

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: analysis service resource, d spatial image, data analysis service, data or information resource, database, production service resource, 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: 20260905T132555+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 634 mentions in open access literature.

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

Karimkhanilouei S, et al. (2026) Innovative Peptide Therapeutics for SARS-CoV-2: Design, Docking, and Functional Analysis. Iranian journal of pharmaceutical research : IJPR, 25(1), e160762.

Alam MJ, et al. (2026) Molecular Docking and MD Modeling Techniques for the Development of Novel ROS1 Kinase Inhibitors. Pharmaceuticals (Basel, Switzerland), 19(2).

Arunachalam L, et al. (2026) Mechanistic elucidation of a terpenoid nano-bionemeticide for the management of root-knot nematodes, Meloidogyne incognita infecting tomato. Scientific reports, 16(1).

Yuka SA, et al. (2026) In Silico Structure-Guided Design of Peptide Candidates Targeting ??-Secretase Subunit Assembly. Proteins, 94(8), 1518.

Silva RMB, et al. (2026) A single viral enzyme drives tRNA-dependent hypermodification of DNA at adenine. Nature communications, 17(1).

Liu Q, et al. (2026) Structural basis for selective thymidine binding by the Borrelia burgdorferi substrate-binding protein BmpA. The Journal of biological chemistry, 302(7),

113206.

Sripath K, et al. (2026) Proteome-Based Antigen Screening and Multi-Epitope Design Against *Cutibacterium acnes*: An In Silico Study. *Biology*, 15(12).

Araneda J, et al. (2026) In silico design of a multiantigenic and multiepitope chimeric protein as a vaccine candidate against *Renibacterium salmoninarum*. *Frontiers in cellular and infection microbiology*, 16, 1814020.

Naveed M, et al. (2026) Immunoinformatics-driven design of a multi-epitope vaccine against Seoul Virus: Structural, dynamic, and immunogenic profiling. *Clinics (Sao Paulo, Brazil)*, 81, 100991.

Smatti MK, et al. (2026) Functional and structural characterization of the SARS-CoV-2 spike N481K mutation. *Archives of virology*, 171(7).

Nandish V, et al. (2026) Comparative pangenomics of *Pasteurella multocida* uncovers adhesins specific to capsular serogroup B strains associated with bovine host tropism. *BMC microbiology*, 26(1).

Dell'Oca M, et al. (2026) NEDAMSS syndrome-related truncating and missense mutations are associated with aberrant liquid-liquid phase separation of IRF2BPL. *Nature communications*, 17(1).

Syaban MFR, et al. (2026) Structural basis underlying the autoinhibition of the formin FHOD1 and its phosphorylation-dependent activation. *The Journal of biological chemistry*, 302(2), 111109.

Zhao J, et al. (2026) Extracellular Vesicle-Mediated O-GlcNAcase Transfer Drives Neuronal Necroptosis to Facilitate Gallbladder Cancer Perineural Invasion. *Cancer research*, 86(6), 1392.

Akwelle RN, et al. (2026) In Silico Design and Computational Characterization of Novel Chimeric Multiepitope Antigens for Mpox Serosurveillance: An Immunoinformatics Approach. *Health science reports*, 9(6), e72702.

Li D, et al. (2026) Post-Translational Modifications Modulate the HLA-DR3 Restricted Epitope Landscape of Sjögren's Associated Autoantigens. *Medicina (Kaunas, Lithuania)*, 62(6).

Mukhtar O, et al. (2026) LFA-1 interaction with GBP-130 on *Plasmodium falciparum*-infected red blood cells mediates NK cell activation and parasite control. *eLife*, 15.

Bhatt TC, et al. (2026) Discovery of age and blood group associated variability in nattokinase mediated thrombolysis and its relevance to cardiovascular management. *Scientific reports*, 16(1).

Akter S, et al. (2026) Immunoinformatics approach to engineer a multi-epitope vaccine against SdrG in skin commensal *Staphylococcus epidermidis*. *PloS one*, 21(3), e0327534.

Cong X, et al. (2026) Ethanol Regulates Bitterness Perception of the Trp-Ile-Lys-Lys (WIKK) Peptide by Activating the Human Bitter Receptor T2R47. *Foods (Basel, Switzerland)*, 15(4).