

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

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: 20260728T043435+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 479 mentions in open access literature.

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

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

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.

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

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

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

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).

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).

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

Zacharopoulou M, et al. (2025) Local Ionic Conditions Modulate the Aggregation Propensity and Influence the Structural Polymorphism of γ -Synuclein. *Journal of the American Chemical Society*, 147(16), 13131.

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.

Gyawu RF, et al. (2025) Molecular interactions of the NaV1.5 C-terminal domain: CaM sequestered the IQ motif from the CTD. *The Journal of biological chemistry*, 301(12), 110871.

Watanabe Y, et al. (2025) Structural basis for phosphatidylcholine synthesis by bacterial phospholipid N-methyltransferases. *The Journal of biological chemistry*, 301(5), 108507.

Orzel B, et al. (2025) The Coordination Chemistry of Two Peptidic Models of NFeoB and Core CFeoB Regions of FeoB Protein: Complexes of Fe(II), Mn(II), and Zn(II). *Inorganic chemistry*, 64(10), 5038.

Feichtlbauer P, et al. (2025) Deceptive *Ceropegia sandersonii* uses an arabinogalactan for trapping its fly pollinators. *The New phytologist*, 246(6), 2738.

Aleshintsev A, et al. (2025) ParB C-terminal lysine residues are essential for dimerization, in vitro DNA sliding and in vivo function. *bioRxiv : the preprint server for biology*.

Jeong J, et al. (2025) NSD2 inhibitors rewire chromatin to treat lung and pancreatic cancers. *Nature*.

Fatalska A, et al. (2024) Recruitment of trimeric eIF2 by phosphatase non-catalytic subunit PPP1R15B. *Molecular cell*, 84(3), 506.

Shukla S, et al. (2024) Disorder in CENP-ACse4 tail-chaperone interaction facilitates binding with Ame1/Okp1 at the kinetochore. *Structure (London, England : 1993)*, 32(6), 690.