

# 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/>

**Proper Citation:** Structural Biology Grid (RRID:SCR\_003511)

**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 or information resource, data repository, data set, service resource, storage service 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:** 20260905T132505+0000

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## Ratings and Alerts

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

No alerts have been found for Structural Biology Grid.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 60 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

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.

Pisa R, et al. (2025) Lipid bilayer thinning near a ubiquitin ligase selects ER membrane proteins for degradation. bioRxiv : the preprint server for biology.

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

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.

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

Sanchez JC, et al. (2024) High-Resolution Cryo-EM Structure Determination of ??-synuclein - A Prototypical Amyloid Fibril. *bioRxiv : the preprint server for biology*.

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.

Wankowicz SA, et al. (2023) Uncovering Protein Ensembles: Automated Multiconformer Model Building for X-ray Crystallography and Cryo-EM. *bioRxiv : the preprint server for biology*.

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.