

# Current developments in *Coot* for macromolecular Cryo- $\mu$ microscopy and Crystallographic Data

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Current developments in <i>Coot</i> for macromolecular model building of Electron Cryo-EM microscopy and Crystallographic Data. <i>Protein Science</i> , 2020, 29, 1055-1064.	3.1	412
2	Neutralizing Antibody Responses Induced by HIV-1 Envelope Glycoprotein SOSIP Trimers Derived from Elite Neutralizers. <i>Journal of Virology</i> , 2020, 94, .	1.5	11
3	Single-particle cryo-EM at atomic resolution. <i>Nature</i> , 2020, 587, 152-156.	13.7	572
4	Elongational stalling activates mitoribosome-associated quality control. <i>Science</i> , 2020, 370, 1105-1110.	6.0	74
5	A tunable LIC1-adaptor interaction modulates dynein activity in a cargo-specific manner. <i>Nature Communications</i> , 2020, 11, 5695.	5.8	41
6	Three-Dimensional Structures of Carbohydrates and Where to Find Them. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7702.	1.8	22
7	Mapping the immunogenic landscape of near-native HIV-1 envelope trimers in non-human primates. <i>PLoS Pathogens</i> , 2020, 16, e1008753.	2.1	61
8	Structure of a human 48 <i>S</i> translational initiation complex. <i>Science</i> , 2020, 369, 1220-1227.	6.0	138
9	De novo design of picomolar SARS-CoV-2 miniprotein inhibitors. <i>Science</i> , 2020, 370, 426-431.	6.0	464
10	Targeting HIV Env immunogens to B cell follicles in nonhuman primates through immune complex or protein nanoparticle formulations. <i>Npj Vaccines</i> , 2020, 5, 72.	2.9	39
11	The Impression of a Nonexisting Catalytic Effect: The Role of CotB2 in Guiding the Complex Biosynthesis of Cyclooctat-9-en-7-ol. <i>Journal of the American Chemical Society</i> , 2020, 142, 21562-21574.	6.6	20
12	Structural basis for membrane insertion by the human ER membrane protein complex. <i>Science</i> , 2020, 369, 433-436.	6.0	127
13	The MiDAC histone deacetylase complex is essential for embryonic development and has a unique multivalent structure. <i>Nature Communications</i> , 2020, 11, 3252.	5.8	51
14	Cryo-EM Structure and Molecular Dynamics Analysis of the Fluoroquinolone Resistant Mutant of the AcrB Transporter from Salmonella. <i>Microorganisms</i> , 2020, 8, 943.	1.6	25
15	Comparison of CryoEM and X-ray structures of dimethylformamidase. <i>Progress in Biophysics and Molecular Biology</i> , 2021, 160, 66-78.	1.4	3
16	Covid-19.bioreproducibility.org: A web resource for SARS-CoV-2 related structural models. <i>Protein Science</i> , 2021, 30, 115-124.	3.1	15
17	Lysozyme conformational changes with ionic liquids: Spectroscopic, small angle x-ray scattering and crystallographic study. <i>Journal of Colloid and Interface Science</i> , 2021, 585, 433-443.	5.0	24
18	Structure and substrate specificity determinants of the taurine biosynthetic enzyme cysteine sulphinic acid decarboxylase. <i>Journal of Structural Biology</i> , 2021, 213, 107674.	1.3	3

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19	A Thermophilic Bacterial Esterase for Scavenging Nerve Agents: A Kinetic, Biophysical and Structural Study. <i>Molecules</i> , 2021, 26, 657.	1.7	1
21	Structure of the SARS-CoV-2 RNA-dependent RNA polymerase in the presence of favipiravir-RTP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	144
22	Adaptive Cartesian and torsional restraints for interactive model rebuilding. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 438-446.	1.1	16
23	Structural basis for VPS34 kinase activation by Rab1 and Rab5 on membranes. <i>Nature Communications</i> , 2021, 12, 1564.	5.8	50
25	Functional elucidation of TfuA in peptide backbone thioamidation. <i>Nature Chemical Biology</i> , 2021, 17, 585-592.	3.9	21
26	Structure of human telomerase holoenzyme with bound telomeric DNA. <i>Nature</i> , 2021, 593, 449-453.	13.7	106
27	Structure of the human Mediator-RNA polymerase II pre-initiation complex. <i>Nature</i> , 2021, 594, 129-133.	13.7	73
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31	Structural basis for conformational equilibrium of the catalytic spliceosome. <i>Molecular Cell</i> , 2021, 81, 1439-1452.e9.	4.5	26
32	Recognizing and validating ligands with CheckMyBlob. <i>Nucleic Acids Research</i> , 2021, 49, W86-W92.	6.5	9
35	Structural basis of substrate recognition and thermal protection by a small heat shock protein. <i>Nature Communications</i> , 2021, 12, 3007.	5.8	22
36	Cryo-EM structure of metazoan TRAPPIII, the multi-subunit complex that activates the GTPase Rab1. <i>EMBO Journal</i> , 2021, 40, e107608.	3.5	26
38	Structural basis of omega-3 fatty acid transport across the blood-brain barrier. <i>Nature</i> , 2021, 595, 315-319.	13.7	61
39	Cryo-EM structure of the photosynthetic RC-LH1-PufX supercomplex at 2.8-Å... resolution. <i>Science Advances</i> , 2021, 7, .	4.7	29
42	Structural basis for SARS-CoV-2 envelope protein recognition of human cell junction protein PALS1. <i>Nature Communications</i> , 2021, 12, 3433.	5.8	69
44	Structural basis of ABCF-mediated resistance to pleuromutilin, lincosamide, and streptogramin A antibiotics in Gram-positive pathogens. <i>Nature Communications</i> , 2021, 12, 3577.	5.8	40
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46	Conformational changes of loops highlight a potential binding site in <i>Rhodococcus equi</i> VapB. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 246-253.	0.4	3

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48	Structure of the TELO2-TTI1-TTI2 complex and its function in TOR recruitment to the R2TP chaperone. <i>Cell Reports</i> , 2021, 36, 109317.	2.9	20
49	Structure of <i>Escherichia coli</i> respiratory complex I reconstituted into lipid nanodiscs reveals an uncoupled conformation. <i>ELife</i> , 2021, 10, .	2.8	36
50	Structural basis of early translocation events on the ribosome. <i>Nature</i> , 2021, 595, 741-745.	13.7	60
51	The X-ray structure of <i>L</i> -threonine dehydrogenase from the common hospital pathogen <i>Clostridium difficile</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 269-274.	0.4	1
52	SARS-CoV-2 RBD antibodies that maximize breadth and resistance to escape. <i>Nature</i> , 2021, 597, 97-102.	13.7	385
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59	Multiple Occurrences of a 168-Nucleotide Deletion in SARS-CoV-2 ORF8, Unnoticed by Standard Amplicon Sequencing and Variant Calling Pipelines. <i>Viruses</i> , 2021, 13, 1870.	1.5	7
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61	Nucleolar maturation of the human small subunit processome. <i>Science</i> , 2021, 373, eabj5338.	6.0	63
62	Bipartite binding and partial inhibition links DEPTOR and mTOR in a mutually antagonistic embrace. <i>ELife</i> , 2021, 10, .	2.8	5
64	The structure of an Hsp90-immunophilin complex reveals cochaperone recognition of the client maturation state. <i>Molecular Cell</i> , 2021, 81, 3496-3508.e5.	4.5	46
65	Structure-based classification of tauopathies. <i>Nature</i> , 2021, 598, 359-363.	13.7	409
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78	Cryo-EM structure of native human uromodulin, a zona pellucida module polymer. <i>EMBO Journal</i> , 2020, 39, e106807.	3.5	31
79	Structure of the bacterial ribosome at 2 Å... resolution. <i>ELife</i> , 2020, 9, .	2.8	151
80	Structural basis for PRC2 decoding of active histone methylation marks H3K36me2/3. <i>ELife</i> , 2020, 9, .	2.8	73
81	Cryo-Electron Microscopy Structure and Interactions of the Human Cytomegalovirus gHgLgO Trimer with Platelet-Derived Growth Factor Receptor Alpha. <i>MBio</i> , 2021, 12, e0262521.	1.8	2
82	Michaelis-like complex of SARS-CoV-2 main protease visualized by room-temperature X-ray crystallography. <i>IUCr</i> , 2021, 8, 973-979.	1.0	25
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93	Structure of the TELO2-TTI1-TTI2 Complex and its Function in TOR Recruitment to the R2TP Chaperone. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
96	Structural basis of glycan276-dependent recognition by HIV-1 broadly neutralizing antibodies. <i>Cell Reports</i> , 2021, 37, 109922.	2.9	5

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98	Structure of the hexameric fungal plasma membrane proton pump in its autoinhibited state. <i>Science Advances</i> , 2021, 7, eabj5255.	4.7	20
100	Broadening access to cryoEM through centralized facilities. <i>Trends in Biochemical Sciences</i> , 2022, 47, 106-116.	3.7	9
101	The X-ray structure of juvenile hormone diol kinase from the silkworm <i>Bombyx mori</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 465-472.	0.4	0
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108	Mapping inhibitory sites on the RNA polymerase of the 1918 pandemic influenza virus using nanobodies. <i>Nature Communications</i> , 2022, 13, 251.	5.8	14
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110	Crystal structure of a human MUC16 SEA domain reveals insight into the nature of the CA125 tumor marker. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1210-1218.	1.5	10
111	Cryo-EM structures of amyloid- $\beta$ 42 filaments from human brains. <i>Science</i> , 2022, 375, 167-172.	6.0	228
112	<i>Pseudomonas aeruginosa</i> C-Terminal Processing Protease CtpA Assembles into a Hexameric Structure That Requires Activation by a Spiral-Shaped Lipoprotein-Binding Partner. <i>MBio</i> , 2022, 13, e0368021.	1.8	7
114	An engineered protein-based submicromolar competitive inhibitor of the <i>Staphylococcus aureus</i> virulence factor aureolysin. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 534-544.	1.9	5
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120	The regulatory domains of the lipid exporter ABCA1 form domain swapped latches. <i>PLoS ONE</i> , 2022, 17, e0262746.	1.1	4
123	Structure of the NLRP3 decamer bound to the cytokine release inhibitor CRID3. <i>Nature</i> , 2022, 604, 184-189.	13.7	109
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140	Structural basis of lipopolysaccharide maturation by the O-antigen ligase. <i>Nature</i> , 2022, 604, 371-376.	13.7	25
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148	Structural basis for the helical filament formation of <i>Escherichia coli</i> glutamine synthetase. <i>Protein Science</i> , 2022, 31, e4304.	3.1	5
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167	Neutralizing Antibodies against Lassa Virus Lineage I. <i>MBio</i> , 2022, 13, .	1.8	12
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187	Selective TnsC recruitment enhances the fidelity of RNA-guided transposition. <i>Nature</i> , 2022, 609, 384-393.	13.7	34
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