

Resource Summary Report

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Integrative Modeling Platform

RRID:SCR_002982

Type: Tool

Proper Citation

Integrative Modeling Platform (RRID:SCR_002982)

Resource Information

URL: <http://integrativemodeling.org/>

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Description: An open source C++ and Python toolbox for solving complex modeling problems, and a number of applications for tackling some common problems in a user-friendly way. Its broad goal is to contribute to a comprehensive structural characterization of biomolecules ranging in size and complexity from small peptides to large macromolecular assemblies, by integrating data from diverse biochemical and biophysical experiments. It can also be used from the Chimera molecular modeling system, or via one of several web applications.

Abbreviations: IMP

Synonyms: IMP - the Integrative Modeling Platform, Integrative Modeling Platform (IMP), IMP the Integrative Modeling Platform

Resource Type: software resource, software toolkit

Defining Citation: [PMID:22272186](#)

Keywords: integrative modeling, structure determination, hybrid modeling, macromolecular assembly, c++, python, peptide, biomolecule, model, structural characterization, structure

Funding: NIGMS R01 GM083960

Availability: GNU Lesser General Public License, v2.1 or later, Acknowledgement requested, GNU General Public License

Resource Name: Integrative Modeling Platform

Resource ID: SCR_002982

Alternate IDs: SciRes_000187

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250519T204904+0000

Ratings and Alerts

No rating or validation information has been found for Integrative Modeling Platform.

No alerts have been found for Integrative Modeling Platform.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 49 mentions in open access literature.

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

Ketaren NE, et al. (2024) Nanobody repertoire generated against the spike protein of ancestral SARS-CoV-2 remains efficacious against the rapidly evolving virus. eLife, 12.

Zhang Y, et al. (2024) A new discrete-geometry approach for integrative docking of proteins using chemical crosslinks. bioRxiv : the preprint server for biology.

Clark T, et al. (2024) Cell Maps for Artificial Intelligence: AI-Ready Maps of Human Cell Architecture from Disease-Relevant Cell Lines. bioRxiv : the preprint server for biology.

Singh D, et al. (2024) The molecular architecture of the nuclear basket. Cell, 187(19), 5267.

Arvindekar S, et al. (2024) Optimizing representations for integrative structural modeling using Bayesian model selection. Bioinformatics (Oxford, England), 40(3).

Singh D, et al. (2024) The Molecular Architecture of the Nuclear Basket. bioRxiv : the preprint server for biology.

Pasani S, et al. (2024) The molecular architecture of the desmosomal outer dense plaque by integrative structural modeling. *Protein science : a publication of the Protein Society*, 33(12), e5217.

Latham AP, et al. (2024) Integrative spatiotemporal modeling of biomolecular processes: application to the assembly of the Nuclear Pore Complex. *bioRxiv : the preprint server for biology*.

Ketaren NE, et al. (2023) Nanobody repertoire generated against the spike protein of ancestral SARS-CoV-2 remains efficacious against the rapidly evolving virus. *bioRxiv : the preprint server for biology*.

Arvindekar S, et al. (2023) Optimizing representations for integrative structural modeling using Bayesian model selection. *bioRxiv : the preprint server for biology*.

Otsuka S, et al. (2023) A quantitative map of nuclear pore assembly reveals two distinct mechanisms. *Nature*, 613(7944), 575.

Pasani S, et al. (2023) The molecular architecture of the desmosomal outer dense plaque by integrative structural modeling. *bioRxiv : the preprint server for biology*.

Rafiei A, et al. (2022) Doublecortin engages the microtubule lattice through a cooperative binding mode involving its C-terminal domain. *eLife*, 11.

Akey CW, et al. (2022) Comprehensive structure and functional adaptations of the yeast nuclear pore complex. *Cell*, 185(2), 361.

Brilot AF, et al. (2021) CM1-driven assembly and activation of yeast γ -tubulin small complex underlies microtubule nucleation. *eLife*, 10.

Mast FD, et al. (2021) Nanobody Repertoires for Exposing Vulnerabilities of SARS-CoV-2. *bioRxiv : the preprint server for biology*.

Ziemianowicz DS, et al. (2021) IMProv: A Resource for Cross-link-Driven Structure Modeling that Accommodates Protein Dynamics. *Molecular & cellular proteomics : MCP*, 20, 100139.

Hepburn M, et al. (2021) The active DNA-PK holoenzyme occupies a tensed state in a staggered synaptic complex. *Structure (London, England : 1993)*, 29(5), 467.

Sali A, et al. (2021) From integrative structural biology to cell biology. *The Journal of biological chemistry*, 296, 100743.

Kaake RM, et al. (2021) Characterization of an A3G-VifHIV-1-CRL5-CBF γ Structure Using a Cross-linking Mass Spectrometry Pipeline for Integrative Modeling of Host-Pathogen Complexes. *Molecular & cellular proteomics : MCP*, 20, 100132.