

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 14, 2026

CYANA

RRID:SCR_014229

Type: Tool

Proper Citation

CYANA (RRID:SCR_014229)

Resource Information

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

Proper Citation: CYANA (RRID:SCR_014229)

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, data processing software, software application, software resource

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: 20260912T195814+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 [SPARC SAWG](#) .

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).

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.

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

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*.

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.

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.

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.

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.

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.

Vögele J, et al. (2024) Structure of an internal loop motif with three consecutive U•U mismatches from stem-loop 1 in the 3'-UTR of the SARS-CoV-2 genomic RNA. Nucleic acids research, 52(11), 6687.

Parrón-Ballesteros J, et al. (2024) Long-chain fatty acids block allergic reaction against lipid transfer protein Sola I 7 from tomato seeds. Protein science : a publication of the Protein Society, 33(9), e5154.