

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

Bsoft

RRID:SCR_016503

Type: Tool

Proper Citation

Bsoft (RRID:SCR_016503)

Resource Information

URL: <https://lsbr.niams.nih.gov/bsoft/>

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Description: Software package and a platform for the processing of electron micrographs in structural biology. Supports different image file formats used in electron microscopy (including MRC, SPIDER, IMAGIC, SUPRIM, and PIF)., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: Bsoft

Synonyms: Bernard's Software

Resource Type: image processing software, software resource, software application, data processing software

Defining Citation: [DOI:10.1006/jsbi.2001.4339](https://doi.org/10.1006/jsbi.2001.4339)

Keywords: image, processing, structural, biology, electron, microscopy, different, format, support

Funding: European Union EC BIO4CT960472;
NIAMS

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Bsoft

Resource ID: SCR_016503

License: GPL

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260804T043649+0000

Ratings and Alerts

No rating or validation information has been found for Bsoft.

No alerts have been found for Bsoft.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Lopez AJ, et al. (2023) Structure and function of Plasmodium actin II in the parasite mosquito stages. PLoS pathogens, 19(3), e1011174.

Tan ZY, et al. (2023) Heterogeneous non-canonical nucleosomes predominate in yeast cells in situ. eLife, 12.

Vahokoski J, et al. (2022) High-resolution structures of malaria parasite actomyosin and actin filaments. PLoS pathogens, 18(4), e1010408.

Kayama Y, et al. (2021) Below 3 Å structure of apoferritin using a multipurpose TEM with a side entry cryoholder. Scientific reports, 11(1), 8395.

Arimura Y, et al. (2021) Structural features of nucleosomes in interphase and metaphase chromosomes. Molecular cell, 81(21), 4377.

Khanra N, et al. (2021) Architecture and structural dynamics of the heteromeric GluK2/K5 kainate receptor. eLife, 10.

Tsutsumi N, et al. (2021) Structural basis for the constitutive activity and immunomodulatory properties of the Epstein-Barr virus-encoded G protein-coupled receptor BILF1. Immunity, 54(7), 1405.

Zhou BR, et al. (2021) Distinct Structures and Dynamics of Chromatosomes with Different Human Linker Histone Isoforms. Molecular cell, 81(1), 166.

Wang J, et al. (2020) Cryo-EM structures of PAC1 receptor reveal ligand binding mechanism. Cell research, 30(5), 436.

Jin W, et al. (2020) Structural Basis for pri-miRNA Recognition by Drosha. Molecular cell, 78(3), 423.

Isom GL, et al. (2020) LetB Structure Reveals a Tunnel for Lipid Transport across the Bacterial Envelope. Cell, 181(3), 653.

Yoder N, et al. (2020) The His-Gly motif of acid-sensing ion channels resides in a reentrant 'loop' implicated in gating and ion selectivity. *eLife*, 9.

Dedden D, et al. (2019) The Architecture of Talin1 Reveals an Autoinhibition Mechanism. *Cell*, 179(1), 120.

Krishna Kumar K, et al. (2019) Structure of a Signaling Cannabinoid Receptor 1-G Protein Complex. *Cell*, 176(3), 448.

Herzik MA, et al. (2019) A Multi-model Approach to Assessing Local and Global Cryo-EM Map Quality. *Structure (London, England : 1993)*, 27(2), 344.

Walter JD, et al. (2019) Cryo-EM structures and functional characterization of murine Slc26a9 reveal mechanism of uncoupled chloride transport. *eLife*, 8.

Svidritskiy E, et al. (2019) Extensive ribosome and RF2 rearrangements during translation termination. *eLife*, 8.

Gamerding M, et al. (2019) Early Scanning of Nascent Polypeptides inside the Ribosomal Tunnel by NAC. *Molecular cell*, 75(5), 996.

Ge J, et al. (2018) Structure of mouse protocadherin 15 of the stereocilia tip link in complex with LHFPL5. *eLife*, 7.

Phulera S, et al. (2018) Cryo-EM structure of the benzodiazepine-sensitive $\alpha 1\beta 2\gamma 2$ tri-heteromeric GABAA receptor in complex with GABA. *eLife*, 7.