

Resource Summary Report

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Sparky

RRID:SCR_014228

Type: Tool

Proper Citation

Sparky (RRID:SCR_014228)

Resource Information

URL: <https://www.cgl.ucsf.edu/home/sparky/>

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Description: A graphical NMR assignment and integration program for proteins, nucleic acids, and other polymers. Sparky displays NMR spectra, the peaks of which users may pick, assign, and integrate using a graphical interface. Users can work with any number of 2, 3 or 4 dimensional spectra simultaneously. Spectra for input to Sparky can be produced with processing programs NMRPipe, Felix, VNMR, XWinNMR or UXNMR. Output consists of text peak lists showing assignments, chemical shifts, volumes, line widths, etc.

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

Keywords: graphical nmr, protein integration, nucleic acid integration

Availability: Free, Acknowledgement requested

Resource Name: Sparky

Resource ID: SCR_014228

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Record Creation Time: 20220129T080319+0000

Record Last Update: 20260829T182443+0000

Ratings and Alerts

No rating or validation information has been found for Sparky .

No alerts have been found for Sparky .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 488 mentions in open access literature.

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

Dupuy P, et al. (2026) Membrane-associated effluxosomes coordinate multi-metal resistance in Mycobacterium tuberculosis. The EMBO journal, 45(7), 2306.

Zhang G, et al. (2026) Characterization of the interaction between human cytochrome c and transfer RNAphe. Magnetic resonance letters, 6(1), 200219.

Kelly B, et al. (2026) Sulfur partitioning from cysteine controls T cell proliferation and effector function. Cell, 189(12), 3669.

Aleshintsev A, et al. (2026) Bacillus subtilis ParB C-terminal lysine residues are essential for dimerization and in vivo function, indicating their roles in DNA sliding. Nucleic acids research, 54(5).

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

Bai J, et al. (2026) Construction of Zn²⁺ Chelated Dodecapeptide Assembled Hydrogel with Bio-Adhesive and Bone Regeneration Functions. Gels (Basel, Switzerland), 12(6).

Kurbah I, et al. (2026) Amide 1H and 15N NMR signal assignments of all naturally-occurring di-ubiquitins. Biomolecular NMR assignments, 20(1).

Colombo G, et al. (2026) Molecular basis and cellular effects of Janus-class-driven cytoplasmic PYK2 coacervates. Communications biology, 9(1), 186.

Yeh JC, et al. (2026) Antimicrobial peptide-induced inner membrane hyperpolarization is associated with antibiotic sensitization and attenuated MIC escalation in multidrug-resistant Gram-negative pathogens. npj antimicrobials and resistance, 4(1).

Gong X, et al. (2025) Molecular bases of the interactions of ATG16L1 with FIP200 and ATG8 family proteins. Nature communications, 16(1), 9035.

Lång HKM, et al. (2025) A TOM1 variant impairs interaction with TOLLIP, autophagosome-lysosome fusion and regulation of innate immunity. Disease models & mechanisms, 18(9).

Litschko C, et al. (2025) Transition transferases prime bacterial capsule polymerization. *Nature chemical biology*, 21(1), 120.

Ikenoue T, et al. (2025) De Novo Peptides That Induce the Liquid-Liquid Phase Separation of γ -Synuclein. *Journal of the American Chemical Society*, 147(27), 24113.

Shoman M, et al. (2025) Expanding the CarD interaction network: CrsL is a novel transcription regulator in actinobacteria. *Nucleic acids research*, 53(22).

Lotz R, et al. (2025) Alternative splicing in the DBD linker region of p63 modulates binding to DNA and iASPP in vitro. *Cell death & disease*, 16(1), 4.

Klaushofer R, et al. (2025) Structural insights into proprotein convertase activation facilitate the engineering of highly specific furin inhibitors. *Nature communications*, 16(1), 8206.

Liebau J, et al. (2025) 4D structural biology-quantitative dynamics in the eukaryotic RNA exosome complex. *Nature communications*, 16(1), 7896.

Mattsson J, et al. (2025) Exploring Helical Fraying Linked to Dynamics and Catalysis in Adenylate Kinase. *Biochemistry*, 64(20), 4281.

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.

Du Z, et al. (2025) The sequence-structure-function relationship of intrinsic ER γ disorder. *Nature*, 638(8052), 1130.