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

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

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260912T200229+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 55 mentions in open access literature.

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

Nde J, et al. (2026) Multicomplex Integrative Structural Modeling of a Human Histone Deacetylase Interactome. bioRxiv : the preprint server for biology.

Mondal D, et al. (2025) Recognizing amino acid sidechains in a medium resolution cryo-electron density map. bioRxiv : the preprint server for biology.

Latham AP, et al. (2025) Integrative spatiotemporal modeling of biomolecular processes: Application to the assembly of the nuclear pore complex. Proceedings of the National Academy of Sciences of the United States of America, 122(11), e2415674122.

Schaffer LV, et al. (2025) Multimodal cell maps as a foundation for structural and functional genomics. Nature, 642(8066), 222.

Kozai T, et al. (2025) Karyopherins remodel the dynamic organization of the nuclear pore complex transport barrier. Nature cell biology, 27(12), 2089.

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

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.

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. Cell, 187(19), 5267.

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.

Liu X, et al. (2024) An integrated structural model of the DNA damage-responsive H3K4me3 binding WDR76:SPIN1 complex with the nucleosome. Proceedings of the National Academy of Sciences of the United States of America, 121(33), e2318601121.

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.