# **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:** storage service resource, data set, data or information resource, service resource, computational hosting, data repository

**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

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

**Record Creation Time:** 20220129T080219+0000

Record Last Update: 20250509T055615+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 53 mentions in open access literature.

**Listed below are recent publications.** The full list is available at <u>dkNET</u>.

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.

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 É, et al. (2022) Captured snapshots of PARP1 in the active state reveal the mechanics of PARP1 allostery. Molecular cell, 82(16), 2939.

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

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.

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

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.

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.

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).

Raman S, et al. (2021) A GPC2 antibody-drug conjugate is efficacious against neuroblastoma and small-cell lung cancer via binding a conformational epitope. Cell reports. Medicine, 2(7), 100344.

Gui M, et al. (2021) De novo identification of mammalian ciliary motility proteins using cryo-EM. Cell, 184(23), 5791.

Caillat C, et al. (2021) Structure of HIV-1 gp41 with its membrane anchors targeted by neutralizing antibodies. eLife, 10.