Resource Summary Report

Generated by dkNET on May 19, 2025

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

Funding:

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: 20250420T014240+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 129 mentions in open access literature.

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

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

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.

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.

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.

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).

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

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

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.

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.

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.

Yang F, et al. (2019) A Novel SNPs in Alpha-Lactalbumin Gene Effects on Lactation Traits in Chinese Holstein Dairy Cows. Animals : an open access journal from MDPI, 10(1).

Iuchi S, et al. (2019) Lysine-specific demethylase 2A enhances binding of various nuclear factors to CpG-rich genomic DNAs by action of its CXXC-PHD domain. Scientific reports, 9(1), 5496.

Zhu LJ, et al. (2019) Mutation of CarO participates in drug resistance in imipenem-resistant Acinetobacter baumannii. Journal of clinical laboratory analysis, 33(8), e22976.

Gupta S, et al. (2019) Structural determinants governing ?-arrestin2 interaction with PDZ proteins and recruitment to CRFR1. Cellular signalling, 63, 109361.