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

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: 20250409T060531+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 469 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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).

Shanto PC, et al. (2025) 3D bio-printed proteinaceous bioactive scaffold loaded with dual growth factor enhanced chondrogenesis and in situ cartilage regeneration. Bioactive materials, 46, 365.

Rahman MM, et al. (2025) Designing of an mRNA vaccine against high-risk human papillomavirus targeting the E6 and E7 oncoproteins exploiting immunoinformatics and dynamic simulation. PloS one, 20(1), e0313559.

Lu D, et al. (2025) Structural basis of the bifunctionality of Marinobacter salinexigens ZYF650T glucosylglycerol phosphorylase in glucosylglycerol catabolism. The Journal of biological chemistry, 301(2), 108127.

Xiong EH, et al. (2024) Functional genomic analysis of genes important for Candida albicans fitness in diverse environmental conditions. Cell reports, 43(8), 114601.

Nishio S, et al. (2024) ZP2 cleavage blocks polyspermy by modulating the architecture of the egg coat. Cell, 187(6), 1440.

Murtaza A, et al. (2024) Advancing PEDV Vaccination: Comparison between Inactivated and Flagellin N-Terminus-Adjuvanted Subunit Vaccines. Vaccines, 12(2).

Biswas S, et al. (2024) An in silico approach to develop potential therapies against Middle East Respiratory Syndrome Coronavirus (MERS-CoV). Heliyon, 10(4), e25837.

Díaz-Valdez J, et al. (2024) EhVps35, a retromer component, is involved in the recycling of the EhADH and Gal/GalNac virulent proteins of Entamoeba histolytica. Frontiers in parasitology, 3, 1356601.

Ehsasatvatan M, et al. (2024) Designing and immunomolecular analysis of a new broad-spectrum multiepitope vaccine against divergent human papillomavirus types. PloS one, 19(12), e0311351.

Mursaleen S, et al. (2024) Genome-level therapeutic targets identification and chimeric Vaccine designing against the Blastomyces dermatitidis. Heliyon, 10(16), e36153.

Martínez-Valencia D, et al. (2024) The Entamoeba histolytica Vps26 (EhVps26) retromeric protein is involved in phagocytosis: Bioinformatic and experimental approaches. PloS one, 19(8), e0304842.

Gayathri K, et al. (2024) Computational analysis of phytocompounds in Centella asiatica for its antifibrotic and drug-likeness properties - Herb to drug study. Heliyon, 10(13), e33762.

Zhou P, et al. (2024) One HA stalk topping multiple heads as a novel influenza vaccine. Emerging microbes & infections, 13(1), 2290838.

Sarvmeili J, et al. (2024) Immunoinformatics design of a structural proteins driven multi-epitope candidate vaccine against different SARS-CoV-2 variants based on fynomer. Scientific reports, 14(1), 10297.

Arratia LM, et al. (2024) Experimental and computational evidence that Calpain-10 binds to the carboxy terminus of NaV1.2 and NaV1.6. Scientific reports, 14(1), 6761.

Sethi G, et al. (2024) Immunoinformatics and structural aided approach to develop multi-epitope based subunit vaccine against Mycobacterium tuberculosis. Scientific reports, 14(1), 15923.

Al Mutairi F, et al. (2024) Biallelic HMGXB4 loss-of-function variant causes intellectual disability, developmental delay, and dysmorphic features. Heliyon, 10(15), e35361.

Oladipo EK, et al. (2024) Exploring the nuclear proteins, viral capsid protein, and early antigen protein using immunoinformatic and molecular modeling approaches to design a vaccine candidate against Epstein Barr virus. Scientific reports, 14(1), 16798.