

Resource Summary Report

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CYANA

RRID:SCR_014229

Type: Tool

Proper Citation

CYANA (RRID:SCR_014229)

Resource Information

URL: http://www.cyana.org/wiki/index.php/Main_Page

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Description: Software for automated structure calculation of biological macromolecules on basis of conformational constraints from nuclear magnetic resonance. Program for automated NMR protein structure calculation. CYANA requires a sufficient list of assigned chemical shifts and lists of cross-peak positions and columns from 2D, 3D, or 4D NOESY spectra in order to calculate the assignment of the NOESY cross-peaks and the 3D structure of the protein in solution.

Resource Type: data analysis software, software application, software resource, data processing software

Defining Citation: [PMID:15318003](#), [PMID:25801209](#)

Keywords: protein structure, nmr, noesy, 3d structure, bio.tools

Availability: Available to the academic community, Available to commercial user, Pay for license

Resource Name: CYANA

Resource ID: SCR_014229

Alternate IDs: SCR_021949, biotools:cyana

Alternate URLs: <http://www.las.jp/english/products/cyana.html>, <https://bio.tools/cyana>, [https://dbpedia.org/page/CYANA_\(software\)](https://dbpedia.org/page/CYANA_(software))

License: Separate licenses are available for academic and commercial users

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260807T042818+0000

Ratings and Alerts

No rating or validation information has been found for CYANA.

No alerts have been found for CYANA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 428 mentions in open access literature.

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

Nguyen CKX, et al. (2026) Characterization of flexible RNA binding by tandem RNA recognition motifs through integrative ensemble modelling. *Nucleic acids research*, 54(6).

Shehadeh F, et al. (2026) CAMPER: mechanistic artificial intelligence for designing peptides that target MRSA persisters. *Nature communications*, 17(1).

Safronova VN, et al. (2026) Marine Antimicrobial Peptide as a Promising Alternative to Polymyxin B. *Marine drugs*, 24(5).

Reddy PP, et al. (2025) Structural analysis of genetic variants of the human tumor suppressor PALB2 coiled-coil domain. *Bioscience reports*, 45(3).

Peck Y, et al. (2025) Structural characterisation of a cysteine-rich conotoxin, sigma(??)S-GVIIIa, extracted from the defensive venom of the marine cone snail *Conus geographus*. *The Biochemical journal*, 482(11), 639.

Agarwal R, et al. (2025) SA-XV, a 15-amino acid fragment of host defense peptide S100A12, targets mitochondria and is protective against fungal infections. *The Journal of biological chemistry*, 301(10), 110743.

Machado LESF, et al. (2025) NMR study of the interaction between MinC and FtsZ and modeling of the FtsZ:MinC complex. *The Journal of biological chemistry*, 301(3), 108169.

Paredes A, et al. (2025) The response regulator BqsR/CarR controls ferrous iron (Fe²⁺) acquisition in *Pseudomonas aeruginosa*. *bioRxiv : the preprint server for biology*.

Bello-Madruga R, et al. (2025) Mining the heparinome for cryptic antimicrobial peptides that selectively kill Gram-negative bacteria. *Molecular systems biology*, 21(7), 889.

Procino E, et al. (2025) Greening the Solid-Phase Peptide Synthesis of the First Bicyclic Analogue of the Arc Repressor and Its Binding to DNA. *The Journal of organic chemistry*, 90(46), 16423.

Kuzmenkov AI, et al. (2025) Spider venom peptides with unique fold selectively block Shaker-type potassium channels. *Cellular and molecular life sciences : CMLS*, 82(1), 300.

Morita K, et al. (2025) Solution structure of the C-terminal domain of the measles virus V protein in its free form and mechanistic analysis of STAT2 targeting. *Journal of virology*, 99(10), e0073925.

Henen MA, et al. (2025) Protocol for converting assigned nuclear Overhauser enhancement spectroscopy series peaks into exact distance restraints using MATLAB- or CYANA-eNORA. *STAR protocols*, 6(1), 103653.

Openy J, et al. (2025) Backbone Alterations in Cyclic Peptides Influence Both Membrane Permeability and Biological Activity. *Journal of medicinal chemistry*, 68(22), 24108.

Polonio P, et al. (2025) Structural basis for amyloid fibril assembly by the master cell-signaling regulator receptor-interacting protein kinase 1. *Nature communications*, 16(1), 9607.

Carlson ES, et al. (2025) The specificity and structure of DNA cross-linking by the gut bacterial genotoxin colibactin. *Science (New York, N.Y.)*, 390(6777), eady3571.

Cointry V, et al. (2025) Metal-sensing properties of the disordered loop from the Arabidopsis metal transceptor IRT1. *The Biochemical journal*, 482(9), 451.

Zhang H, et al. (2025) Machine learning and genetic algorithm-guided directed evolution for the development of antimicrobial peptides. *Journal of advanced research*, 68, 415.

Nguyen MH, et al. (2024) Analysis of the structure and interactions of the SARS-CoV-2 ORF7b accessory protein. *Proceedings of the National Academy of Sciences of the United States of America*, 121(46), e2407731121.

Abdullah SJ, et al. (2024) Structures, Interactions and Activity of the N-Terminal Truncated Variants of Antimicrobial Peptide Thanatin. *Antibiotics (Basel, Switzerland)*, 13(1).