

New tools for automated high-resolution cryo-EM struc

ELife

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Structure of transcribing RNA polymerase II-nucleosome complex. <i>Nature Communications</i> , 2018, 9, 5432.	5.8	85
2	Inhibition of bacterial ubiquitin ligases by SidJ-calmodulin catalysed glutamylation. <i>Nature</i> , 2019, 572, 382-386.	13.7	98
3	CryoTEM with a Cold Field Emission Gun That Moves Structural Biology into a New Stage. <i>Microscopy and Microanalysis</i> , 2019, 25, 998-999.	0.2	45
4	T3S injectisome needle complex structures in four distinct states reveal the basis of membrane coupling and assembly. <i>Nature Microbiology</i> , 2019, 4, 2010-2019.	5.9	58
5	Imaging of Unstained DNA Origami Triangles with Electron Microscopy. <i>Small Methods</i> , 2019, 3, 1900393.	4.6	7
6	Cryo-EM structures capture the transport cycle of the P4-ATPase flippase. <i>Science</i> , 2019, 365, 1149-1155.	6.0	143
7	Structure and conformational plasticity of the intact <i>Thermus thermophilus</i> V/A-type ATPase. <i>Science</i> , 2019, 365, .	6.0	47
8	Atomic structures of an entire contractile injection system in both the extended and contracted states. <i>Nature Microbiology</i> , 2019, 4, 1885-1894.	5.9	45
9	Structural Basis for Tetherin Antagonism as a Barrier to Zoonotic Lentiviral Transmission. <i>Cell Host and Microbe</i> , 2019, 26, 359-368.e8.	5.1	26
10	Structural basis of Cullin 2 RING E3 ligase regulation by the COP9 signalosome. <i>Nature Communications</i> , 2019, 10, 3814.	5.8	40
11	Conformation space of a heterodimeric ABC exporter under turnover conditions. <i>Nature</i> , 2019, 571, 580-583.	13.7	185
12	Similarities and differences between native HIV-1 envelope glycoprotein trimers and stabilized soluble trimer mimetics. <i>PLoS Pathogens</i> , 2019, 15, e1007920.	2.1	61
13	Unique Structural Features of the Mitochondrial AAA+ Protease AFG3L2 Reveal the Molecular Basis for Activity in Health and Disease. <i>Molecular Cell</i> , 2019, 75, 1073-1085.e6.	4.5	58
14	Structural basis for transcription antitermination at bacterial intrinsic terminator. <i>Nature Communications</i> , 2019, 10, 3048.	5.8	18
15	Structure of the eukaryotic protein O-mannosyltransferase Pmt1-Pmt2 complex. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 704-711.	3.6	38
16	Structural basis of TFIIH activation for nucleotide excision repair. <i>Nature Communications</i> , 2019, 10, 2885.	5.8	112
17	Evolutionary compaction and adaptation visualized by the structure of the dormant microsporidian ribosome. <i>Nature Microbiology</i> , 2019, 4, 1798-1804.	5.9	60
18	Asymmetric analysis reveals novel virus capsid features. <i>Biophysical Reviews</i> , 2019, 11, 603-609.	1.5	14

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19	Structure of the <i>Helicobacter pylori</i> Cag type IV secretion system. <i>ELife</i> , 2019, 8, .	2.8	78
20	Interpretation of medium resolution cryoEM maps of multi-protein complexes. <i>Current Opinion in Structural Biology</i> , 2019, 58, 166-174.	2.6	18
21	A one-gate elevator mechanism for the human neutral amino acid transporter ASCT2. <i>Nature Communications</i> , 2019, 10, 3427.	5.8	76
22	Structure and mechanism of the cation-chloride cotransporter NKCC1. <i>Nature</i> , 2019, 572, 488-492.	13.7	89
23	Microfluidic protein isolation and sample preparation for high-resolution cryo-EM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 15007-15012.	3.3	41
24	Structure of the substrate-engaged SecA-SecY protein translocation machine. <i>Nature Communications</i> , 2019, 10, 2872.	5.8	55
25	Toxic Activation of an AAA+ Protease by the Antibacterial Drug Cyclomarin A. <i>Cell Chemical Biology</i> , 2019, 26, 1169-1179.e4.	2.5	36
26	Cryo-electron microscopy structure and analysis of the P-Rex1-G12I3 signaling scaffold. <i>Science Advances</i> , 2019, 5, eaax8855.	4.7	28
27	Structure of ribosome-bound azole-modified peptide phazolicin rationalizes its species-specific mode of bacterial translation inhibition. <i>Nature Communications</i> , 2019, 10, 4563.	5.8	45
28	Structural and functional insights into the tetrameric photosystem I from heterocyst-forming cyanobacteria. <i>Nature Plants</i> , 2019, 5, 1087-1097.	4.7	57
29	Cas9 Allosteric Inhibition by the Anti-CRISPR Protein AcrIIA6. <i>Molecular Cell</i> , 2019, 76, 922-937.e7.	4.5	44
30	Structural basis for the docking of mTORC1 on the lysosomal surface. <i>Science</i> , 2019, 366, 468-475.	6.0	132
31	Cryo-EM structure of the bacterial Ton motor subcomplex ExbB-ExbD provides information on structure and stoichiometry. <i>Communications Biology</i> , 2019, 2, 358.	2.0	60
32	Structure, Function, and Evolution of the <i>Pseudomonas aeruginosa</i> Lysine Decarboxylase LdcA. <i>Structure</i> , 2019, 27, 1842-1854.e4.	1.6	9
33	Structure and Function of the Proteasome Activator PA28 of the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Microscopy and Microanalysis</i> , 2019, 25, 1324-1325.	0.2	0
34	Stanford-SLAC Cryo-EM Center (S ² C ²). <i>Microscopy and Microanalysis</i> , 2019, 25, 2658-2659.	0.2	1
35	High-End Data Collection for Single-Particle Cryo-EM. <i>Microscopy and Microanalysis</i> , 2019, 25, 2688-2689.	0.2	0
36	A packing for A-form DNA in an icosahedral virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 22591-22597.	3.3	23

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37	Structure of the Decorated Ciliary Doublet Microtubule. <i>Cell</i> , 2019, 179, 909-922.e12.	13.5	186
38	Structural consequences of the interaction of RbgA with a 50S ribosomal subunit assembly intermediate. <i>Nucleic Acids Research</i> , 2019, 47, 10414-10425.	6.5	38
39	Dynamic modulation of the lipid translocation groove generates a conductive ion channel in Ca ²⁺ -bound nhTMEM16. <i>Nature Communications</i> , 2019, 10, 4972.	5.8	23
40	Conservative transcription in three steps visualized in a double-stranded RNA virus. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1023-1034.	3.6	33
41	Structural mechanism of a Rag GTPase activation checkpoint by the lysosomal folliculin complex. <i>Science</i> , 2019, 366, 971-977.	6.0	108
42	Cryo-EM Structure of the Human FLCN-FNIP2-Rag-Ragulator Complex. <i>Cell</i> , 2019, 179, 1319-1329.e8.	13.5	98
43	LDAF1 and Seipin Form a Lipid Droplet Assembly Complex. <i>Developmental Cell</i> , 2019, 51, 551-563.e7.	3.1	152
44	Structural Basis of H2B Ubiquitination-Dependent H3K4 Methylation by COMPASS. <i>Molecular Cell</i> , 2019, 76, 712-723.e4.	4.5	80
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47	Structures of a RAG-like transposase during cut-and-paste transposition. <i>Nature</i> , 2019, 575, 540-544.	13.7	30
48	CryoEM reconstruction approaches to resolve asymmetric features. <i>Advances in Virus Research</i> , 2019, 105, 73-91.	0.9	19
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50	Structure of a P element transposaseâ€“DNA complex reveals unusual DNA structures and GTP-DNA contacts. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1013-1022.	3.6	30
51	Structure and mechanism of mitochondrial proton-translocating transhydrogenase. <i>Nature</i> , 2019, 573, 291-295.	13.7	55
52	Atomic structure of the Epstein-Barr virus portal. <i>Nature Communications</i> , 2019, 10, 3891.	5.8	28
53	Visualizing structural transitions of ligand-dependent gating of the TRPM2 channel. <i>Nature Communications</i> , 2019, 10, 3740.	5.8	34
54	Structure and mechanogating of the mammalian tactile channel PIEZO2. <i>Nature</i> , 2019, 573, 225-229.	13.7	218

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56	Structural basis of nucleosome recognition and modification by MLL methyltransferases. <i>Nature</i> , 2019, 573, 445-449.	13.7	134
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58	Agonist Selectivity and Ion Permeation in the $\alpha 3 \beta 4$ Ganglionic Nicotinic Receptor. <i>Neuron</i> , 2019, 104, 501-511.e6.	3.8	131
59	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
60	Structure Determination by Single-Particle Cryo-Electron Microscopy: Only the Sky (and Intrinsic) Tj ETQq1 1 0.784314 rgBT /Overlock 1.8 50		
61	Structural basis of assembly of the human T cell receptor-CD3 complex. <i>Nature</i> , 2019, 573, 546-552.	13.7	218
62	Heparin-induced tau filaments are polymorphic and differ from those in Alzheimer's and Pick's diseases. <i>ELife</i> , 2019, 8, .	2.8	309
63	The cryo-EM structure of the acid activatable pore-forming immune effector Macrophage-expressed gene 1. <i>Nature Communications</i> , 2019, 10, 4288.	5.8	65
64	Filling Adeno-Associated Virus Capsids: Estimating Success by Cryo-Electron Microscopy. <i>Human Gene Therapy</i> , 2019, 30, 1449-1460.	1.4	25
65	Cryo-EM structure of a dimeric B-Raf:14-3-3 complex reveals asymmetry in the active sites of B-Raf kinases. <i>Science</i> , 2019, 366, 109-115.	6.0	127
66	The Architecture of Talin1 Reveals an Autoinhibition Mechanism. <i>Cell</i> , 2019, 179, 120-131.e13.	13.5	93
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68	Autoinhibition and activation mechanisms of the eukaryotic lipid flippase Drs2p-Cdc50p. <i>Nature Communications</i> , 2019, 10, 4142.	5.8	51
69	Tubulin lattice in cilia is in a stressed form regulated by microtubule inner proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19930-19938.	3.3	61
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71	Structural insights into the mechanism of human soluble guanylate cyclase. <i>Nature</i> , 2019, 574, 206-210.	13.7	102
72	Cryo-EM structure and dynamics of eukaryotic DNA polymerase ϵ holoenzyme. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 955-962.	3.6	40

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73	Structural Definition of a Neutralization-Sensitive Epitope on the MERS-CoV S1-NTD. <i>Cell Reports</i> , 2019, 28, 3395-3405.e6.	2.9	63
74	High-quality, high-throughput cryo-electron microscopy data collection via beam tilt and astigmatism-free beam-image shift. <i>Journal of Structural Biology</i> , 2019, 208, 107396.	1.3	91
75	Active site rearrangement and structural divergence in prokaryotic respiratory oxidases. <i>Science</i> , 2019, 366, 100-104.	6.0	90
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83	Structural and biochemical analyses of the nuclear pore complex component ELYS identify residues responsible for nucleosome binding. <i>Communications Biology</i> , 2019, 2, 163.	2.0	17
84	Cryo-EM reveals the structural basis of long-range electron transport in a cytochrome-based bacterial nanowire. <i>Communications Biology</i> , 2019, 2, 219.	2.0	120
85	The big picture of chromatin biology by cryo-EM. <i>Current Opinion in Structural Biology</i> , 2019, 58, 76-87.	2.6	12
86	Structure and autoregulation of a P4-ATPase lipid flippase. <i>Nature</i> , 2019, 571, 366-370.	13.7	126
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88	Iron-Sequestering Nanocompartments as Multiplexed Electron Microscopy Gene Reporters. <i>ACS Nano</i> , 2019, 13, 8114-8123.	7.3	33
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90	Immunization expands B cells specific to HIV-1 V3 glycan in mice and macaques. <i>Nature</i> , 2019, 570, 468-473.	13.7	145

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95	Structural basis for selective stalling of human ribosome nascent chain complexes by a drug-like molecule. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 501-509.	3.6	67
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105	Structure of the DNA-Bound Spacer Capture Complex of a Type II CRISPR-Cas System. <i>Molecular Cell</i> , 2019, 75, 90-101.e5.	4.5	35
106	Cryo-Electron Microscopy Methodology: Current Aspects and Future Directions. <i>Trends in Biochemical Sciences</i> , 2019, 44, 837-848.	3.7	176
107	Fusion of DARPIn to Aldolase Enables Visualization of Small Protein by Cryo-EM. <i>Structure</i> , 2019, 27, 1148-1155.e3.	1.6	32
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110	Structural basis for eIF2B inhibition in integrated stress response. <i>Science</i> , 2019, 364, 495-499.	6.0	91
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121	An allosteric mechanism for potent inhibition of human ATP-citrate lyase. <i>Nature</i> , 2019, 568, 566-570.	13.7	105
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146	Structural determinants of microtubule minus end preference in CAMSAP CCK domains. <i>Nature Communications</i> , 2019, 10, 5236.	5.8	36
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153	High-resolution cryo-EM structures of respiratory complex I: Mechanism, assembly, and disease. <i>Science Advances</i> , 2019, 5, eaax9484.	4.7	109
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1109	Inhibition of bacterial binding through dysfunction of bacterial adhesion pili. <i>Microscopy and Microanalysis</i> , 2021, 27, 828-831.	0.2	0
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