

Resource Summary Report

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CSA - Catalytic Site Atlas

RRID:SCR_013099

Type: Tool

Proper Citation

CSA - Catalytic Site Atlas (RRID:SCR_013099)

Resource Information

URL: <http://www.ebi.ac.uk/thornton-srv/databases/CSA/>

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Description: The Catalytic Site Atlas (CSA) is a database documenting enzyme active sites and catalytic residues in enzymes of 3D structure. We defined a classification of catalytic residues which includes only those residues thought to be directly involved in some aspect of the reaction catalyzed by an enzyme. The CSA contains 2 types of entry: 1. Original hand-annotated entries, derived from the primary literature. References for these entries are given. 2. Homologous entries, found by PSI-BLAST alignment (using an e value cut-off of 0.00005) to one of the original entries. The equivalent residues, which align in sequence to the catalytic residues found in the original entry are documented. Access to the CSA is via PDB code, SWISS-PROT entry or E.C. number. Accessing via PDB code takes you straight to the CSA entry for that PDB, while accessing via SWISS-PROT or E.C. number gives a list of all PDB codes for structures assigned that particular SWISS-PROT identifier or E.C. number. Structures with entries in the CSA are given as hyperlinks. Each CSA entry lists the catalytic residues found in that entry, using PDB residue numbering. Each site is also marked with an evidence tag, which is either Literature reference or PSI-BLAST hit. If the entry is a PSI-BLAST hit you can follow the link to the original entry. You may download the CSA. JESS, an algorithm for constraint-based structural template matching and its application to 3D templates used by the CSA, is available for download.

Abbreviations: CSA

Synonyms: Catalytic Site Atlas

Resource Type: software resource, data or information resource, database

Defining Citation: [PMID:14681376](#)

Keywords: enzyme, enzyme 3d structure, enzyme catalysis, enzyme structure, catalysis, catalytic site, catalytic residue, gold standard

Resource Name: CSA - Catalytic Site Atlas

Resource ID: SCR_013099

Alternate IDs: nif-0000-02699, r3d100010815

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260806T054552+0000

Ratings and Alerts

No rating or validation information has been found for CSA - Catalytic Site Atlas.

No alerts have been found for CSA - Catalytic Site Atlas.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Grinspon RP, et al. (2021) Diagnosis of Male Central Hypogonadism During Childhood. Journal of the Endocrine Society, 5(11), bvab145.

Wackett LP, et al. (2018) Microbial biocatalysis databases: An annotated selection of World Wide Web sites relevant to the topics in microbial biotechnology. Microbial biotechnology, 11(2), 429.

Tang A, et al. (2018) Mechanism of Pseudomonas aeruginosa Small Protease (PASP), a Corneal Virulence Factor. Investigative ophthalmology & visual science, 59(15), 5993.

Masso M, et al. (2015) Modeling functional changes to Escherichia coli thymidylate synthase upon single residue replacements: a structure-based approach. PeerJ, 3, e721.

Radusky LG, et al. (2015) An integrated structural proteomics approach along the druggable genome of Corynebacterium pseudotuberculosis species for putative druggable targets. BMC genomics, 16 Suppl 5(Suppl 5), S9.

Sridhar S, et al. (2015) Analyses of the Sequence and Structural Properties Corresponding to Pentapeptide and Large Palindromes in Proteins. PloS one, 10(10), e0139568.

Radusky L, et al. (2014) TuberQ: a Mycobacterium tuberculosis protein druggability database. Database : the journal of biological databases and curation, 2014, bau035.

Furnham N, et al. (2014) The Catalytic Site Atlas 2.0: cataloging catalytic sites and residues identified in enzymes. *Nucleic acids research*, 42(Database issue), D485.

Nilmeier JP, et al. (2013) Rapid catalytic template searching as an enzyme function prediction procedure. *PloS one*, 8(5), e62535.

Sehna D, et al. (2013) MOLE 2.0: advanced approach for analysis of biomacromolecular channels. *Journal of cheminformatics*, 5(1), 39.

Suplatov DA, et al. (2011) Comparative Bioinformatic Analysis of Active Site Structures in Evolutionarily Remote Homologues of α , β -Hydrolase Superfamily Enzymes. *Acta naturae*, 3(1), 93.

Devos D, et al. (2006) Harry Potter and the structural biologist's (Key)stone. *Genome biology*, 7(12), 333.

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

Yang LW, et al. (2005) Coupling between catalytic site and collective dynamics: a requirement for mechanochemical activity of enzymes. *Structure (London, England : 1993)*, 13(6), 893.