

Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

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: 20260905T133143+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 [PRECISE-TBI](#) .

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.