

Resource Summary Report

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NCBI Structure: Cn3D

RRID:SCR_004861

Type: Tool

Proper Citation

NCBI Structure: Cn3D (RRID:SCR_004861)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/Structure/CN3D/cn3d.shtml>

Proper Citation: NCBI Structure: Cn3D (RRID:SCR_004861)

Description: Cn3D is a helper application for your web browser that allows you to view 3-dimensional structures from NCBI's Entrez retrieval service. Cn3D runs on Windows, Macintosh, and Unix. Cn3D simultaneously displays structure, sequence, and alignment, and now has powerful annotation and alignment editing features. Cn3D is a tool for visualization of three-dimensional structures with emphasis on interactive examination of sequence-structure relationships and superposition of geometrically similar structures. Can be used to display MMDB structures, superpositions of VAST related structures, and conserved core motifs identified in conserved domains.

Synonyms: Cn3D

Resource Type: d visualization software

Defining Citation: [PMID:10838572](#)

Keywords: gold standard, bio.tools

Resource Name: NCBI Structure: Cn3D

Resource ID: SCR_004861

Alternate IDs: biotools:cn3d, nlx_84208

Alternate URLs: <https://bio.tools/cn3d>

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260905T132525+0000

Ratings and Alerts

No rating or validation information has been found for NCBI Structure: Cn3D.

No alerts have been found for NCBI Structure: Cn3D.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 133 mentions in open access literature.

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

Rottenberg H, et al. (2025) Adaptive evolution of cytochrome b in songbirds. *Biology open*, 14(4).

Wu W, et al. (2024) Evolution of the WRKY Family in Angiosperms and Functional Diversity under Environmental Stress. *International journal of molecular sciences*, 25(6).

Valadés-Alcaraz A, et al. (2024) Development and characterization of high-affinity aptamers for HIV protease detection. *Heliyon*, 10(22), e38234.

Gleason RJ, et al. (2023) Developmentally programmed histone H3 expression regulates cellular plasticity at the parental-to-early embryo transition. *Science advances*, 9(14), eadh0411.

Pozdniakova NV, et al. (2022) Using ELP Repeats as a Scaffold for De Novo Construction of Gadolinium-Binding Domains within Multifunctional Recombinant Proteins for Targeted Delivery of Gadolinium to Tumour Cells. *International journal of molecular sciences*, 23(6).

Hult AK, et al. (2022) A new missense variant in exon 7 of the ABO gene, c.662G>A, in a family with Bw phenotype. *Transfusion*, 62(10), E55.

Song S, et al. (2021) Allo-Specific Humoral Responses: New Methods for Screening Donor-Specific Antibody and Characterization of HLA-Specific Memory B Cells. *Frontiers in immunology*, 12, 705140.

Fogeron ML, et al. (2021) Easy Synthesis of Complex Biomolecular Assemblies: Wheat Germ Cell-Free Protein Expression in Structural Biology. *Frontiers in molecular biosciences*, 8, 639587.

Tripathi A, et al. (2021) Trypanosoma brucei Tim50 Possesses PAP Activity and Plays a Critical Role in Cell Cycle Regulation and Parasite Infectivity. *mBio*, 12(5), e0159221.

Yang M, et al. (2020) NCBI's Conserved Domain Database and Tools for Protein Domain Analysis. *Current protocols in bioinformatics*, 69(1), e90.

Kim YM, et al. (2020) The GBA p.G85E mutation in Korean patients with non-neuronopathic Gaucher disease: founder and neuroprotective effects. *Orphanet journal of*

rare diseases, 15(1), 318.

Gu J, et al. (2020) Transcriptome Analysis of Carbohydrate Metabolism Genes and Molecular Regulation of Sucrose Transport Gene LoSUT on the Flowering Process of Developing Oriental Hybrid Lily 'Sorbonne' Bulb. *International journal of molecular sciences*, 21(9).

Kinoshita M, et al. (2020) Epidemiological survey of serum titers from adults against various Gram-negative bacterial V-antigens. *PloS one*, 15(3), e0220924.

Youkharibache P, et al. (2020) Pseudo-Symmetric Assembly of Protodomains as a Common Denominator in the Evolution of Polytopic Helical Membrane Proteins. *Journal of molecular evolution*, 88(4), 319.

Martínez-Montañés F, et al. (2020) Phosphoproteomic Analysis across the Yeast Life Cycle Reveals Control of Fatty Acyl Chain Length by Phosphorylation of the Fatty Acid Synthase Complex. *Cell reports*, 32(6), 108024.

Lee MC, et al. (2020) Human Labor Pain Is Influenced by the Voltage-Gated Potassium Channel KV6.4 Subunit. *Cell reports*, 32(3), 107941.

Eun Kang J, et al. (2020) SeSaMe PS Function: Functional Analysis of the Whole Metagenome Sequencing Data of the Arbuscular Mycorrhizal Fungi. *Genomics, proteomics & bioinformatics*, 18(5), 613.

Chen Y, et al. (2020) Structure analysis of the receptor binding of 2019-nCoV. *Biochemical and biophysical research communications*, 525(1), 135.

Gadermaier E, et al. (2019) Characterization of a sandwich ELISA for quantification of total human soluble neuropilin-1. *Journal of clinical laboratory analysis*, 33(7), e22944.

Laforet M, et al. (2019) Modifying a covarying protein-DNA interaction changes substrate preference of a site-specific endonuclease. *Nucleic acids research*, 47(20), 10830.