

# Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

## Collaborative Computing Project for NMR

RRID:SCR\_016983

Type: Tool

---

### Proper Citation

Collaborative Computing Project for NMR (RRID:SCR\_016983)

---

### Resource Information

**URL:** <https://www.ccpn.ac.uk/>

**Proper Citation:** Collaborative Computing Project for NMR (RRID:SCR\_016983)

**Description:** Project provides tools and knowledge to maximize the impact of the biological NMR studies. CCPN software facilitates data analysis and software integration. Project promotes the exchange of knowledge and provides training and best practices for the NMR community and has leading role in the development of NMR data sharing standard and coordination of NMR instrumentation proposals. Includes CCPN Data Model for macromolecular NMR and related areas, CcpNmr suite of programs like Analysis for spectrum visualization, resonance assignment and analysis, ChemBuild to create chemical structure templates in an NMR aware manner, FormatConverter for data exchange with common textual NMR formats and SpecView for swift, format independent peak and spectrum visualization.

**Abbreviations:** CCPN

**Synonyms:** CCPN, Collaborative Computing Project for NMR, The Collaborative Computing Project for NMR

**Resource Type:** portal, narrative resource, project portal, discussion, data or information resource, forum

**Defining Citation:** [PMID:15613391](#)

**Keywords:** collaborative, computing, project, NMR, software, data, standard, protein, molecule, spectroscopy, global

**Funding:** Medical Research Council ;  
Astra-Zeneca ;  
Genentech ;  
Dupont Pharma ;  
GlaxoSmithKline ;

BBSRC

**Availability:** Free for non profit, Public, Acknowledgement requested

**Resource Name:** Collaborative Computing Project for NMR

**Resource ID:** SCR\_016983

**Alternate URLs:** <https://sourceforge.net/projects/ccpn/>

**License:** GNU GPL, CCPN licence

**Record Creation Time:** 20220129T080333+0000

**Record Last Update:** 20260805T044402+0000

---

## Ratings and Alerts

No rating or validation information has been found for Collaborative Computing Project for NMR.

No alerts have been found for Collaborative Computing Project for NMR.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Baskaran K, et al. (2024) Restraint Validation of Biomolecular Structures Determined by NMR in the Protein Data Bank. bioRxiv : the preprint server for biology.

Goretzki B, et al. (2024) Dual BACH1 regulation by complementary SCF-type E3 ligases. Cell, 187(26), 7585.

Estelle AB, et al. (2022) Native state fluctuations in a peroxiredoxin active site match motions needed for catalysis. Structure (London, England : 1993), 30(2), 278.

Boisvert O, et al. (2022) Zinc Fingers 10 and 11 of Miz-1 undergo conformational exchange to achieve specific DNA binding. Structure (London, England : 1993), 30(4), 623.

Wu H, et al. (2022) Structural characterization of a dimerization interface in the CD28 transmembrane domain. Structure (London, England : 1993), 30(6), 803.

Zacharchenko T, et al. (2022) Structural basis of Apt48 inhibition of the BCL6 BTB domain. Structure (London, England : 1993), 30(3), 396.

Ludzia P, et al. (2021) Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. *Structure* (London, England : 1993), 29(9), 1014.

Fonseca-Ornelas L, et al. (2021) Altered conformation of  $\alpha$ -synuclein drives dysfunction of synaptic vesicles in a synaptosomal model of Parkinson's disease. *Cell reports*, 36(1), 109333.

Weinhäupl K, et al. (2021) Architecture and assembly dynamics of the essential mitochondrial chaperone complex TIM9·10·12. *Structure* (London, England : 1993), 29(9), 1065.

Sicorello A, et al. (2021) Capturing the Conformational Ensemble of the Mixed Folded Polyglutamine Protein Ataxin-3. *Structure* (London, England : 1993), 29(1), 70.

Karami Y, et al. (2021) Computational and biochemical analysis of type IV pilus dynamics and stability. *Structure* (London, England : 1993), 29(12), 1397.

Gomara MJ, et al. (2020) Importance of structure-based studies for the design of a novel HIV-1 inhibitor peptide. *Scientific reports*, 10(1), 14430.

Rivière G, et al. (2020) NMR Characterization of the Influence of Zinc(II) Ions on the Structural and Dynamic Behavior of the New Delhi Metallo- $\beta$ -Lactamase-1 and on the Binding with Flavonols as Inhibitors. *ACS omega*, 5(18), 10466.

Dekoninck K, et al. (2020) Defining the function of OmpA in the Rcs stress response. *eLife*, 9.

Li M, et al. (2019) Surface-Binding to Cardiolipin Nanodomains Triggers Cytochrome c Pro-apoptotic Peroxidase Activity via Localized Dynamics. *Structure* (London, England : 1993), 27(5), 806.

Ji Z, et al. (2019) Kibra Modulates Learning and Memory via Binding to Dendrin. *Cell reports*, 26(8), 2064.

Yan R, et al. (2019) The Structure of the Pro-domain of Mouse proNGF in Contact with the NGF Domain. *Structure* (London, England : 1993), 27(1), 78.

Slack RL, et al. (2019) Conformational Changes in HIV-1 Reverse Transcriptase that Facilitate Its Maturation. *Structure* (London, England : 1993), 27(10), 1581.

Bardiaux B, et al. (2019) Structure and Assembly of the Enterohemorrhagic *Escherichia coli* Type 4 Pilus. *Structure* (London, England : 1993), 27(7), 1082.

Newcomer RL, et al. (2019) The phage  $\lambda$  capsid decoration protein has a novel OB-fold and an unusual capsid binding strategy. *eLife*, 8.