

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

Crystallography and NMR System (CNS)

RRID:SCR_014223

Type: Tool

Proper Citation

Crystallography and NMR System (CNS) (RRID:SCR_014223)

Resource Information

URL: <http://cns-online.org/v1.2/>

Proper Citation: Crystallography and NMR System (CNS) (RRID:SCR_014223)

Description: Software designed to provide a multi-level hierarchical approach for the most commonly used algorithms in macromolecular structure determination. Features include heavy atom searching, experimental phasing (including MAD and MIR), density modification, crystallographic refinement with maximum likelihood targets, and NMR structure calculation using NOEs, J-coupling, chemical shift, and dipolar coupling data. Modules, libraries, utility programs, tutorials, and a syntax manual are available on the website.

Abbreviations: CNS

Synonyms: Crystallography and NMR System

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

Defining Citation: [PMID:9757107](#)

Keywords: structure determination, software suite, macromolecular structure determination, data visualization software, bio.tools

Availability: Available to academic institutions, Request form must be submitted

Resource Name: Crystallography and NMR System (CNS)

Resource ID: SCR_014223

Alternate IDs: biotools:cnssolve

Alternate URLs: <https://bio.tools/cnssolve>

License: License for non-profit institutions is available at <http://cns-online.org/v1.2/>

Record Creation Time: 20220129T080319+0000

Record Last Update: 20260728T043436+0000

Ratings and Alerts

No rating or validation information has been found for Crystallography and NMR System (CNS).

No alerts have been found for Crystallography and NMR System (CNS).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Nishio S, et al. (2024) ZP2 cleavage blocks polyspermy by modulating the architecture of the egg coat. *Cell*, 187(6), 1440.

van Dorp S, et al. (2021) Conformational dynamics of auto-inhibition in the ER calcium sensor STIM1. *eLife*, 10.

Svidritskiy E, et al. (2019) Extensive ribosome and RF2 rearrangements during translation termination. *eLife*, 8.

Ramesh K, et al. (2018) Homologous Lympho-Epithelial Kazal-type Inhibitor Domains Delay Blood Coagulation by Inhibiting Factor X and XI with Differential Specificity. *Structure (London, England : 1993)*, 26(9), 1178.

Saio T, et al. (2018) Oligomerization of a molecular chaperone modulates its activity. *eLife*, 7.

Svidritskiy E, et al. (2018) Conformational Control of Translation Termination on the 70S Ribosome. *Structure (London, England : 1993)*, 26(6), 821.

Wasmuth EV, et al. (2017) Structure and reconstitution of yeast Mpp6-nuclear exosome complexes reveals that Mpp6 stimulates RNA decay and recruits the Mtr4 helicase. *eLife*, 6.

Joshi A, et al. (2014) Solution and crystal structures of a C-terminal fragment of the neuronal isoform of the polypyrimidine tract binding protein (nPTB). *PeerJ*, 2, e305.