

Features and development of *Coot*

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Crystal structure of oxygen-evolving photosystem II at atomic resolution. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2010, 66, s124-s125.	0.3	2
3	Three factors that modulate the activity of class D β -lactamases and interfere with the post-translational carboxylation of Lys70. <i>Biochemical Journal</i> , 2010, 432, 495-506.	1.7	40
4	Intragenic deletions and a deep intronic mutation affecting pre-mRNA splicing in the dihydropyrimidine dehydrogenase gene as novel mechanisms causing 5-fluorouracil toxicity. <i>Human Genetics</i> , 2010, 128, 529-538.	1.8	101
5	X-ray structure determination of the glycine cleavage system protein H of <i>Mycobacterium tuberculosis</i> using an inverse Compton synchrotron X-ray source. <i>Journal of Structural and Functional Genomics</i> , 2010, 11, 91-100.	1.2	23
6	Unmet challenges of structural genomics. <i>Current Opinion in Structural Biology</i> , 2010, 20, 587-597.	2.6	49
7	Crystal structure of the LMAN1 ϵ CRD/MCFD2 transport receptor complex provides insight into combined deficiency of factor V and factor VIII. <i>FEBS Letters</i> , 2010, 584, 878-882.	1.3	23
8	RapiData: a practical course in macromolecular X-ray diffraction data measurement and structure solving at the NSLS. <i>Journal of Applied Crystallography</i> , 2010, 43, 1238-1241.	1.9	0
9	ResDe: a new tool for visual definition of distance restraints for crystallographic refinement. <i>Journal of Applied Crystallography</i> , 2010, 43, 1540-1542.	1.9	1
10	Macromolecular crystal data phased by negative-stained electron-microscopy reconstructions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 514-521.	2.5	11
11	High-resolution X-ray crystal structure of bovine H-protein at 0.88 \AA resolution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 698-708.	2.5	9
12	Structure at 1.5 \AA resolution of cytochrome <i>c</i> ₅₅₂ with its flexible linker segment, a membrane-anchored protein from <i>Paracoccus denitrificans</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 850-854.	2.5	6
13	Atomic resolution studies of haloalkane dehalogenases DhaA04, DhaA14 and DhaA15 with engineered access tunnels. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 962-969.	2.5	12
14	Percentile-based spread: a more accurate way to compare crystallographic models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 970-978.	2.5	18
15	Structures of the nucleotide-binding domain of the human ABCB6 transporter and its complexes with nucleotides. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 979-987.	2.5	12
16	Crystallization of small proteins assisted by green fluorescent protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1059-1066.	2.5	31
17	Comparison of a nontoxic variant of <i>Clostridium perfringens</i> β -toxin with the toxic wild-type strain. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 1067-1074.	2.5	5
18	Refined structures of placental alkaline phosphatase show a consistent pattern of interactions at the peripheral site. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 866-870.	0.7	17
19	Structural studies of the catalytic core of the primate foamy virus (PFV-1) integrase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 881-886.	0.7	3

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21	Structure of the <i>Francisella tularensis</i> enoyl-acyl carrier protein reductase (FabI) in complex with NAD ⁺ and triclosan. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1436-1440.	0.7	11
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23	Crystal structure of <i>Bacillus subtilis</i> SPP1 phage gp23.1, a putative chaperone. <i>Protein Science</i> , 2010, 19, 1812-1816.	3.1	11
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25	Stabilization of mutant p53 via alkylation of cysteines and effects on DNA binding. <i>Protein Science</i> , 2010, 19, 2267-2278.	3.1	59
26	Enzyme-ligand interactions that drive active site rearrangements in the <i>Helicobacter pylori</i> 5-methylthioadenosine/S-adenosylhomocysteine nucleosidase. <i>Protein Science</i> , 2010, 19, 2498-2510.	3.1	29
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34	Glycoprotein organization of Chikungunya virus particles revealed by X-ray crystallography. <i>Nature</i> , 2010, 468, 709-712.	13.7	524
35	The Crystal Structure of the Dachshund Domain of Human SnoN Reveals Flexibility in the Putative Protein Interaction Surface. <i>PLoS ONE</i> , 2010, 5, e12907.	1.1	13
36	Quantitative High-Throughput Screening Identifies 8-Hydroxyquinolines as Cell-Active Histone Demethylase Inhibitors. <i>PLoS ONE</i> , 2010, 5, e15535.	1.1	194
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44	Structural and Kinetic Characterization of 4-Hydroxy-4-methyl-2-oxoglutarate/4-Carboxy-4-hydroxy-2-oxoadipate Aldolase, a Protocatechuate Degradation Enzyme Evolutionarily Convergent with the HpaI and DmpG Pyruvate Aldolases. <i>Journal of Biological Chemistry</i> , 2010, 285, 36608-36615.	1.6	28
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2035	Structural and Biochemical Characterization of <i>Chlamydia trachomatis</i> Hypothetical Protein CT263 Supports That Menaquinone Synthesis Occurs through the Futasoline Pathway. <i>Journal of Biological Chemistry</i> , 2014, 289, 32214-32229.	1.6	23
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8116	Structure-guided identification of function: role of <i>Capsicum annuum</i> vicilin during oxidative stress. <i>Biochemical Journal</i> , 2018, 475, 3057-3071.	1.7	15
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13860	An ultrapotent pan- β -coronavirus lineage B (β -CoV-B) neutralizing antibody locks the receptor-binding domain in closed conformation by targeting its conserved epitope. <i>Protein and Cell</i> , 2022, 13, 655-675.	4.8	25
13861	Disease-associated mutations impacting BC-loop flexibility trigger long-range transthyretin tetramer destabilization and aggregation. <i>Journal of Biological Chemistry</i> , 2021, 297, 101039.	1.6	8
13862	Structures of synthetic nanobody-SARS-CoV-2 receptor-binding domain complexes reveal distinct sites of interaction. <i>Journal of Biological Chemistry</i> , 2021, 297, 101202.	1.6	28
13863	A lipoprotein allosterically activates the CwID amidase during <i>Clostridioides difficile</i> spore formation. <i>PLoS Genetics</i> , 2021, 17, e1009791.	1.5	8
13865	Structure of mycobacterial CIII2CIV2 respiratory supercomplex bound to the tuberculosis drug candidate telacebec (Q203). <i>ELife</i> , 2021, 10, .	2.8	19
13866	The CRL4 ^{DCAF1} cullin-RING ubiquitin ligase is activated following a switch in oligomerization state. <i>EMBO Journal</i> , 2021, 40, e108008.	3.5	19
13867	Structural basis of P[II] rotavirus evolution and host ranges under selection of histo-blood group antigens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	9
13868	Functional characterization and structural bases of two class I diterpene synthases in pimarane-type diterpene biosynthesis. <i>Communications Chemistry</i> , 2021, 4, .	2.0	6
13869	Structural characterization of human peptidyl-arginine deiminase type III by X-ray crystallography. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 334-340.	0.4	2
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13872	Cryo-EM reveals new species-specific proteins and symmetry elements in the <i>Legionella pneumophila</i> Dot/Icm T4SS. <i>ELife</i> , 2021, 10, .	2.8	22
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13876	Directed evolution of prenylated FMN-dependent Fdc supports efficient in vivo isobutene production. <i>Nature Communications</i> , 2021, 12, 5300.	5.8	11
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14690	Structural characterization of free-state and product-state <i>Mycobacterium tuberculosis</i> methionyl-tRNA synthetase reveals an induced-fit ligand-recognition mechanism. IUCrJ, 2018, 5, 478-490.	1.0	10
14691	<i>De novo</i> protein structure determination by heavy-atom soaking in lipidic cubic phase and SIRAS phasing using serial synchrotron crystallography. IUCrJ, 2018, 5, 524-530.	1.0	12
14692	Twist and turn: a revised structural view on the unpaired bubble of class II CPD photolyase in complex with damaged DNA. IUCrJ, 2018, 5, 608-618.	1.0	7
14693	Homology-based loop modeling yields more complete crystallographic protein structures. IUCrJ, 2018, 5, 585-594.	1.0	27
14694	Structural basis for light control of cell development revealed by crystal structures of a myxobacterial phytochrome. IUCrJ, 2018, 5, 619-634.	1.0	33
14695	Structures of collagen IV globular domains: insight into associated pathologies, folding and network assembly. IUCrJ, 2018, 5, 765-779.	1.0	12
14696	Computational design of symmetrical eight-bladed \hat{I}^2 -propeller proteins. IUCrJ, 2019, 6, 46-55.	1.0	33
14697	Homochiral and racemic MicroED structures of a peptide repeat from the ice-nucleation protein InaZ. IUCrJ, 2019, 6, 197-205.	1.0	16
14698	Nanobeam precession-assisted 3D electron diffraction reveals a new polymorph of hen egg-white lysozyme. IUCrJ, 2019, 6, 178-188.	1.0	56
14699	A three-domain copper-nitrite reductase with a unique sensing loop. IUCrJ, 2019, 6, 248-258.	1.0	15
14700	Calixarene-mediated assembly of a small antifungal protein. IUCrJ, 2019, 6, 238-247.	1.0	51
14701	Structure of mammalian plasma fetuin-B and its mechanism of selective metallopeptidase inhibition. IUCrJ, 2019, 6, 317-330.	1.0	28
14702	Ice formation and solvent nanoconfinement in protein crystals. IUCrJ, 2019, 6, 346-356.	1.0	11
14703	Determination of the molecular basis for coprogen import by Gram-negative bacteria. IUCrJ, 2019, 6, 401-411.	1.0	19
14704	Dose-resolved serial synchrotron and XFEL structures of radiation-sensitive metalloproteins. IUCrJ, 2019, 6, 543-551.	1.0	65
14705	The structural characterization of a glucosylglycerate hydrolase provides insights into the molecular mechanism of mycobacterial recovery from nitrogen starvation. IUCrJ, 2019, 6, 572-585.	1.0	16
14706	Specific radiation damage is a lesser concern at room temperature. IUCrJ, 2019, 6, 665-680.	1.0	42

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14707	On-chip crystallization for serial crystallography experiments and on-chip ligand-binding studies. IUCrJ, 2019, 6, 714-728.	1.0	41
14708	Ligand pathways in neuroglobin revealed by low-temperature photodissociation and docking experiments. IUCrJ, 2019, 6, 832-842.	1.0	8
14709	1 kHz fixed-target serial crystallography using a multilayer monochromator and an integrating pixel detector. IUCrJ, 2019, 6, 927-937.	1.0	35
14710	Structural insights into stressosome assembly. IUCrJ, 2019, 6, 938-947.	1.0	11
14711	The DRSâ€‘AIMP2â€‘EPRS subcomplex acts as a pivot in the multi-tRNA synthetase complex. IUCrJ, 2019, 6, 958-967.	1.0	12
14712	Why is interoperability between the two fields of chemical crystallography and protein crystallography so difficult?. IUCrJ, 2019, 6, 788-793.	1.0	11
14713	High-throughput structures of proteinâ€‘ligand complexes at room temperature using serial femtosecond crystallography. IUCrJ, 2019, 6, 1074-1085.	1.0	36
14714	Crystal structure of the putative cyclase IdmH from the indanomycin nonribosomal peptide synthase/polyketide synthase. IUCrJ, 2019, 6, 1120-1133.	1.0	8
14715	Mutagenesis facilitated crystallization of GLP-1R. IUCrJ, 2019, 6, 996-1006.	1.0	13
14716	Structure-based mechanism of cysteine-switch latency and of catalysis by pappalysin-family metallopeptidases. IUCrJ, 2020, 7, 18-29.	1.0	9
14717	Structural and kinetic insights into flavin-containing monooxygenase and calponin-homology domains in human MICAL3. IUCrJ, 2020, 7, 90-99.	1.0	10
14718	3D-MiXD: 3D-printed X-ray-compatible microfluidic devices for rapid, low-consumption serial synchrotron crystallography data collection in flow. IUCrJ, 2020, 7, 207-219.	1.0	43
14719	Structural insights into conformational switching in latency-associated peptide between transforming growth factor Î²-1 bound and unbound states. IUCrJ, 2020, 7, 238-252.	1.0	5
14720	The resolution revolution in cryoEM requires high-quality sample preparation: a rapid pipeline to a high-resolution map of yeast fatty acid synthase. IUCrJ, 2020, 7, 220-227.	1.0	16
14721	The structural study of mutation-induced inactivation of human muscarinic receptor M4. IUCrJ, 2020, 7, 294-305.	1.0	9
14722	Comparing serial X-ray crystallography and microcrystal electron diffraction (MicroED) as methods for routine structure determination from small macromolecular crystals. IUCrJ, 2020, 7, 306-323.	1.0	32
14723	High-resolution cryo-EM reconstructions in the presence of substantial aberrations. IUCrJ, 2020, 7, 445-452.	1.0	11
14724	<i>Plasmodium vivax</i> and human hexokinases share similar active sites but display distinct quaternary architectures. IUCrJ, 2020, 7, 453-461.	1.0	6

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14725	A complete compendium of crystal structures for the human SEPT3 subgroup reveals functional plasticity at a specific septin interface. IUCrJ, 2020, 7, 462-479.	1.0	28
14726	Crystal structure of the NS3-like helicase from Alongshan virus. IUCrJ, 2020, 7, 375-382.	1.0	13
14727	The active form of quinol-dependent nitric oxide reductase from <i>Neisseria meningitidis</i> is a dimer. IUCrJ, 2020, 7, 404-415.	1.0	10
14728	Atomic structures determined from digitally defined nanocrystalline regions. IUCrJ, 2020, 7, 490-499.	1.0	8
14729	Structures of substrate- and product-bound forms of a multi-domain copper nitrite reductase shed light on the role of domain tethering in protein complexes. IUCrJ, 2020, 7, 557-565.	1.0	5
14730	Paired refinement under the control of PAIREF. IUCrJ, 2020, 7, 681-692.	1.0	18
14731	Induced DNA bending by unique dimerization of HigA antitoxin. IUCrJ, 2020, 7, 748-760.	1.0	6
14732	Millisecond time-resolved serial oscillation crystallography of a blue-light photoreceptor at a synchrotron. IUCrJ, 2020, 7, 728-736.	1.0	12
14733	Structural insights into the regulation of SigB activity by RsbV and RsbW. IUCrJ, 2020, 7, 737-747.	1.0	11
14734	Crystal structures of SARS-CoV-2 ADP-ribose phosphatase: from the apo form to ligand complexes. IUCrJ, 2020, 7, 814-824.	1.0	92
14735	Anaerobic fixed-target serial crystallography. IUCrJ, 2020, 7, 901-912.	1.0	12
14736	Structural insights into the effect of active-site mutation on the catalytic mechanism of carbonic anhydrase. IUCrJ, 2020, 7, 985-994.	1.0	7
14737	Novel approaches for the lipid sponge phase crystallization of the <i>Rhodobacter sphaeroides</i> photosynthetic reaction center. IUCrJ, 2020, 7, 1084-1091.	1.0	6
14738	Room-temperature X-ray crystallography reveals the oxidation and reactivity of cysteine residues in SARS-CoV-2 3CL M ^{pro} : insights into enzyme mechanism and drug design. IUCrJ, 2020, 7, 1028-1035.	1.0	49
14739	Harnessing the power of an X-ray laser for serial crystallography of membrane proteins crystallized in lipidic cubic phase. IUCrJ, 2020, 7, 976-984.	1.0	15
14740	Continuous flexibility analysis of SARS-CoV-2 spike prefusion structures. IUCrJ, 2020, 7, 1059-1069.	1.0	39
14741	Molecular determinants of vascular transport of dexamethasone in COVID-19 therapy. IUCrJ, 2020, 7, 1048-1058.	1.0	12
14742	High-resolution cryo-EM using beam-image shift at 200 keV. IUCrJ, 2020, 7, 1179-1187.	1.0	14

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14744	Cloning, expression, purification and preliminary X-ray crystallographic analysis of mouse protein arginine methyltransferase 7. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 80-86.	0.4	8
14745	Structure of the human MLH1 N-terminus: implications for predisposition to Lynch syndrome. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 981-985.	0.4	21
14746	Structure of the SPRY domain of the human RNA helicase DDX1, a putative interaction platform within a DEAD-box protein. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1176-1188.	0.4	14
14747	An active siteâ€“(tail interaction in the structure of hexahistidine-tagged <i>Thermoplasma acidophilum</i> citrate synthase. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1292-1299.	0.4	7
14748	1.25â€“(Å... resolution structure of an RNA 20-mer that binds to the TREX2 complex. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1318-1321.	0.4	4
14749	Purification, crystallization and structural elucidation of <sc>D</sc>-galactaro-1,4-lactone cycloisomerase from <i>Agrobacterium tumefaciens</i> involved in pectin degradation. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 36-41.	0.4	7
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14751	The use of noncrystallographic symmetry averaging to solve structures from data affected by perfect hemihedral twinning. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 188-197.	0.4	5
14752	Characterization of the NTPR and BD1 interacting domains of the human PICHâ€“(BEND3 complex. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 646-651.	0.4	5
14753	Structural analysis of a function-associated loop mutant of the substrate-recognition domain of Fbs1 ubiquitin ligase. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 619-626.	0.4	6
14754	1.65â€“(Å... resolution structure of the AraC-family transcriptional activator ToxT from <i>Vibrio cholerae</i>. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 726-731.	0.4	13
14755	The crystal structure of dihydrodipicolinate reductase from the human-pathogenic bacterium <i>Bartonella henselae</i> strain Houston-1 at 2.3â€“(Å... resolution. Acta Crystallographica Section F, Structural Biology Communications, 2016, 72, 885-891.	0.4	4
14756	Crystal structures of human Fabs targeting the Bexsero meningococcal vaccine antigen NHBA. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 305-314.	0.4	5
14757	Crystal structure of N-acetylmannosamine kinase from <i>Fusobacterium nucleatum</i> . Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 356-362.	0.4	8
14758	The structure of a complex of the lactonohydrolase zearalenone hydrolase with the hydrolysis product of zearalenone at 1.60â€“(Å... resolution. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 376-381.	0.4	15
14759	Crystal structure of a family 6 cellobiohydrolase from the basidiomycete <i>Phanerochaete chrysosporium</i>. Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 398-403.	0.4	8
14760	Crystal structure of type II NADH:quinone oxidoreductase from <i>Caldalkalibacillus thermarum</i> with an improved resolution of 2.15â€“(Å... Acta Crystallographica Section F, Structural Biology Communications, 2017, 73, 541-549.	0.4	10

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14761	Periplasmic form of dipeptidyl aminopeptidase IV from <i>Pseudoxanthomonas mexicana</i> WO24: purification, kinetic characterization, crystallization and X-ray crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2017, 73, 601-606.	0.4	1
14762	Crystal structure of cytoplasmic acetoacetyl-CoA thiolase from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 6-13.	0.4	4
14763	Crystal structure of the MSMEG_4306 gene product from <i>Mycobacterium smegmatis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 166-173.	0.4	1
14764	Crystal structure of an inferred ancestral bacterial pyruvate decarboxylase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 179-186.	0.4	3
14765	Structure of the tandem PX-PH domains of Bem3 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 315-321.	0.4	5
14766	TssA from <i>Burkholderia cenocepacia</i> : expression, purification, crystallization and crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 536-542.	0.4	1
14767	Crystal structures and kinetics of <i>N</i> -acetylneuraminase lyase from <i>Fusobacterium nucleatum</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 725-732.	0.4	5
14768	Structural studies of a glycoside hydrolase family 3 β -glucosidase from the model fungus <i>Neurospora crassa</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 787-796.	0.4	7
14769	Crystal structure of the <i>Agrobacterium tumefaciens</i> type VI effector- ϵ immunity complex. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 810-816.	0.4	3
14770	Iterative screen optimization maximizes the efficiency of macromolecular crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 123-131.	0.4	8
14771	High-resolution structure of a Y27W mutant of the Dishevelled2 DIX domain. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 116-122.	0.4	6
14772	Carbonic anhydrase II in complex with carboxylic acid-based inhibitors. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 166-170.	0.4	7
14773	Neutron and X-ray analysis of the Fenna-Matthews-Olson photosynthetic antenna complex from <i>Prosthecochloris aestuarii</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 171-175.	0.4	3
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14775	High-resolution crystal structure of the reduced Grx1 from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 392-396.	0.4	3
14776	Structural basis for oligomerization of the prokaryotic peptide transporter PepT _{So2} . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 348-358.	0.4	10
14777	Structure of the Prx6-subfamily 1-Cys peroxiredoxin from <i>Sulfolobus islandicus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 428-434.	0.4	6
14778	Crystal structure of (<i>S</i>)-3- <i>O</i> -geranylgeranyl glycerol phosphate synthase from <i>Thermoplasma acidophilum</i> in complex with the substrate <i>sn</i> -glycerol 1-phosphate. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 470-479.	0.4	3

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14779	Structure of the archaeal chemotaxis protein CheY in a domain-swapped dimeric conformation. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 576-585.	0.4	10
14780	Structure of GTP cyclohydrolase I from <i>Listeria monocytogenes</i> , a potential anti-infective drug target. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 586-592.	0.4	4
14781	Structure of the dihydrolipoamide succinyltransferase catalytic domain from <i>Escherichia coli</i> in a novel crystal form: a tale of a common protein crystallization contaminant. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 616-624.	0.4	6
14782	Structure of an RNA helix with pyrimidine mismatches and cross-strand stacking. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 652-656.	0.4	4
14783	Structure determination of the human TRPV1 ankyrin-repeat domain under nonreducing conditions. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 130-137.	0.4	7
14784	Structure of the <i>Mycobacterium smegmatis</i> $\hat{1}$ -maltose-1-phosphate synthase GlgM. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 175-181.	0.4	7
14785	Crystal structure of <i>Arabidopsis thaliana</i> casein kinase 2 $\hat{1}$. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 182-191.	0.4	3
14786	Structure of the 4-hydroxy-tetrahydrodipicolinate synthase from the thermoacidophilic methanotroph <i>Methylophilum fumariolicum</i> SolV and the phylogeny of the aminotransferase pathway. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 199-208.	0.4	4
14787	Enhanced X-ray diffraction of <i>in vivo</i> -grown $\hat{1}$ / ₄ NS crystals by viscous jets at XFELs. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 278-289.	0.4	8
14788	Proline/alanine-rich sequence (PAS) polypeptides as an alternative to PEG precipitants for protein crystallization. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 320-325.	0.4	6
14789	Structural characterization of borneol dehydrogenase from <i>Pseudomonas</i> sp. TCU-HL1. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 309-313.	0.4	4
14790	Crystal structure of the FYCO1 RUN domain suggests possible interfaces with small GTPases. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 326-333.	0.4	5
14791	Crystal structure of GH30-7 endoxylanase C from the filamentous fungus <i>Talaromyces cellulolyticus</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 341-349.	0.4	6
14792	Structural characterization of three noncanonical NTF2-like superfamily proteins: implications for polyketide biosynthesis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 372-383.	0.4	11
14793	Binding of inhibitors to active-site mutants of CD1, the enigmatic catalytic domain of histone deacetylase 6. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 428-437.	0.4	5
14794	The structure of the Moco carrier protein from <i>Rippkaea orientalis</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 453-463.	0.4	6
14795	Multiple crystal forms of human MacroD2. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 477-482.	0.4	3
14796	Crystallization and structure of ebselen bound to Cys141 of human inositol monophosphatase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 469-476.	0.4	9

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14797	Structure of the substrate-binding domain of <i>Plasmodium falciparum</i> heat-shock protein 70-x. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 495-500.	0.4	8
14798	Crystal structure of barley agmatine coumaroyltransferase, an N-acyltransferase from the BAHD superfamily. Acta Crystallographica Section F, Structural Biology Communications, 2020, 76, 590-596.	0.4	7
14799	Using yeast surface display to engineer a soluble and crystallizable construct of hematopoietic progenitor kinase 1 (HPK1). Acta Crystallographica Section F, Structural Biology Communications, 2021, 77, 22-28.	0.4	6
14800	Neutron and X-ray single-crystal diffraction from protein microcrystals via magnetically oriented microcrystal arrays in gels. Acta Crystallographica Section D: Structural Biology, 2016, 72, 823-829.	1.1	5
14801	RoboDiff: combining a sample changer and goniometer for highly automated macromolecular crystallography experiments. Acta Crystallographica Section D: Structural Biology, 2016, 72, 966-975.	1.1	35
14802	Using more than 801,296 small-molecule crystal structures to aid in protein structure refinement and analysis. Acta Crystallographica Section D: Structural Biology, 2017, 73, 234-239.	1.1	6
14803	Structure and conformational plasticity of the U6 small nuclear ribonucleoprotein core. Acta Crystallographica Section D: Structural Biology, 2017, 73, 1-8.	1.1	5
14804	Ligand fitting with CCP4. Acta Crystallographica Section D: Structural Biology, 2017, 73, 158-170.	1.1	18
14805	Validation and extraction of molecular-geometry information from small-molecule databases. Acta Crystallographica Section D: Structural Biology, 2017, 73, 103-111.	1.1	19
14806	Low-dose fixed-target serial synchrotron crystallography. Acta Crystallographica Section D: Structural Biology, 2017, 73, 373-378.	1.1	91
14807	Binding of hydroxycitrate to human ATP-citrate lyase. Acta Crystallographica Section D: Structural Biology, 2017, 73, 660-671.	1.1	23
14808	Structural basis for the regulation of chemotaxis by MapZ in the presence of c-di-GMP. Acta Crystallographica Section D: Structural Biology, 2017, 73, 683-691.	1.1	26
14809	Gyreandgimble: a maximum-likelihood replacement for Patterson correlation refinement. Acta Crystallographica Section D: Structural Biology, 2018, 74, 279-289.	1.1	14
14810	<i>Fragon</i> : rapid high-resolution structure determination from ideal protein fragments. Acta Crystallographica Section D: Structural Biology, 2018, 74, 205-214.	1.1	25
14811	Automated map sharpening by maximization of detail and connectivity. Acta Crystallographica Section D: Structural Biology, 2018, 74, 545-559.	1.1	218
14812	Domain swap in the C-terminal ubiquitin-like domain of human doublecortin. Acta Crystallographica Section D: Structural Biology, 2018, 74, 450-462.	1.1	10
14813	Cryoprotectant-free high-pressure cooling and dynamic nuclear polarization for more sensitive detection of hydrogen in neutron protein crystallography. Acta Crystallographica Section D: Structural Biology, 2018, 74, 787-791.	1.1	5
14814	<i>SIMBAD</i> : a sequence-independent molecular-replacement pipeline. Acta Crystallographica Section D: Structural Biology, 2018, 74, 595-605.	1.1	25

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14815	Real-space refinement in <i>PHENIX</i> for cryo-EM and crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 531-544.	1.1	2,065
14816	Current approaches for the fitting and refinement of atomic models into cryo-EM maps using <i>CCP-EM</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 492-505.	1.1	93
14817	The impact of cryosolution thermal contraction on proteins and protein crystals: volumes, conformation and order. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 922-938.	1.1	8
14818	Resolving polymorphs and radiation-driven effects in microcrystals using fixed-target serial synchrotron crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 151-159.	1.1	35
14819	Identification of the site of oxidase substrate binding in <i>Scytalidium thermophilum</i> catalase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 979-985.	1.1	5
14820	Crystallography on a chip – without the chip: sheet-on-sheet sandwich. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 1000-1007.	1.1	51
14821	The structure of the AliC GH13 α -amylase from <i>Alicyclobacillus</i> sp. reveals the accommodation of starch branching points in the α -amylase family. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 1-7.	1.1	15
14822	Iron-sulfur clusters have no right angles. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 16-20.	1.1	16
14823	Structural studies of a surface-entropy reduction mutant of O-GlcNAcase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 70-78.	1.1	5
14824	The crystal structure of the <i>N</i> -acetylglucosamine 2-epimerase from <i>Nostoc</i> sp. KVJ10 reveals the true dimer. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 90-100.	1.1	6
14825	Crystal structure of <i>Mycobacterium tuberculosis</i> FadB2 implicated in mycobacterial β -oxidation. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 101-108.	1.1	7
14826	Coping with strong translational noncrystallographic symmetry and extreme anisotropy in molecular replacement with <i>Phaser</i> : human Rab27a. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 342-353.	1.1	8
14827	Engineered variants provide new insight into the structural properties important for activity of the highly dynamic, trimeric protein disulfide isomerase ScsC from <i>Proteus mirabilis</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 296-307.	1.1	5
14828	Long-wavelength <i>Mesh&Collect</i> native SAD phasing from microcrystals. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 192-199.	1.1	8
14829	Building and rebuilding N-glycans in protein structure models. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 416-425.	1.1	19
14830	Structural analysis of a replication protein encoded by a plasmid isolated from a multiple sclerosis patient. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 498-504.	1.1	5
14831	Analysis and validation of macromolecular <i>B</i> values. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 505-518.	1.1	14
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15140	Dna2 nuclease-helicase structure, mechanism and regulation by Rpa. <i>ELife</i> , 2015, 4, .	2.8	93
15141	Structural determinants of nuclear export signal orientation in binding to exportin CRM1. <i>ELife</i> , 2015, 4, .	2.8	79
15142	Binary architecture of the Nav1.2- β 2 signaling complex. <i>ELife</i> , 2016, 5, .	2.8	37
15143	cryo-EM structures of the <i>E. coli</i> replicative DNA polymerase reveal its dynamic interactions with the DNA sliding clamp, exonuclease and β . <i>ELife</i> , 2015, 4, .	2.8	75
15144	Structural basis of nucleic-acid recognition and double-strand unwinding by the essential neuronal protein Pur-alpha. <i>ELife</i> , 2016, 5, .	2.8	35
15145	The near-atomic cryoEM structure of a flexible filamentous plant virus shows homology of its coat protein with nucleoproteins of animal viruses. <i>ELife</i> , 2015, 4, e11795.	2.8	61
15146	Mutation in ATG5 reduces autophagy and leads to ataxia with developmental delay. <i>ELife</i> , 2016, 5, .	2.8	161
15147	The Sec7 N-terminal regulatory domains facilitate membrane-proximal activation of the Arf1 GTPase. <i>ELife</i> , 2016, 5, .	2.8	17

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15148	Toxoplasma gondii peptide ligands open the gate of the HLA class I binding groove. <i>ELife</i> , 2016, 5, .	2.8	88
15149	Evolutionary diversification of the trypanosome haptoglobin-haemoglobin receptor from an ancestral haemoglobin receptor. <i>ELife</i> , 2016, 5, .	2.8	28
15150	Molecular mechanism of activation-triggered subunit exchange in Ca ²⁺ /calmodulin-dependent protein kinase II. <i>ELife</i> , 2016, 5, .	2.8	89
15151	Structural basis for DNA 5' end resection by RecJ. <i>ELife</i> , 2016, 5, e14294.	2.8	54
15152	Bile salt receptor complex activates a pathogenic type III secretion system. <i>ELife</i> , 2016, 5, .	2.8	68
15153	Mechanism of B-box 2 domain-mediated higher-order assembly of the retroviral restriction factor TRIM5 β . <i>ELife</i> , 2016, 5, .	2.8	81
15154	Structural elucidation of a novel mechanism for the bacteriophage-based inhibition of the RNA degradosome. <i>ELife</i> , 2016, 5, .	2.8	47
15155	The Ki-67 and RepoMan mitotic phosphatases assemble via an identical, yet novel mechanism. <i>ELife</i> , 2016, 5, .	2.8	50
15156	Crystal structure of an HIV assembly and maturation switch. <i>ELife</i> , 2016, 5, .	2.8	119
15157	Automated structure refinement of macromolecular assemblies from cryo-EM maps using Rosetta. <i>ELife</i> , 2016, 5, .	2.8	407
15158	Mechanism for nuclease regulation in RecBCD. <i>ELife</i> , 2016, 5, .	2.8	36
15159	bMERB domains are bivalent Rab8 family effectors evolved by gene duplication. <i>ELife</i> , 2016, 5, .	2.8	51
15160	Mechanistic signs of double-barreled structure in a fluoride ion channel. <i>ELife</i> , 2016, 5, .	2.8	33
15161	NPAS1-ARNT and NPAS3-ARNT crystal structures implicate the bHLH-PAS family as multi-ligand binding transcription factors. <i>ELife</i> , 2016, 5, .	2.8	58
15162	Structural characterization of encapsulated ferritin provides insight into iron storage in bacterial nanocompartments. <i>ELife</i> , 2016, 5, .	2.8	77
15163	Molecular basis of sidekick-mediated cell-cell adhesion and specificity. <i>ELife</i> , 2016, 5, .	2.8	36
15164	Structure of the active form of human origin recognition complex and its ATPase motor module. <i>ELife</i> , 2017, 6, .	2.8	44
15165	β -Protocadherin structural diversity and functional implications. <i>ELife</i> , 2016, 5, .	2.8	54

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15166	Structural basis for inhibition of erythrocyte invasion by antibodies to Plasmodium falciparum protein CyRPA. <i>ELife</i> , 2017, 6, .	2.8	47
15167	Structural insights into the mechanism of the DEAH-box RNA helicase Prp43. <i>ELife</i> , 2017, 6, .	2.8	80
15168	Cryo-EM structures of the autoinhibited E. coli ATP synthase in three rotational states. <i>ELife</i> , 2016, 5, .	2.8	132
15169	Structure of the transporter associated with antigen processing trapped by herpes simplex virus. <i>ELife</i> , 2016, 5, .	2.8	78
15170	Structure of protein O-mannose kinase reveals a unique active site architecture. <i>ELife</i> , 2016, 5, .	2.8	33
15171	Structural basis for the hijacking of endosomal sorting nexin proteins by Chlamydia trachomatis. <i>ELife</i> , 2017, 6, .	2.8	55
15172	Mechanistic insights into neurotransmitter release and presynaptic plasticity from the crystal structure of Munc13-1 C1C2BMUN. <i>ELife</i> , 2017, 6, .	2.8	103
15173	Chlamydia interfere with an interaction between the mannose-6-phosphate receptor and sorting nexins to counteract host restriction. <i>ELife</i> , 2017, 6, .	2.8	61
15174	Structural basis for the inhibition of RecBCD by Gam and its synergistic antibacterial effect with quinolones. <i>ELife</i> , 2016, 5, .	2.8	50
15175	Structural insights into the molecular mechanisms of myasthenia gravis and their therapeutic implications. <i>ELife</i> , 2017, 6, .	2.8	22
15176	Crystal structure and dynamics of a lipid-induced potential desensitized-state of a pentameric ligand-gated channel. <i>ELife</i> , 2017, 6, .	2.8	67
15177	Structural basis of protein translocation by the Vps4-Vta1 AAA ATPase. <i>ELife</i> , 2017, 6, .	2.8	123
15178	Epistatic mutations in PUMA BH3 drive an alternate binding mode to potently and selectively inhibit anti-apoptotic Bfl-1. <i>ELife</i> , 2017, 6, .	2.8	33
15179	Structure of a AAA+ unfoldase in the process of unfolding substrate. <i>ELife</i> , 2017, 6, .	2.8	119
15180	A widespread family of serine/threonine protein phosphatases shares a common regulatory switch with proteasomal proteases. <i>ELife</i> , 2017, 6, .	2.8	28
15181	Pirating conserved phage mechanisms promotes promiscuous staphylococcal pathogenicity island transfer. <i>ELife</i> , 2017, 6, .	2.8	25
15182	Structural basis for interdomain communication in SHIP2 providing high phosphatase activity. <i>ELife</i> , 2017, 6, .	2.8	32
15183	Structural insights into the light-driven auto-assembly process of the water-oxidizing Mn ₄ CaO ₅ -cluster in photosystem II. <i>ELife</i> , 2017, 6, .	2.8	62

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15184	A broadly distributed toxin family mediates contact-dependent antagonism between gram-positive bacteria. <i>ELife</i> , 2017, 6, .	2.8	132
15185	The structure of a LAIR1-containing human antibody reveals a novel mechanism of antigen recognition. <i>ELife</i> , 2017, 6, .	2.8	11
15186	Structure and in situ organisation of the <i>Pyrococcus furiosus</i> archaeellum machinery. <i>ELife</i> , 2017, 6, .	2.8	83
15187	Structure-based analysis of CysZ-mediated cellular uptake of sulfate. <i>ELife</i> , 2018, 7, .	2.8	10
15188	Cryo-EM structure of the SAGA and NuA4 coactivator subunit Tra1 at 3.7 angstrom resolution. <i>ELife</i> , 2017, 6, .	2.8	38
15189	A novel SH2 recognition mechanism recruits Spt6 to the doubly phosphorylated RNA polymerase II linker at sites of transcription. <i>ELife</i> , 2017, 6, .	2.8	61
15190	Computational design of environmental sensors for the potent opioid fentanyl. <i>ELife</i> , 2017, 6, .	2.8	78
15191	A Histidine pH sensor regulates activation of the Ras-specific guanine nucleotide exchange factor RasGRP1. <i>ELife</i> , 2017, 6, .	2.8	32
15192	Structure and reconstitution of yeast Mpp6-nuclear exosome complexes reveals that Mpp6 stimulates RNA decay and recruits the Mtr4 helicase. <i>ELife</i> , 2017, 6, .	2.8	49
15193	Autoinhibition of ankyrin-B/G membrane target bindings by intrinsically disordered segments from the tail regions. <i>ELife</i> , 2017, 6, .	2.8	27
15194	Rift Valley fever phlebovirus NSs protein core domain structure suggests molecular basis for nuclear filaments. <i>ELife</i> , 2017, 6, .	2.8	20
15195	Structural insight into TPX2-stimulated microtubule assembly. <i>ELife</i> , 2017, 6, .	2.8	87
15196	Molecular determinants of permeation in a fluoride-specific ion channel. <i>ELife</i> , 2017, 6, .	2.8	20
15197	Human LINE-1 retrotransposition requires a metastable coiled coil and a positively charged N-terminus in L1ORF1p. <i>ELife</i> , 2018, 7, .	2.8	31
15198	Hexameric and pentameric complexes of the ExbBD energizer in the Ton system. <i>ELife</i> , 2018, 7, .	2.8	45
15199	Specific Eph receptor-cytoplasmic effector signaling mediated by SAM-SAM domain interactions. <i>ELife</i> , 2018, 7, .	2.8	35
15200	Viral GPCR US28 can signal in response to chemokine agonists of nearly unlimited structural degeneracy. <i>ELife</i> , 2018, 7, .	2.8	41
15201	The universally-conserved transcription factor RfaH is recruited to a hairpin structure of the non-template DNA strand. <i>ELife</i> , 2018, 7, .	2.8	45

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15202	Structures reveal opening of the store-operated calcium channel Orai. <i>ELife</i> , 2018, 7, .	2.8	77
15203	Structure of the human lipid-gated cation channel TRPC3. <i>ELife</i> , 2018, 7, .	2.8	104
15204	Single-particle cryo-EM structure of a voltage-activated potassium channel in lipid nanodiscs. <i>ELife</i> , 2018, 7, .	2.8	80
15205	Germline VRC01 antibody recognition of a modified clade C HIV-1 envelope trimer and a glycosylated HIV-1 gp120 core. <i>ELife</i> , 2018, 7, .	2.8	32
15206	Crystal structure of the full Swi2/Snf2 remodeler Mot1 in the resting state. <i>ELife</i> , 2018, 7, .	2.8	4
15207	Membrane insertion of $\hat{\pm}$ -xenorhabdysin in near-atomic detail. <i>ELife</i> , 2018, 7, .	2.8	27
15208	Structural basis for Scc3-dependent cohesin recruitment to chromatin. <i>ELife</i> , 2018, 7, .	2.8	69
15209	Distinct and evolutionary conserved structural features of the human nuclear exosome complex. <i>ELife</i> , 2018, 7, .	2.8	47
15210	Structural principles of SNARE complex recognition by the AAA+ protein NSF. <i>ELife</i> , 2018, 7, .	2.8	67
15211	Structural basis of tubulin recruitment and assembly by microtubule polymerases with tumor overexpressed gene (TOG) domain arrays. <i>ELife</i> , 2018, 7, .	2.8	32
15212	Unified mechanisms for self-RNA recognition by RIG-I Singleton-Merten syndrome variants. <i>ELife</i> , 2018, 7, .	2.8	26
15213	Translational initiation factor eIF5 replaces eIF1 on the 40S ribosomal subunit to promote start-codon recognition. <i>ELife</i> , 2018, 7, .	2.8	76
15214	Ligand discrimination and gating in cyclic nucleotide-gated ion channels from apo and partial agonist-bound cryo-EM structures. <i>ELife</i> , 2018, 7, .	2.8	39
15215	Biosynthesis of histone messenger RNA employs a specific 3' end endonuclease. <i>ELife</i> , 2018, 7, .	2.8	14
15216	BRCT domains of the DNA damage checkpoint proteins TOPBP1/Rad4 display distinct specificities for phosphopeptide ligands. <i>ELife</i> , 2018, 7, .	2.8	34
15217	Molecular basis of synaptic specificity by immunoglobulin superfamily receptors in <i>Drosophila</i> . <i>ELife</i> , 2019, 8, .	2.8	35
15218	Mechanisms of opening and closing of the bacterial replicative helicase. <i>ELife</i> , 2018, 7, .	2.8	16
15219	CryoEM structures of open dimers of gyrase A in complex with DNA illuminate mechanism of strand passage. <i>ELife</i> , 2018, 7, .	2.8	26

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15220	Lipidation-independent vacuolar functions of Atg8 rely on its noncanonical interaction with a vacuole membrane protein. <i>ELife</i> , 2018, 7, .	2.8	34
15221	Molecular basis for activation of lecithin:cholesterol acyltransferase by a compound that increases HDL cholesterol. <i>ELife</i> , 2018, 7, .	2.8	37
15222	An unexpected INAD PDZ tandem-mediated $plc\hat{1}^2$ binding in <i>Drosophila</i> photo receptors. <i>ELife</i> , 2018, 7, .	2.8	9
15223	DNA translocation mechanism of an XPD family helicase. <i>ELife</i> , 2018, 7, .	2.8	38
15224	High resolution cryo-EM structure of the helical RNA-bound Hantaan virus nucleocapsid reveals its assembly mechanisms. <i>ELife</i> , 2019, 8, .	2.8	28
15225	Architectural principles for Hfq/Crc-mediated regulation of gene expression. <i>ELife</i> , 2019, 8, .	2.8	46
15226	Structural basis of Ca^{2+} -dependent activation and lipid transport by a TMEM16 scramblase. <i>ELife</i> , 2019, 8, .	2.8	87
15227	Molecular mechanisms of gating in the calcium-activated chloride channel bestrophin. <i>ELife</i> , 2019, 8, .	2.8	34
15228	Importin-9 wraps around the H2A-H2B core to act as nuclear importer and histone chaperone. <i>ELife</i> , 2019, 8, .	2.8	47
15229	Cryo-EM reveals distinct conformations of <i>E. coli</i> ATP synthase on exposure to ATP. <i>ELife</i> , 2019, 8, .	2.8	48
15230	Structure of Vps4 with circular peptides and implications for translocation of two polypeptide chains by AAA+ ATPases. <i>ELife</i> , 2019, 8, .	2.8	41
15231	tRNA ligase structure reveals kinetic competition between non-conventional mRNA splicing and mRNA decay. <i>ELife</i> , 2019, 8, .	2.8	24
15232	The structure of the Ctf19c/CCAN from budding yeast. <i>ELife</i> , 2019, 8, .	2.8	71
15233	The complete structure of the human TFIIF core complex. <i>ELife</i> , 2019, 8, .	2.8	91
15234	Self-capping of nucleoprotein filaments protects the Newcastle disease virus genome. <i>ELife</i> , 2019, 8, .	2.8	18
15235	Structural basis for mammalian nucleotide sugar transport. <i>ELife</i> , 2019, 8, .	2.8	25
15236	Structural mechanisms of phospholipid activation of the human TPC2 channel. <i>ELife</i> , 2019, 8, .	2.8	103
15237	Binding and transport of D-aspartate by the glutamate transporter homolog GltTk. <i>ELife</i> , 2019, 8, .	2.8	24

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15238	The dynamic conformational landscape of the protein methyltransferase SETD8. <i>ELife</i> , 2019, 8, .	2.8	38
15239	Near-infrared dual bioluminescence imaging in mouse models of cancer using infraluciferin. <i>ELife</i> , 2019, 8, .	2.8	47
15240	Cryo-EM structures of remodeler-nucleosome intermediates suggest allosteric control through the nucleosome. <i>ELife</i> , 2019, 8, .	2.8	70
15241	Large protein organelles form a new iron sequestration system with high storage capacity. <i>ELife</i> , 2019, 8, .	2.8	92
15242	A dedicated diribonuclease resolves a key bottleneck for the terminal step of RNA degradation. <i>ELife</i> , 2019, 8, .	2.8	21
15243	HIV-1 integrase tetramers are the antiviral target of pyridine-based allosteric integrase inhibitors. <i>ELife</i> , 2019, 8, .	2.8	41
15244	Mechanism of pharmacochaperoning in a mammalian KATP channel revealed by cryo-EM. <i>ELife</i> , 2019, 8, .	2.8	68
15245	Structural and functional characterization of an otopetrin family proton channel. <i>ELife</i> , 2019, 8, .	2.8	20
15246	A chemical probe of CARM1 alters epigenetic plasticity against breast cancer cell invasion. <i>ELife</i> , 2019, 8, .	2.8	32
15247	Ctf4 organizes sister replisomes and Pol δ into a replication factory. <i>ELife</i> , 2019, 8, .	2.8	42
15248	Cryo-EM analyses reveal the common mechanism and diversification in the activation of RET by different ligands. <i>ELife</i> , 2019, 8, .	2.8	37
15249	Protein engineering expands the effector recognition profile of a rice NLR immune receptor. <i>ELife</i> , 2019, 8, .	2.8	118
15250	The structure of the yeast Ctf3 complex. <i>ELife</i> , 2019, 8, .	2.8	15
15251	Ternary structure of the outer membrane transporter FoxA with resolved signalling domain provides insights into TonB-mediated siderophore uptake. <i>ELife</i> , 2019, 8, .	2.8	48
15252	Activation mechanism of the insulin receptor revealed by cryo-EM structure of the fully liganded receptorâ€“ligand complex. <i>ELife</i> , 2019, 8, .	2.8	123
15253	Crystal structure of dopamine receptor D4 bound to the subtype selective ligand, L745870. <i>ELife</i> , 2019, 8, .	2.8	19
15254	Structural basis for AcrVA4 inhibition of specific CRISPR-Cas12a. <i>ELife</i> , 2019, 8, .	2.8	41
15255	Regulation of Eag1 gating by its intracellular domains. <i>ELife</i> , 2019, 8, .	2.8	25

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15256	Decoding WW domain tandem-mediated target recognitions in tissue growth and cell polarity. <i>ELife</i> , 2019, 8, .	2.8	38
15257	Structural model for differential cap maturation at growing microtubule ends. <i>ELife</i> , 2020, 9, .	2.8	44
15258	Ligand recognition and gating mechanism through three ligand-binding sites of human TRPM2 channel. <i>ELife</i> , 2019, 8, .	2.8	70
15259	The mechanosensitive ion channel TRAAK is localized to the mammalian node of Ranvier. <i>ELife</i> , 2019, 8, .	2.8	74
15260	Molecular basis of force-from-lipids gating in the mechanosensitive channel MscS. <i>ELife</i> , 2019, 8, .	2.8	84
15261	Allosteric activation of the nitric oxide receptor soluble guanylate cyclase mapped by cryo-electron microscopy. <i>ELife</i> , 2019, 8, .	2.8	66
15262	Activation of a nucleotide-dependent RCK domain requires binding of a cation cofactor to a conserved site. <i>ELife</i> , 2019, 8, .	2.8	8
15263	Unstructured regions in IRE1 β specify BiP-mediated destabilisation of the luminal domain dimer and repression of the UPR. <i>ELife</i> , 2019, 8, .	2.8	35
15264	The kinesin-5 tail domain directly modulates the mechanochemical cycle of the motor domain for anti-parallel microtubule sliding. <i>ELife</i> , 2020, 9, .	2.8	40
15265	Molecular structures of the human Slo1 K ⁺ channel in complex with β 4. <i>ELife</i> , 2019, 8, .	2.8	91
15266	Modulation of the <i>Erwinia</i> ligand-gated ion channel (ELIC) and the 5-HT ₃ receptor via a common vestibule site. <i>ELife</i> , 2020, 9, .	2.8	16
15267	Structural basis for the activation of PLC- β 3 isozymes by phosphorylation and cancer-associated mutations. <i>ELife</i> , 2019, 8, .	2.8	52
15268	Structural insights into mRNA reading frame regulation by tRNA modification and slippery codon-anticodon pairing. <i>ELife</i> , 2020, 9, .	2.8	28
15269	Structural basis of transcription inhibition by the DNA mimic protein Ocr of bacteriophage T7. <i>ELife</i> , 2020, 9, .	2.8	8
15270	Fatal amyloid formation in a patient's antibody light chain is caused by a single point mutation. <i>ELife</i> , 2020, 9, .	2.8	33
15271	Casein kinase 1 dynamics underlie substrate selectivity and the PER2 circadian phosphoswitch. <i>ELife</i> , 2020, 9, .	2.8	52
15272	Cryo-EM structure of the potassium-chloride cotransporter KCC4 in lipid nanodiscs. <i>ELife</i> , 2020, 9, .	2.8	36
15273	The inner junction complex of the cilia is an interaction hub that involves tubulin post-translational modifications. <i>ELife</i> , 2020, 9, .	2.8	1,191

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15274	The structure of the endogenous ESX-3 secretion system. <i>ELife</i> , 2019, 8, .	2.8	61
15275	Structural basis for COMPASS recognition of an H2B-ubiquitinated nucleosome. <i>ELife</i> , 2020, 9, .	2.8	79
15276	Cryo-EM structures demonstrate human IMPDH2 filament assembly tunes allosteric regulation. <i>ELife</i> , 2020, 9, .	2.8	56
15277	Structural basis for pharmacological modulation of the TRPC6 channel. <i>ELife</i> , 2020, 9, .	2.8	74
15278	Gating and selectivity mechanisms for the lysosomal K ⁺ channel TMEM175. <i>ELife</i> , 2020, 9, .	2.8	24
15279	The primary structural photoresponse of phytochrome proteins captured by a femtosecond X-ray laser. <i>ELife</i> , 2020, 9, .	2.8	78
15280	New approach for membrane protein reconstitution into peptidiscs and basis for their adaptability to different proteins. <i>ELife</i> , 2020, 9, .	2.8	57
15281	An asymmetric sheath controls flagellar supercoiling and motility in the leptospira spirochete. <i>ELife</i> , 2020, 9, .	2.8	26
15282	Structural basis for ion selectivity in TMEM175 K ⁺ channels. <i>ELife</i> , 2020, 9, .	2.8	27
15283	Insights into herpesvirus assembly from the structure of the pUL7:pUL51 complex. <i>ELife</i> , 2020, 9, .	2.8	27
15284	Structure of the human BBSome core complex. <i>ELife</i> , 2020, 9, .	2.8	59
15285	Structure of the AAA protein Msp1 reveals mechanism of mislocalized membrane protein extraction. <i>ELife</i> , 2020, 9, .	2.8	38
15286	Architecture of the chromatin remodeler RSC and insights into its nucleosome engagement. <i>ELife</i> , 2019, 8, .	2.8	68
15287	A complex IRES at the 5'-UTR of a viral mRNA assembles a functional 48S complex via an uAUG intermediate. <i>ELife</i> , 2020, 9, .	2.8	19
15288	Local frustration determines loop opening during the catalytic cycle of an oxidoreductase. <i>ELife</i> , 2020, 9, .	2.8	13
15289	Limited dishevelled/Axin oligomerization determines efficiency of Wnt/ β^2 -catenin signal transduction. <i>ELife</i> , 2020, 9, .	2.8	41
15290	CRISPR-Cas12a exploits R-loop asymmetry to form double-strand breaks. <i>ELife</i> , 2020, 9, .	2.8	80
15291	Dynamics at the serine loop underlie differential affinity of cryptochromes for CLOCK:BMAL1 to control circadian timing. <i>ELife</i> , 2020, 9, .	2.8	50

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15292	Kin discrimination in social yeast is mediated by cell surface receptors of the Flo11 adhesin family. <i>ELife</i> , 2020, 9, .	2.8	30
15293	mRNA stem-loops can pause the ribosome by hindering A-site tRNA binding. <i>ELife</i> , 2020, 9, .	2.8	40
15294	PrkA controls peptidoglycan biosynthesis through the essential phosphorylation of ReoM. <i>ELife</i> , 2020, 9, .	2.8	39
15295	Nucleosome-CHD4 chromatin remodeler structure maps human disease mutations. <i>ELife</i> , 2020, 9, .	2.8	52
15296	The His-Gly motif of acid-sensing ion channels resides in a reentrant α -loop TM implicated in gating and ion selectivity. <i>ELife</i> , 2020, 9, .	2.8	64
15297	Mechanical inhibition of isolated Vo from V/A-ATPase for proton conductance. <i>ELife</i> , 2020, 9, .	2.8	11
15298	An ER translocon for multi-pass membrane protein biogenesis. <i>ELife</i> , 2020, 9, .	2.8	85
15299	Structural insights into human acid-sensing ion channel 1a inhibition by snake toxin mambalgin1. <i>ELife</i> , 2020, 9, .	2.8	29
15300	Structure of substrate-bound SMG1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. <i>ELife</i> , 2020, 9, .	2.8	25
15301	Biochemical basis for the regulation of biosynthesis of antiparasitics by bacterial hormones. <i>ELife</i> , 2020, 9, .	2.8	3
15302	The architecture of EMC reveals a path for membrane protein insertion. <i>ELife</i> , 2020, 9, .	2.8	81
15303	Bacterial OTU deubiquitinases regulate substrate ubiquitination upon <i>Legionella</i> infection. <i>ELife</i> , 2020, 9, .	2.8	23
15304	Large domain movements through the lipid bilayer mediate substrate release and inhibition of glutamate transporters. <i>ELife</i> , 2020, 9, .	2.8	43
15305	Cannabidiol interactions with voltage-gated sodium channels. <i>ELife</i> , 2020, 9, .	2.8	40
15306	Structural basis for histone variant H3tK27me3 recognition by PHF1 and PHF19. <i>ELife</i> , 2020, 9, .	2.8	17
15307	Cryo-EM structures of human ZnT8 in both outward- and inward-facing conformations. <i>ELife</i> , 2020, 9, .	2.8	46
15308	EDF1 coordinates cellular responses to ribosome collisions. <i>ELife</i> , 2020, 9, .	2.8	96
15309	Structural ordering of the <i>Plasmodium berghei</i> circumsporozoite protein repeats by inhibitory antibody 3D11. <i>ELife</i> , 2020, 9, .	2.8	15

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15310	Ebola and Marburg virus matrix layers are locally ordered assemblies of VP40 dimers. <i>ELife</i> , 2020, 9, .	2.8	41
15311	Ciliate mitoribosome illuminates evolutionary steps of mitochondrial translation. <i>ELife</i> , 2020, 9, .	2.8	35
15312	Cryo-EM reveals species-specific components within the <i>Helicobacter pylori</i> Cag type IV secretion system core complex. <i>ELife</i> , 2020, 9, .	2.8	36
15313	Structural analysis of the <i>Legionella pneumophila</i> Dot/Icm type IV secretion system core complex. <i>ELife</i> , 2020, 9, .	2.8	43
15314	Cryo-EM structure of the lysosomal chloride-proton exchanger CLC-7 in complex with OSTM1. <i>ELife</i> , 2020, 9, .	2.8	41
15315	Transport of DNA within cohesin involves clamping on top of engaged heads by Scc2 and entrapment within the ring by Scc3. <i>ELife</i> , 2020, 9, .	2.8	67
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