

Resource Summary Report

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Hetero-compound Information Centre- Uppsala

RRID:SCR_007710

Type: Tool

Proper Citation

Hetero-compound Information Centre- Uppsala (RRID:SCR_007710)

Resource Information

URL: <http://xray.bmc.uu.se/hicup/>

Proper Citation: Hetero-compound Information Centre- Uppsala (RRID:SCR_007710)

Description: HIC-Up, the Hetero-compound Information Centre - Uppsala, a freely accessible resource for structural biologists who are dealing dealing with hetero-compounds ("small molecules"). This site contains information about hetero-compounds encountered in files from the Protein Data Bank (PDB). For every compound, a subset of the following information is available: Coordinate files (PDB and text files) Visualisation files (Chime and VRML) Dictionary files (X-PLOR/CNS, O, TNT) Links to off-site databases and servers (PDBsum, EDS, PRODRG, Relibase, MSDchem, ChemDB, Jena HCD, etc.) Miscellaneous files and information

Synonyms: HIC-Up

Resource Type: data or information resource, database

Keywords: hetero-compounds, software

Resource Name: Hetero-compound Information Centre- Uppsala

Resource ID: SCR_007710

Alternate IDs: nif-0000-02960

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260912T200150+0000

Ratings and Alerts

No rating or validation information has been found for Hetero-compound Information Centre- Uppsala.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Corrêa TLR, et al. (2021) A novel mechanism of β -glucosidase stimulation through a monosaccharide binding-induced conformational change. International journal of biological macromolecules, 166, 1188.

Rendón JL, et al. (2018) Insight into the Mechanistic Basis of the Hysteretic-Like Kinetic Behavior of Thioredoxin-Glutathione Reductase (TGR). Enzyme research, 2018, 3215462.

Smith BA, et al. (2018) Potential roles of inorganic phosphate on the progression of initially bound glucopyranose toward the nonenzymatic glycation of human hemoglobin: mechanistic diversity and impacts on site selectivity. Cogent biology, 4.

Maurya AK, et al. (2017) Bioprocess for the production of recombinant HAP phytase of the thermophilic mold Sporotrichum thermophile and its structural and biochemical characteristics. International journal of biological macromolecules, 94(Pt A), 36.

Papadovasilaki M, et al. (2015) Biophysical and enzymatic properties of aminoglycoside adenyltransferase AadA6 from Pseudomonas aeruginosa. Biochemistry and biophysics reports, 4, 152.

Shanmuga Priya A, et al. (2013) Improvement on dissolution rate of inclusion complex of Rifabutin drug with β -cyclodextrin. International journal of biological macromolecules, 62, 472.

Sommer B, et al. (2013) Membrane Packing Problems: A short Review on computational Membrane Modeling Methods and Tools. Computational and structural biotechnology journal, 5, e201302014.

Megli CJ, et al. (2011) Crystal structure of the Vibrio cholerae colonization factor TcpF and identification of a functional immunogenic site. Journal of molecular biology, 409(2), 146.

Koropatkin NM, et al. (2010) SusG: a unique cell-membrane-associated alpha-amylase from a prominent human gut symbiont targets complex starch molecules. Structure (London, England : 1993), 18(2), 200.

Nash RP, et al. (2010) The mechanism and control of DNA transfer by the conjugative relaxase of resistance plasmid pCU1. Nucleic acids research, 38(17), 5929.

Ding J, et al. (2010) Crystal structure of human programmed cell death 10 complexed with inositol-(1,3,4,5)-tetrakisphosphate: a novel adaptor protein involved in human cerebral

cavernous malformation. *Biochemical and biophysical research communications*, 399(4), 587.

Maugé C, et al. (2010) Crystal structure and catalytic mechanism of leucoanthocyanidin reductase from *Vitis vinifera*. *Journal of molecular biology*, 397(4), 1079.

Hoffman RM, et al. (2009) Structure of the inhibitor W7 bound to the regulatory domain of cardiac troponin C. *Biochemistry*, 48(24), 5541.

Duclert-Savatier N, et al. (2009) Insights into the enzymatic mechanism of 6-phosphogluconolactonase from *Trypanosoma brucei* using structural data and molecular dynamics simulation. *Journal of molecular biology*, 388(5), 1009.

Koropatkin NM, et al. (2008) Starch catabolism by a prominent human gut symbiont is directed by the recognition of amylose helices. *Structure (London, England : 1993)*, 16(7), 1105.

Desveaux D, et al. (2007) Type III effector activation via nucleotide binding, phosphorylation, and host target interaction. *PLoS pathogens*, 3(3), e48.

Kleywegt GJ, et al. (2007) Crystallographic refinement of ligand complexes. *Acta crystallographica. Section D, Biological crystallography*, 63(Pt 1), 94.

Guruprasad K, et al. (2005) Computational tools for the analysis of heteroatom groups and their neighbours in protein tertiary structure. *International journal of biological macromolecules*, 37(1-2), 35.

Shin JM, et al. (2005) PDB-Ligand: a ligand database based on PDB for the automated and customized classification of ligand-binding structures. *Nucleic acids research*, 33(Database issue), D238.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.