

Resource Summary Report

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Structural Biology Grid

RRID:SCR_003511

Type: Tool

Proper Citation

Structural Biology Grid (RRID:SCR_003511)

Resource Information

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

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Description: Computing resources structural biologists need to discover the shapes of the molecules of life, it provides access to web-enabled structural biology applications, data sharing facilities, biological data sets, and other resources valuable to the computational structural biology community. Consortium includes X-ray crystallography, NMR and electron microscopy laboratories worldwide. SBGrid Service Center is located at Harvard Medical School. SBGrid's NIH-compliant Service Center supports SBGrid operations and provides members with access to Software Maintenance, Computing Access, and Training. Consortium benefits include: * remote management of your customized collection of structural biology applications on Linux and Mac workstations; * access to commercial applications exclusively licensed to members of the Consortium, such as NMRPipe, Schrodinger Suite (limited tokens) and the Incentive version of Pymol; remote management of supporting scientific applications (e.g., bioinformatics, computational chemistry and utilities); * access to SBGrid seminars and events; and * advice about hardware configurations, operating system installations and high performance computing. Membership is restricted to academic/non-profit research laboratories that use X-ray crystallography, 2D crystallography, NMR, EM, tomography and other experimental structural biology technologies in their research. Most new members are fully integrated with SBGrid within 2 weeks of the initial application.

Abbreviations: SBGrid

Synonyms: SBGrid Software Consortium, SBGrid Science Portal, SBGrid Consortium

Resource Type: computational hosting, data set, storage service resource, data repository, service resource, data or information resource

Defining Citation: [PMID:22514186](#)

Keywords: structure, x-ray crystallography, nuclear magnetic resonance, electron microscopy, structural biology, software application, computation, chemistry, meeting, software service, molecule, data sharing, biomedical

Funding: NSF

Availability: Membership is restricted to academic/non-profit research laboratories that use X-ray crystallography, 2D crystallography, NMR, EM, Tomography and other experimental structural biology technologies in their research., The community can contribute to this resource

Resource Name: Structural Biology Grid

Resource ID: SCR_003511

Alternate IDs: nif-0000-37641, r3d100010234

Alternate URLs: <https://doi.org/10.17616/R3NS3R>

Old URLs: <http://sbgrid.org/index.php>

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260805T044055+0000

Ratings and Alerts

No rating or validation information has been found for Structural Biology Grid.

No alerts have been found for Structural Biology Grid.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 56 mentions in open access literature.

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

Li S, et al. (2025) The structure of basal body inner junctions from Tetrahymena revealed by electron cryo-tomography. The EMBO journal, 44(7), 1975.

Jeong TK, et al. (2025) CODANIN-1 sequesters ASF1 by using a histone H3 mimic helix to regulate the histone supply. Nature communications, 16(1), 2181.

Carpentier R, et al. (2025) Structure of the Huntingtin F-actin complex reveals its role in cytoskeleton organization. Science advances, 11(38), eadw4124.

Flowers J, et al. (2024) Expanding Automated Multiconformer Ligand Modeling to Macrocycles and Fragments. *bioRxiv : the preprint server for biology*.

Abe KM, et al. (2024) Small LEA proteins mitigate air-water interface damage to fragile cryo-EM samples during plunge freezing. *Nature communications*, 15(1), 7705.

Wankowicz SA, et al. (2024) Automated multiconformer model building for X-ray crystallography and cryo-EM. *eLife*, 12.

David L, et al. (2024) NINJ1 mediates plasma membrane rupture by cutting and releasing membrane disks. *Cell*, 187(9), 2224.

Dong Y, et al. (2024) Structural transitions enable interleukin-18 maturation and signaling. *Immunity*, 57(7), 1533.

Kroon-Batenburg LMJ, et al. (2023) Making your raw data available to the macromolecular crystallography community. *Acta crystallographica. Section F, Structural biology communications*, 79(Pt 10), 267.

Abhiraman GC, et al. (2023) A structural blueprint for interleukin-21 signal modulation. *Cell reports*, 42(6), 112657.

Hajam IA, et al. (2023) Functional divergence of a bacterial enzyme promotes healthy or acneic skin. *Nature communications*, 14(1), 8061.

Tsutsumi N, et al. (2023) Structure of the thrombopoietin-MPL receptor complex is a blueprint for biasing hematopoiesis. *Cell*, 186(19), 4189.

Rouleau-Turcotte ??, et al. (2022) Captured snapshots of PARP1 in the active state reveal the mechanics of PARP1 allostery. *Molecular cell*, 82(16), 2939.

Heo Y, et al. (2022) Cryo-EM structure of the human somatostatin receptor 2 complex with its agonist somatostatin delineates the ligand-binding specificity. *eLife*, 11.

Kucharska I, et al. (2022) Structural basis of Plasmodium vivax inhibition by antibodies binding to the circumsporozoite protein repeats. *eLife*, 11.

Yen M, et al. (2022) Facile discovery of surrogate cytokine agonists. *Cell*, 185(8), 1414.

Sever N, et al. (2021) Mechanism of Lamellar Body Formation by Lung Surfactant Protein B. *Molecular cell*, 81(1), 49.

Lilic M, et al. (2021) Structural basis of transcriptional activation by the Mycobacterium tuberculosis intrinsic antibiotic-resistance transcription factor WhiB7. *Molecular cell*, 81(14), 2875.

Sharif H, et al. (2021) Dipeptidyl peptidase 9 sets a threshold for CARD8 inflammasome formation by sequestering its active C-terminal fragment. *Immunity*, 54(7), 1392.

Kelly CM, et al. (2021) The hypervariable region of atlastin-1 is a site for intrinsic and extrinsic regulation. *The Journal of cell biology*, 220(11).