Resource Summary Report

Generated by dkNET on May 21, 2025

CCPN Analysis

RRID:SCR_016984
Type: Tool

Proper Citation

CCPN Analysis (RRID:SCR_016984)

Resource Information

URL: https://www.ccpn.ac.uk/v2-software/software/analysis

Proper Citation: CCPN Analysis (RRID:SCR_016984)

Description: Software package for interactive NMR spectrum visualization, resonance assignment and data analysis. Graphical elements allow to enter information and to view status of data and library functions manipulate the CCPN data model objects to record the scientific information. Software is cross platform and works on Linux, Mac OSX, Windows and Unix.

Abbreviations: CcpNmr Analysis

Synonyms: CcpNmr Analysis, CCPN Analysis v2, CCPN Analysis v3

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

Defining Citation: PMID:21953355, PMID:15815974

Keywords: interactive, NMR, specturm, visualization, resonance, data, analysis

Funding: Deutsche Forschungsgemeinschaft ;
Biotechnology and Biological Sciences Research Council (UK)

Availability: Public, Available for download, Free of charge for non profit institutions, Tutorial available

Resource Name: CCPN Analysis

Resource ID: SCR_016984

License: CCPN licence

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250521T061656+0000

Ratings and Alerts

No rating or validation information has been found for CCPN Analysis.

No alerts have been found for CCPN Analysis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 42 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Rua AJ, et al. (2024) Perturbations in mitochondrial metabolism associated with defective cardiolipin biosynthesis: An in-organello real-time NMR study. bioRxiv : the preprint server for biology.

Soto J, et al. (2024) Dynamics and thermal stability of the bypass polymerase, DinB homolog (Dbh). Frontiers in molecular biosciences, 11, 1364068.

Dawes S, et al. (2024) Chaperone BiP controls ER stress sensor Ire1 through interactions with its oligomers. Life science alliance, 7(10).

Rua AJ, et al. (2024) Perturbations in mitochondrial metabolism associated with defective cardiolipin biosynthesis: An in-organello real-time NMR study. The Journal of biological chemistry, 300(10), 107746.

Rampratap P, et al. (2024) Resolving Atomic-Level Dynamics and Interactions of High-Molecular-Weight Hyaluronic Acid by Multidimensional Solid-State NMR. ACS applied materials & interfaces, 16(33), 43317.

Mahana Y, et al. (2024) Structural evidence for protein-protein interaction between the non-canonical methyl-CpG-binding domain of SETDB proteins and C11orf46. Structure (London, England : 1993), 32(3), 304.

Lete MG, et al. (2023) NMR Investigation of Protein-Carbohydrate Interactions: The Recognition of Glycans by Galectins Engineered with Fluorotryptophan Residues. Chemistry (Weinheim an der Bergstrasse, Germany), 29(5), e202202208.

Aretz J, et al. (2023) Talin and kindlin use integrin tail allostery and direct binding to activate integrins. Nature structural & molecular biology, 30(12), 1913.

Gubensäk N, et al. (2023) Vibrio cholerae's ToxRS bile sensing system. eLife, 12.

Lin CC, et al. (2023) The combined action of the intracellular regions regulates FGFR2 kinase activity. Communications biology, 6(1), 728.

Masone A, et al. (2023) A tetracationic porphyrin with dual anti-prion activity. iScience, 26(9), 107480.

Johansen NT, et al. (2022) Mg2+-dependent conformational equilibria in CorA and an integrated view on transport regulation. eLife, 11.

Martinsen JH, et al. (2022) Structure, dynamics, and stability of the globular domain of human linker histone H1.0 and the role of positive charges. Protein science : a publication of the Protein Society, 31(4), 918.

Jara KA, et al. (2022) Multivalency, autoinhibition, and protein disorder in the regulation of interactions of dynein intermediate chain with dynactin and the nuclear distribution protein. eLife, 11.

Heikkinen HA, et al. (2021) NMR Structure Determinations of Small Proteins Using only One Fractionally 20% 13C- and Uniformly 100% 15N-Labeled Sample. Molecules (Basel, Switzerland), 26(3).

Mahling R, et al. (2021) NaV1.2 EFL domain allosterically enhances Ca2+ binding to sites I and II of WT and pathogenic calmodulin mutants bound to the channel CTD. Structure (London, England : 1993), 29(12), 1339.

Lin CC, et al. (2021) Grb2 binding induces phosphorylation-independent activation of Shp2. Communications biology, 4(1), 437.

Zhou S, et al. (2021) NMR Structure and Dynamics Studies of Yeast Respiratory Supercomplex Factor 2. Structure (London, England : 1993), 29(3), 275.

Cong X, et al. (2021) Molecular insights into the biased signaling mechanism of the ?-opioid receptor. Molecular cell, 81(20), 4165.

Quintana JI, et al. (2021) Galectin-4 N-Terminal Domain: Binding Preferences Toward A and B Antigens With Different Peripheral Core Presentations. Frontiers in chemistry, 9, 664097.