

Resource Summary Report

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Appion Package

RRID:SCR_016734

Type: Tool

Proper Citation

Appion Package (RRID:SCR_016734)

Resource Information

URL: http://emg.nysbc.org/redmine/projects/appion/wiki/Appion_Home

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Description: Software package for processing and analysis of EM images. Appion is integrated with Leginon data acquisition but can also be used stand-alone after uploading images (either digital or scanned micrographs) or particle stacks using a set of provided tools.

Abbreviations: Appion

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

Defining Citation: [PMID:19263523](#)

Keywords: processing, analysis, electron, microscope, image

Funding: ARCS ;
NCRR RR023093;
NCRR RR17573

Availability: Free, Available for download, Freely available

Resource Name: Appion Package

Resource ID: SCR_016734

Alternate URLs: <http://www.appion.org>

License: Apache Open Source License, Version 2.0

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260912T195844+0000

Ratings and Alerts

No rating or validation information has been found for Appion Package.

No alerts have been found for Appion Package.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

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.

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.

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.

Wang X, et al. (2020) Large domain movements through the lipid bilayer mediate substrate release and inhibition of glutamate transporters. *eLife*, 9.

Gilchuk P, et al. (2020) Analysis of a Therapeutic Antibody Cocktail Reveals Determinants for Cooperative and Broad Ebolavirus Neutralization. *Immunity*, 52(2), 388.

Wang N, et al. (2019) Structural Definition of a Neutralization-Sensitive Epitope on the MERS-CoV S1-NTD. *Cell reports*, 28(13), 3395.

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.

Bangaru S, et al. (2019) A Site of Vulnerability on the Influenza Virus Hemagglutinin Head Domain Trimer Interface. *Cell*, 177(5), 1136.

Jiang S, et al. (2019) Interplay between the Kinesin and Tubulin Mechanochemical Cycles Underlies Microtubule Tip Tracking by the Non-motile Ciliary Kinesin Kif7. *Developmental cell*, 49(5), 711.

Gilchuk IM, et al. (2019) Influenza H7N9 Virus Neuraminidase-Specific Human Monoclonal Antibodies Inhibit Viral Egress and Protect from Lethal Influenza Infection in Mice. *Cell host & microbe*, 26(6), 715.

Puchades C, et al. (2019) Unique Structural Features of the Mitochondrial AAA+ Protease AFG3L2 Reveal the Molecular Basis for Activity in Health and Disease. *Molecular cell*, 75(5), 1073.

Ma M, et al. (2019) Structure of the Decorated Ciliary Doublet Microtubule. *Cell*, 179(4), 909.

Chang C, et al. (2019) Bidirectional Control of Autophagy by BECN1 BARA Domain Dynamics. *Molecular cell*, 73(2), 339.

Zhu X, et al. (2019) Structural Basis of Protection against H7N9 Influenza Virus by Human Anti-N9 Neuraminidase Antibodies. *Cell host & microbe*, 26(6), 729.

Borst AJ, et al. (2018) Germline VRC01 antibody recognition of a modified clade C HIV-1 envelope trimer and a glycosylated HIV-1 gp120 core. *eLife*, 7.

Dionne G, et al. (2018) Mechanotransduction by PCDH15 Relies on a Novel cis-Dimeric Architecture. *Neuron*, 99(3), 480.