

Resource Summary Report

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PDBsum

RRID:SCR_006511

Type: Tool

Proper Citation

PDBsum (RRID:SCR_006511)

Resource Information

URL: <http://www.ebi.ac.uk/pdbsum>

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Description: Pictorial database of an at-a-glance overview of the contents of each 3D structure deposited in the Protein Data Bank (PDB). It shows the molecule(s) that make up the structure (ie protein chains, DNA, ligands and metal ions) and schematic diagrams of their interactions. Extensive use is made of the freely available RasMol molecular graphics program to view the molecules and their interactions in 3D. Entries are accessed either by their 4-character PDB code, or by one of the two search boxes provided on the PDBsum home page: text search or sequence search. The information given on each PDBsum entry is spread across several pages, as listed below and accessible from the tabs at the top of the page. Only the relevant tabs will be present on any given page. * Top page - summary information including thumbnail image of structure, molecules in structure, enzyme reaction diagram (where relevant), GO functional assignments, and selected figures from key reference * Protein - wiring diagram, topology diagram(s) by CATH domain, and residue conservation (where available) * DNA/RNA - DNA/RNA sequence and NUCPLOT showing interactions made with protein * Ligands - description of bound molecule and LIGPLOT showing interactions made with protein * Prot-prot - schematic diagrams of any protein-protein interfaces and the residue-residue interactions made across them * Clefts - listing of top ten clefts in the surface of the protein, listed by volume with any bound ligands shown * Links - links to external databases Additionally, it accepts users' own PDB format files and generates a private set of analyses for each uploaded structure.

Abbreviations: PDBsum

Resource Type: data analysis service, data or information resource, database, service resource, d spatial image, production service resource, analysis service resource

Defining Citation: [PMID:18996896](#), [PMID:15608193](#), [PMID:11125097](#), [PMID:9433130](#)

Keywords: 3d structure, protein, molecule, structure, protein chain, dna, ligand, metal ion, interaction, gold standard

Funding: Wellcome Trust

Resource Name: PDBsum

Resource ID: SCR_006511

Alternate IDs: nlx_40623

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260801T042617+0000

Ratings and Alerts

No rating or validation information has been found for PDBsum.

No alerts have been found for PDBsum.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 546 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Malarvizhi GL, et al. (2025) Rationally Designed Functionalized Phytochemical-Conjugated Fullerene Quantum Dots Inhibiting Viral Chaperone Activity and RNA-Dependent RNA Polymerase in Nipah Virus. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 39(15), e70890.

Basharat Z, et al. (2025) Proteome mining of Yersinia Enterocolitica for drug targets and computational inhibitor identification with ADMET, anti-inflammation potential and formulation characteristics. BioData mining, 18(1), 68.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. Heliyon, 11(1), e41714.

Castillo G, et al. (2025) Genome Sequencing Reveals the Potential of Enterobacter sp. Strain UNJFSC003 for Hydrocarbon Bioremediation. Genes, 16(1).

Iqbal MW, et al. (2025) Exploring deleterious non-synonymous SNPs in FUT2 gene, and implications for norovirus susceptibility and gut microbiota composition. Scientific reports, 15(1), 10395.

- Zhu F, et al. (2025) Designing a multi-epitope vaccine against *Pseudomonas aeruginosa* via integrating reverse vaccinology with immunoinformatics approaches. *Scientific reports*, 15(1), 10425.
- Zengin K, et al. (2025) The Function of TER94 of *Spodoptera frugiperda* 9 Cells When Infected With Invertebrate Iridescent Virus-6. *Journal of basic microbiology*, 65(8), e70045.
- Khazani Asforooshani M, et al. (2025) Exploiting subtractive genomics to identify novel drug targets and new immunogenic candidates against *Bordetella pertussis*: an in silico study. *Frontiers in bioinformatics*, 5, 1570054.
- García-Franco A, et al. (2025) Characterization of a consensus-designed trans-cinnamic acid decarboxylase for styrene biosynthesis. *mBio*, 16(6), e0071425.
- Shehri ZSA, et al. (2025) Immuno-informatics analyses of important esophageal cancer associated viruses for multi-epitope vaccine design. *Frontiers in immunology*, 16, 1587224.
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- Jiang J, et al. (2025) A comprehensive strategy for the development of a multi-epitope vaccine targeting *Treponema pallidum*, utilizing heat shock proteins, encompassing the entire process from vaccine design to in vitro evaluation of immunogenicity. *Frontiers in microbiology*, 16, 1551437.
- Hammerstad M, et al. (2025) The methyltransferase NmbA methylates the low-molecular weight thiol bacillithiol, and displays a specific structural architecture. *Redox biology*, 88, 103937.
- Hanif MA, et al. (2025) The role of N185D substitution in enhancing activity of BaqA?C ?-amylase. *Scientific reports*, 15(1), 43521.
- Galuzo R, et al. (2025) CLEC5A Activation in Inflammatory Monocytes: A Mechanism for Enhanced Adaptive Immunity Following COVID-19 mRNA Vaccination in a Preclinical Study. *Viruses*, 17(9).
- Das U, et al. (2025) Identification of potential natural BCL-2 inhibitors for leukemia through an integrated virtual screening approach. *BMC pharmacology & toxicology*, 26(1), 176.
- Asrar B, et al. (2025) In silico investigation of ketamine and methylphenidate drug-drug conjugate for MDD and ADHD treatment using MD simulations and MMGBSA. *Scientific reports*, 15(1), 24565.
- Beig M, et al. (2025) Development of a multi-epitope vaccine against *Acinetobacter baumannii*: A comprehensive approach to combating antimicrobial resistance. *PloS one*, 20(3), e0319191.
- Zubair A, et al. (2025) Targeting HIV-1 conserved regions: An immunoinformatic pathway to vaccine innovation for the Asia. *PloS one*, 20(3), e0317382.

Jia Y, et al. (2025) Design and Evaluation of a Broadly Multivalent Adhesins-Based Multi-Epitope Fusion Antigen Vaccine Against Enterotoxigenic *Escherichia coli* Infection. *Vaccines*, 13(10).