

Resource Summary Report

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[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.

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).

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.

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.

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.

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

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

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

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*.

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

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.

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*.

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).

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

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

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*.

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.

Wu Y, et al. (2024) SAND: Automated Time-Domain Modeling of NMR Spectra Applied to Metabolite Quantification. *Analytical chemistry*, 96(5), 1843.