

Resource Summary Report

Generated by [RRID](#) on Aug 4, 2026

[NMRbox](#)

RRID:SCR_014827

Type: Tool

Proper Citation

NMRbox (RRID:SCR_014827)

Resource Information

URL: <http://nmrbox.org>

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Description: Computing platform for biomolecular NMR available to not-for-profit or government users. It consists of a virtual machine (VM) provisioned with dozens of widely-used NMR software packages, and is available as a cloud-based Platform-as-a-Service (PaaS) or as a downloadable VM for local execution.

Synonyms: , Nuclear Magnetic Resonance box, NMRbox.org

Resource Type: software toolkit, software resource, web application

Keywords: Nuclear Magnetic Resonance, nmr, spectra, computing platform, platform, virtual machine, cloud, software toolbox

Funding: NIGMS P41GM111135

Availability: Account required

Resource Name: NMRbox

Resource ID: SCR_014827

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260804T043552+0000

Ratings and Alerts

No rating or validation information has been found for NMRbox.

No alerts have been found for NMRbox.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 78 mentions in open access literature.

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

Zeinalilathori S, et al. (2026) Structure of the disulfide-rich modules of a striking tandem repeat protein, avian cysteine-rich eggshell membrane protein. Protein science : a publication of the Protein Society, 35(1), e70431.

Li K, et al. (2025) Strategic Acyl Carrier Protein Engineering Enables Functional Type II Polyketide Synthase Reconstitution In Vitro. ACS chemical biology, 20(1), 197.

Hernandez G, et al. (2025) Dynamic ensembles of SARS-CoV-2 N-protein reveal head-to-head coiled-coil-driven oligomerization and phase separation. Nucleic acids research, 53(11).

Jin Y, et al. (2025) T cells detect mevalonate diphosphate via BTN3A3. Cellular and molecular life sciences : CMLS, 82(1), 405.

Rovnyak HB, et al. (2025) Decoherence Principles and Algorithms for One-Dimensional Nonuniform Sampling Schedules for Multidimensional NMR. Analytical chemistry, 97(49), 27091.

Lin QT, et al. (2025) Protocol for deriving distance restraints from AlphaFold for use in solution NMR structure determination. STAR protocols, 6(3), 103988.

Lu X, et al. (2025) Optimization of the PROTAC linker region of the proteasome substrate receptor hRpn13 rationalized by structural modeling with molecular dynamics. The Journal of biological chemistry, 301(6), 108520.

Lv G, et al. (2025) Amyloid fibril structures link CHCHD10 and CHCHD2 to neurodegeneration. Nature communications, 16(1), 7121.

Love DL, et al. (2025) Evaluating metrics of spectral quality in nonuniform sampling. Journal of magnetic resonance open, 23.

Lesovoy D, et al. (2025) Insight into Malt1 activation mechanism through synergetic approach of AlphaFold, MD Simulation and NMR dynamic analyses. bioRxiv : the preprint server for biology.

Boulay A, et al. (2024) A new class of capsid-targeting inhibitors that specifically block HIV-1 nuclear import. EMBO molecular medicine, 16(11), 2918.

Jahangiri A, et al. (2024) Beyond traditional magnetic resonance processing with artificial intelligence. Communications chemistry, 7(1), 244.

Wallerstein J, et al. (2024) Insights into mechanisms of MALT1 allostery from NMR and AlphaFold dynamic analyses. *Communications biology*, 7(1), 868.

Klebansky B, et al. (2024) In Search of Better Peptide-(Derived from PD-L2)-Based Immune Checkpoint Inhibitors. *Biomolecules*, 14(5).

Li W, et al. (2024) Structural basis of nearest-neighbor cooperativity in the ring-shaped gene regulatory protein TRAP from protein engineering and cryo-EM. *bioRxiv : the preprint server for biology*.

Bursch KL, et al. (2024) Cancer-associated polybromo-1 bromodomain 4 missense variants variably impact bromodomain ligand binding and cell growth suppression. *The Journal of biological chemistry*, 300(4), 107146.

Guo C, et al. (2024) Structural Model of Bacteriophage P22 Scaffolding Protein in a Procapsid by Magic-Angle Spinning NMR. *bioRxiv : the preprint server for biology*.

Taujale R, et al. (2024) PyINETA: Open-Source Platform for INADEQUATE-JRES Integration in NMR Metabolomics. *Analytical chemistry*, 96(48), 19029.

Coutinho AL, et al. (2024) Prediction of Successful Amorphous Solid Dispersion Pairs through Liquid State Nuclear Magnetic Resonance. *Molecular pharmaceuticals*, 21(12), 6153.

Dudas EF, et al. (2024) The structural properties of full-length annexin A11. *Frontiers in molecular biosciences*, 11, 1347741.