

Resource Summary Report

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Leginon

RRID:SCR_016731

Type: Tool

Proper Citation

Leginon (RRID:SCR_016731)

Resource Information

URL: http://emg.nysbc.org/redmine/projects/leginon/wiki/Leginon_Homepage

Proper Citation: Leginon (RRID:SCR_016731)

Description: System designed for automated collection of images from a transmission electron microscope.

Resource Type: software application, service resource, data or information resource, data repository, data processing software, software resource, image acquisition software, storage service resource, portal, data acquisition software

Defining Citation: [PMID:15890530](#)

Keywords: automated, collection, acquisition, data, image, electron, microscope

Funding: NCRR RR17573;
NIGMS GM61939;
NSF DBI0352386;
NSF DBI9730056;
NSF DBI9904547

Availability: Free, Available for download, Freely available, Registration suggested

Resource Name: Leginon

Resource ID: SCR_016731

License: Apache License, Version 2.0

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260729T044422+0000

Ratings and Alerts

No rating or validation information has been found for Leginon.

No alerts have been found for Leginon.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 42 mentions in open access literature.

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

Abiona OM, et al. (2025) MERS-CoV spike vaccine-induced N-terminal domain-specific antibodies are more protective than receptor binding domain-specific antibodies. *iScience*, 28(2), 111632.

Schleich FA, et al. (2025) Vaccination of nonhuman primates elicits a broadly neutralizing antibody lineage targeting a quaternary epitope on the HIV-1 Env trimer. *Immunity*, 58(6), 1598.

Dederer V, et al. (2024) A designed ankyrin-repeat protein that targets Parkinson's disease-associated LRRK2. *The Journal of biological chemistry*, 300(7), 107469.

Reimer JM, et al. (2023) Structure of LRRK1 and mechanisms of autoinhibition and activation. *Nature structural & molecular biology*, 30(11), 1735.

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

Huang P, et al. (2022) Structural basis for catalyzed assembly of the Sonic hedgehog-Patched1 signaling complex. *Developmental cell*, 57(5), 670.

Van Tilbeurgh M, et al. (2022) Innate cell markers that predict anti-HIV neutralizing antibody titers in vaccinated macaques. *Cell reports. Medicine*, 3(10), 100751.

Snead DM, et al. (2022) Structural basis for Parkinson's disease-linked LRRK2's binding to microtubules. *Nature structural & molecular biology*, 29(12), 1196.

Melville Z, et al. (2022) High-resolution structure of the membrane-embedded skeletal muscle ryanodine receptor. *Structure (London, England : 1993)*, 30(1), 172.

Puno MR, et al. (2022) Structural basis for RNA surveillance by the human nuclear exosome targeting (NEXT) complex. *Cell*, 185(12), 2132.

Sahoo A, et al. (2022) Structure-guided changes at the V2 apex of HIV-1 clade C trimer enhance elicitation of autologous neutralizing and broad V1V2-scaffold antibodies. *Cell reports*, 38(9), 110436.

Kirchdoerfer RN, et al. (2021) Structure and immune recognition of the porcine epidemic diarrhea virus spike protein. *Structure* (London, England : 1993), 29(4), 385.

Jiang D, et al. (2021) Open-state structure and pore gating mechanism of the cardiac sodium channel. *Cell*, 184(20), 5151.

Wisedchaisri G, et al. (2021) Structural Basis for High-Affinity Trapping of the NaV1.7 Channel in Its Resting State by Tarantula Toxin. *Molecular cell*, 81(1), 38.

Nikolay R, et al. (2021) Snapshots of native pre-50S ribosomes reveal a biogenesis factor network and evolutionary specialization. *Molecular cell*, 81(6), 1200.

Walls AC, et al. (2020) Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein. *Cell*, 181(2), 281.

Oh S, et al. (2020) Gating and selectivity mechanisms for the lysosomal K⁺ channel TMEM175. *eLife*, 9.

Wang C, et al. (2020) Structures reveal gatekeeping of the mitochondrial Ca²⁺ uniporter by MICU1-MICU2. *eLife*, 9.

Hou X, et al. (2020) Cryo-EM structure of the calcium release-activated calcium channel Orai in an open conformation. *eLife*, 9.

Kieuvongngam V, et al. (2020) Structural basis of substrate recognition by a polypeptide processing and secretion transporter. *eLife*, 9.