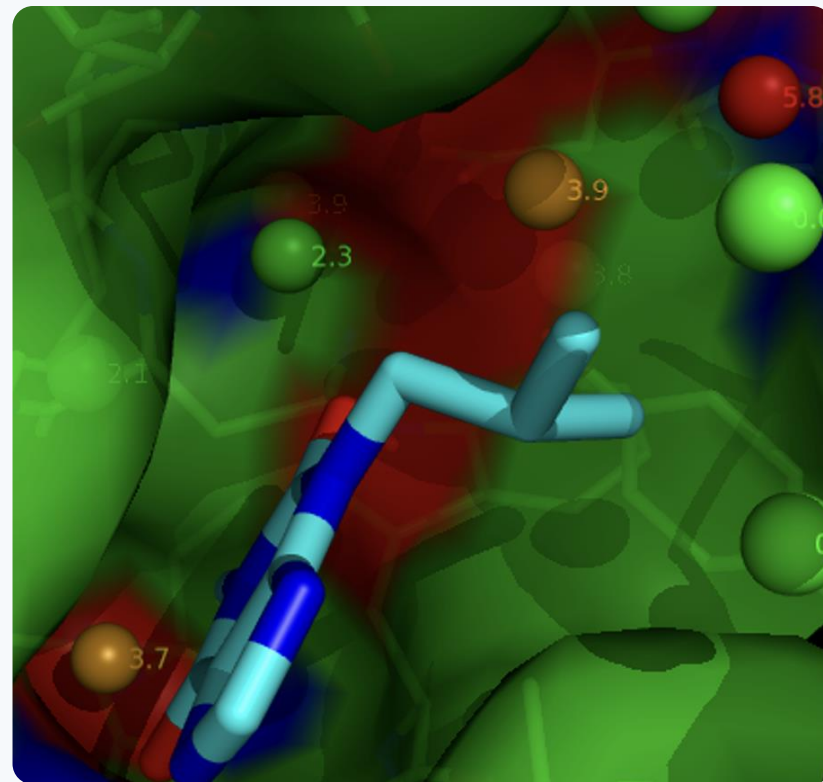
Rank scores:

- 1 ideal H-bond: 1
- 2 ideal H-bonds: 2.3
- 3 ideal H-bonds: 4.0
- Tetrahedral coordination: 6.0

Maximum of 4 protein atoms is counted (≤ 2 donors and ≤ 2 acceptors). Any angle less than 60° is rejected.

Color-coding of Rank score in PyMol:

- **Green:** 0 - 2.3 (easy to replace)
- **Amber:** 2.3 - 4.0 (possible to replace with suitable polar functionalities)
- **Red:** 4.0 - 6.0 (unlikely to replace)



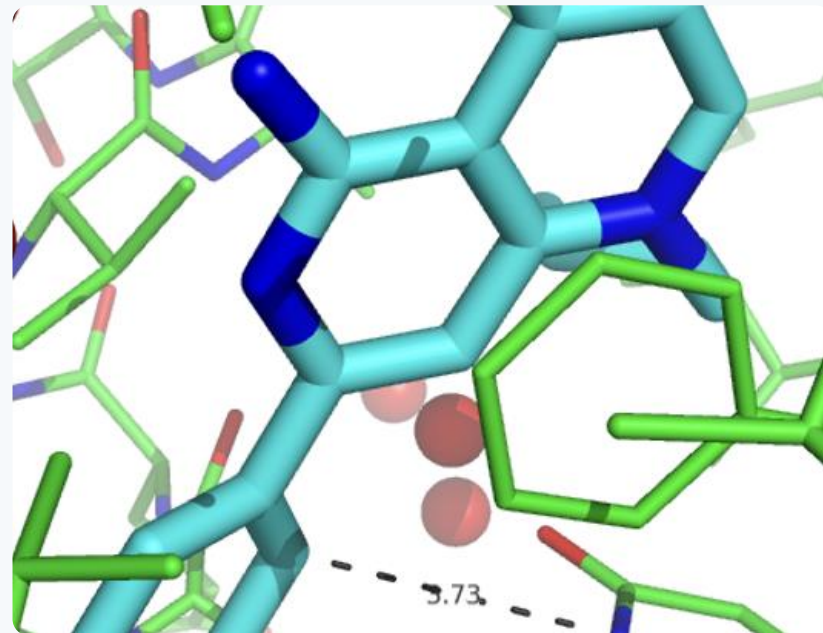
EX. 2R8Q (PDE-B1)

Rank scores provide easy identification of bound water molecules that can be targeted in ligand design experiments.

Identification of unfavourable interactions

- Unfavourable contact if apolar ligand atom replaced by a water molecule fulfills hydrogen bonding requirements.
- Distances and angles are checked for all polar/apolar close-contact pairs.
- Solvent exposure of each atom is taken into account when testing for unfavourable contacts.

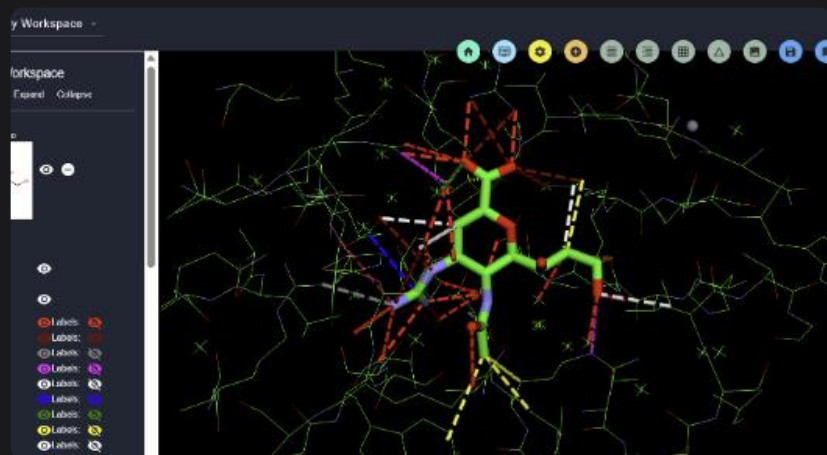
Allows for the detection of desolvation penalties that negatively affect target binding.



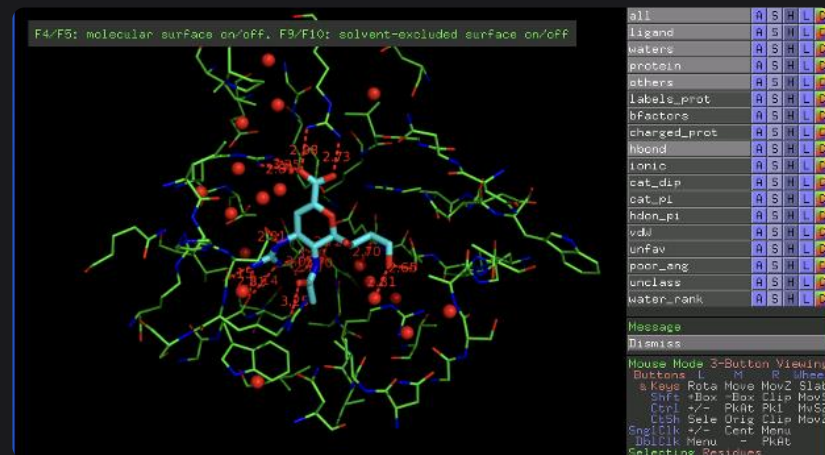
EX. 3HDZ (PDE-5)

No hydrogen bond partner for this buried N atom in the binding site -> contact highlighted as an unfav. interaction.

Proasis



Proasis easy-to-use web interface for exploring Raptor Results.



And enables export directly into PyMol.

Additional features

- Any HET group or any protein-protein interface in any domain of any pdb file can be explored.
- Size of viewed binding site can be modified.
- Interactions can be tabulated, sorted and colour-coded according to requirements.
- Interactions can be further sub-divided into strong/medium/weak.
- All interactions within a binding site or with in a protein can be viewed.
- Buried contacts can be viewed separately from solvated contacts.
- Water mediated hydrogen bonds are automatically highlighted.
- Can easily read results from docking studies, with poses stored in sdf file(s).
- PyMol script creates molecular surface, solvent excluded surface, short-cuts for viewing temperature factors and much more.
- Bond orders from input sdf file, cif library, or detected using automated methods.
- Available as an api resource accessible to all data scientists and inhouse applications.
- Available as a command line tool for linking with data pipelines for AI model building.

Thank you

References

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PyMol – www.pymol.org

Acknowledgments

- Dr. Bernd Kuhn, F.Hoffmann-La Roche Ltd
- Scientists of F.Hoffmann-La Roche Ltd for extensive testing



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