Resource Summary Report

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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/

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Description: Software designed to provide a multi-level hierachical 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 processing software, data visualization software, software application, software resource, 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/

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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 PRECISE-TBI .

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.