Resource Summary Report

Generated by T1D on Jul 28, 2026

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

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: 20260728T043147+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 T1D .

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.

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 ??, 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).