

cisTEM, user-friendly software for single-particle image

ELife

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Protein structural biology using cell-free platform from wheat germ. <i>Advanced Structural and Chemical Imaging</i> , 2018, 4, 13.	4.0	21
3	Mechanisms for Zinc and Proton Inhibition of the GluN1/GluN2A NMDA Receptor. <i>Cell</i> , 2018, 175, 1520-1532.e15.	13.5	85
4	Structures and gating mechanism of human TRPM2. <i>Science</i> , 2018, 362, .	6.0	129
5	Structural Basis of the Proton Sensitivity of Human GluN1-GluN2A NMDA Receptors. <i>Cell Reports</i> , 2018, 25, 3582-3590.e4.	2.9	47
6	Advances in image processing for single-particle analysis by electron cryomicroscopy and challenges ahead. <i>Current Opinion in Structural Biology</i> , 2018, 52, 127-145.	2.6	15
7	Cryo-EM Visualization of an Active High Open Probability CFTR Anion Channel. <i>Biochemistry</i> , 2018, 57, 6234-6246.	1.2	44
8	Architecture of the TRPM2 channel and its activation mechanism by ADP-ribose and calcium. <i>Nature</i> , 2018, 562, 145-149.	13.7	146
9	Reducing effects of particle adsorption to the air-water interface in cryo-EM. <i>Nature Methods</i> , 2018, 15, 793-795.	9.0	167
10	Assessing the quality of single particle reconstructions by atomic model building. <i>Journal of Structural Biology</i> , 2018, 204, 276-282.	1.3	8
11	Cryo-EM structure of the hibernating <i>Thermus thermophilus</i> 100S ribosome reveals a protein-mediated dimerization mechanism. <i>Nature Communications</i> , 2018, 9, 4179.	5.8	34
12	emClarity: software for high-resolution cryo-electron tomography and subtomogram averaging. <i>Nature Methods</i> , 2018, 15, 955-961.	9.0	206
13	Sub-2Å... Ewald curvature corrected structure of an AAV2 capsid variant. <i>Nature Communications</i> , 2018, 9, 3628.	5.8	73
14	Structural Basis for the RNA-Guided Ribonuclease Activity of CRISPR-Cas13d. <i>Cell</i> , 2018, 175, 212-223.e17.	13.5	195
15	Characterization of Membrane Proteins Using Cryo-Electron Microscopy. <i>Current Protocols in Protein Science</i> , 2018, 94, e72.	2.8	1
16	Membrane protein structural biology in the era of single particle cryo-EM. <i>Current Opinion in Structural Biology</i> , 2018, 52, 58-63.	2.6	122
17	Mechanism of premature translation termination on a sense codon. <i>Journal of Biological Chemistry</i> , 2018, 293, 12472-12479.	1.6	21
18	Processing apoferritin with the Appion pipeline. <i>Journal of Structural Biology</i> , 2018, 204, 85-89.	1.3	3
19	Cryo-EM structure of the polycystin 2-11 ion channel. <i>ELife</i> , 2018, 7, .	2.8	43

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20	Structural basis for the regulation of inositol trisphosphate receptors by Ca ²⁺ and IP ₃ . <i>Nature Structural and Molecular Biology</i> , 2018, 25, 660-668.	3.6	89
21	Cryo-EM structures of fungal and metazoan mitochondrial calcium uniporters. <i>Nature</i> , 2018, 559, 580-584.	13.7	129
22	Atomic Resolution Cryo-EM Structure of β -Galactosidase. <i>Structure</i> , 2018, 26, 848-856.e3.	1.6	115
23	Structure and Conformational Dynamics of a COMPASS Histone H3K4 Methyltransferase Complex. <i>Cell</i> , 2018, 174, 1117-1126.e12.	13.5	84
24	Cryo-EM for Small Molecules Discovery, Design, Understanding, and Application. <i>Cell Chemical Biology</i> , 2018, 25, 1318-1325.	2.5	63
25	Cryo-EM in drug discovery: achievements, limitations and prospects. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 471-492.	21.5	304
26	Structural Analysis of <i>Helicobacter pylori</i> VacA Reveals Insights into Oligomerization. <i>Microscopy and Microanalysis</i> , 2019, 25, 1290-1291.	0.2	0
27	Structural determination of the large photosystem II "light-harvesting complex II supercomplex of <i>Chlamydomonas reinhardtii</i> using nonionic amphipol. <i>Journal of Biological Chemistry</i> , 2019, 294, 15003-15013.	1.6	35
28	Securing the future of research computing in the biosciences. <i>PLoS Computational Biology</i> , 2019, 15, e1006958.	1.5	6
29	Tumor Suppressor p53-Mediated Structural Reorganization of the Transcriptional Coactivator p300. <i>Biochemistry</i> , 2019, 58, 3434-3443.	1.2	16
30	Cryo-EM Studies of TMEM16F Calcium-Activated Ion Channel Suggest Features Important for Lipid Scrambling. <i>Cell Reports</i> , 2019, 28, 567-579.e4.	2.9	76
31	Structures of autoinhibited and polymerized forms of CARD9 reveal mechanisms of CARD9 and CARD11 activation. <i>Nature Communications</i> , 2019, 10, 3070.	5.8	33
32	Structures of the Rhodopsin-Transducin Complex: Insights into G-Protein Activation. <i>Molecular Cell</i> , 2019, 75, 781-790.e3.	4.5	74
33	Evolutionary compaction and adaptation visualized by the structure of the dormant microsporidian ribosome. <i>Nature Microbiology</i> , 2019, 4, 1798-1804.	5.9	60
34	Resting-State Structure and Gating Mechanism of a Voltage-Gated Sodium Channel. <i>Cell</i> , 2019, 178, 993-1003.e12.	13.5	142
35	Interpretation of medium resolution cryoEM maps of multi-protein complexes. <i>Current Opinion in Structural Biology</i> , 2019, 58, 166-174.	2.6	18
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39	Cryo-EM Structure of the Human FLCN-FNIP2-Rag-Ragulator Complex. <i>Cell</i> , 2019, 179, 1319-1329.e8.	13.5	98
40	Structural Basis of H2B Ubiquitination-Dependent H3K4 Methylation by COMPASS. <i>Molecular Cell</i> , 2019, 76, 712-723.e4.	4.5	80
41	Cryo-EM reveals active site coordination within a multienzyme pre-rRNA processing complex. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 830-839.	3.6	23
42	Structure of the Centromere Binding Factor 3 Complex from <i>Kluyveromyces lactis</i> . <i>Journal of Molecular Biology</i> , 2019, 431, 4444-4454.	2.0	3
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51	Capabilities of the Falcon III detector for single-particle structure determination. <i>Ultramicroscopy</i> , 2019, 203, 145-154.	0.8	21
52	A small-molecule inhibitor of C5 complement protein. <i>Nature Chemical Biology</i> , 2019, 15, 666-668.	3.9	17
53	In situ Structure of Rotavirus VP1 RNA-Dependent RNA Polymerase. <i>Journal of Molecular Biology</i> , 2019, 431, 3124-3138.	2.0	45
54	The big picture of chromatin biology by cryo-EM. <i>Current Opinion in Structural Biology</i> , 2019, 58, 76-87.	2.6	12
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63	Cryo-EM Structure of Chikungunya Virus in Complex with the Mxra8 Receptor. <i>Cell</i> , 2019, 177, 1725-1737.e16.	13.5	104
64	The Structural Basis for the Binding of Repaglinide to the Pancreatic KATP Channel. <i>Cell Reports</i> , 2019, 27, 1848-1857.e4.	2.9	76
65	Cryo-Electron Microscopy Methodology: Current Aspects and Future Directions. <i>Trends in Biochemical Sciences</i> , 2019, 44, 837-848.	3.7	176
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75	Advances in domain and subunit localization technology for electron microscopy. <i>Biophysical Reviews</i> , 2019, 11, 149-155.	1.5	3
76	Different genetic and morphological outcomes for phages targeted by single or multiple CRISPR-Cas spacers. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180090.	1.8	24
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86	Structural basis of $\hat{\pm}$ -scorpion toxin action on Na ^v channels. <i>Science</i> , 2019, 363, .	6.0	139
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135	An Ultrahigh-Affinity Complement C4b-Specific Nanobody Inhibits In Vivo Assembly of the Classical Pathway Proconvertase. <i>Journal of Immunology</i> , 2020, 205, 1678-1694.	0.4	12
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