

# Sampling the conformational space of the catalytic subu

ELife

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Versatility of Approximating Single-Particle Electron Microscopy Density Maps Using Pseudoatoms and Approximation-Accuracy Control. <i>BioMed Research International</i> , 2016, 2016, 1-11.	0.9	11
2	Accelerated cryo-EM structure determination with parallelisation using GPUs in RELION-2. <i>ELife</i> , 2016, 5, .	2.8	919
4	Identifying and Visualizing Macromolecular Flexibility in Structural Biology. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 47.	1.6	49
5	Substrate recruitment of Î³-secretase and mechanism of clinical presenilin mutations revealed by photoaffinity mapping. <i>EMBO Journal</i> , 2016, 35, 1628-1643.	3.5	104
6	Membrane trafficking and proteolytic activity of Î³-secretase in Alzheimerâ€™s disease. <i>Biological Chemistry</i> , 2016, 397, 827-835.	1.2	6
7	Translational termination without a stop codon. <i>Science</i> , 2016, 354, 1437-1440.	6.0	72
8	Tor forms a dimer through an N-terminal helical solenoid with a complex topology. <i>Nature Communications</i> , 2016, 7, 11016.	5.8	76
9	Cryo-electron Microscopy Analysis of Structurally Heterogeneous Macromolecular Complexes. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 385-390.	1.9	27
10	Breaking Cryo-EM Resolution Barriers to Facilitate Drug Discovery. <i>Cell</i> , 2016, 165, 1698-1707.	13.5	458
11	Ribosome-dependent activation of stringent control. <i>Nature</i> , 2016, 534, 277-280.	13.7	200
12	The Central domain of RyR1 is the transducer for long-range allosteric gating of channel opening. <i>Cell Research</i> , 2016, 26, 995-1006.	5.7	93
13	Structural insights into Ca <sup>2+</sup> -activated long-range allosteric channel gating of RyR1. <i>Cell Research</i> , 2016, 26, 977-994.	5.7	84
14	Atomic structure of the entire mammalian mitochondrial complex I. <i>Nature</i> , 2016, 538, 406-410.	13.7	427
15	Processing of Structurally Heterogeneous Cryo-EM Data in RELION. <i>Methods in Enzymology</i> , 2016, 579, 125-157.	0.4	502
16	Frealign. <i>Methods in Enzymology</i> , 2016, 579, 191-226.	0.4	169
17	Large-Scale Movements of IF3 and tRNA during Bacterial Translation Initiation. <i>Cell</i> , 2016, 167, 133-144.e13.	13.5	135
18	Structural characterization of coatomer in its cytosolic state. <i>Protein and Cell</i> , 2016, 7, 586-600.	4.8	12
19	Resolution advances in cryo-EM enable application to drug discovery. <i>Current Opinion in Structural Biology</i> , 2016, 41, 194-202.	2.6	95

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20	Biophysical mechanism of rhomboid proteolysis: Setting a foundation for therapeutics. <i>Seminars in Cell and Developmental Biology</i> , 2016, 60, 46-51.	2.3	8
21	The changing landscape of membrane protein structural biology through developments in electron microscopy. <i>Molecular Membrane Biology</i> , 2016, 33, 12-22.	2.0	40
22	Cryo-EM structure of the spliceosome immediately after branching. <i>Nature</i> , 2016, 537, 197-201.	13.7	208
23	Probing $\beta$ -secretase substrate interactions at the single amino acid residue level. <i>EMBO Journal</i> , 2016, 35, 1597-1599.	3.5	2
24	Structure of the full-length TRPV2 channel by cryo-EM. <i>Nature Communications</i> , 2016, 7, 11130.	5.8	176
25	Decoding Mammalian Ribosome-mRNA States by Translational GTPase Complexes. <i>Cell</i> , 2016, 167, 1229-1240.e15.	13.5	191
26	Antibody-Based Affinity Cryoelectron Microscopy at 2.6-Å... Resolution. <i>Structure</i> , 2016, 24, 1984-1990.	1.6	34
27	Mechanistic insight into eukaryotic 60S ribosomal subunit biogenesis by cryo-electron microscopy. <i>Rna</i> , 2016, 22, 1643-1662.	1.6	54
28	YphC and YsxC GTPases assist the maturation of the central protuberance, GTPase associated region and functional core of the 50S ribosomal subunit. <i>Nucleic Acids Research</i> , 2016, 44, 8442-8455.	6.5	42
29	Development of Sulfonamide Photoaffinity Inhibitors for Probing Cellular $\beta$ -Secretase. <i>ACS Chemical Neuroscience</i> , 2016, 7, 1166-1173.	1.7	20
30	Atomic structure of Hsp90-Cdc37-Cdk4 reveals that Hsp90 traps and stabilizes an unfolded kinase. <i>Science</i> , 2016, 352, 1542-1547.	6.0	354
31	Toward a structural understanding of co-translational protein translocation. <i>Current Opinion in Cell Biology</i> , 2016, 41, 91-99.	2.6	97
32	An algorithm for estimation and correction of anisotropic magnification distortion of cryo-EM images without need of pre-calibration. <i>Journal of Structural Biology</i> , 2016, 195, 207-215.	1.3	37
33	Elucidation of AMPA receptor-stargazin complexes by cryo-electron microscopy. <i>Science</i> , 2016, 353, 83-86.	6.0	112
34	Cryo-EM structure of the yeast U4/U6.U5 tri-snRNP at 3.7 Å... resolution. <i>Nature</i> , 2016, 530, 298-302.	13.7	184
35	Conformational Changes in Transmembrane Domain 4 of Presenilin 1 Are Associated with Altered Amyloid- $\beta$ 42 Production. <i>Journal of Neuroscience</i> , 2016, 36, 1362-1372.	1.7	25
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37	NGP 555, a $\beta$ -secretase modulator, lowers the amyloid biomarker, A $\beta$ <sub>42</sub> in cerebrospinal fluid while preventing Alzheimer's disease cognitive decline in rodents. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2017, 3, 65-73.	1.8	25

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38	Mapping the Binding Site of BMS-708163 on $\hat{\text{I}}^3$ -Secretase with Cleavable Photoprobes. <i>Cell Chemical Biology</i> , 2017, 24, 3-8.	2.5	40
39	Self-correcting mismatches during high-fidelity DNA replication. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 140-143.	3.6	42
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41	Structural basis of co-translational quality control by ArfA and RF2 bound to ribosome. <i>Nature</i> , 2017, 541, 554-557.	13.7	40
42	Structure of a Pancreatic ATP-Sensitive Potassium Channel. <i>Cell</i> , 2017, 168, 101-110.e10.	13.5	221
43	Cryo-EM Captures the Dynamics of Ion Channel Opening. <i>Cell</i> , 2017, 168, 341-343.	13.5	8
44	Computational methods for analyzing conformational variability of macromolecular complexes from cryo-electron microscopy images. <i>Current Opinion in Structural Biology</i> , 2017, 43, 114-121.	2.6	37
45	cryoSPARC: algorithms for rapid unsupervised cryo-EM structure determination. <i>Nature Methods</i> , 2017, 14, 290-296.	9.0	5,371
46	Initial Substrate Binding of $\hat{\text{I}}^3$ -Secretase: The Role of Substrate Flexibility. <i>ACS Chemical Neuroscience</i> , 2017, 8, 1279-1290.	1.7	23
47	Nmd3 is a structural mimic of $\langle \text{scp} \rangle \text{eIF} \langle / \text{scp} \rangle$ 5A, and activates the cp $\langle \text{scp} \rangle \text{GTP} \langle / \text{scp} \rangle$ ase Lsg1 during 60S ribosome biogenesis. <i>EMBO Journal</i> , 2017, 36, 854-868.	3.5	67
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50	Mechanism of chromatin remodelling revealed by the Snf2-nucleosome structure. <i>Nature</i> , 2017, 544, 440-445.	13.7	193
51	Structure of the MacAB-TolC ABC-type tripartite multidrug efflux pump. <i>Nature Microbiology</i> , 2017, 2, 17070.	5.9	140
52	The Canonical Notch Signaling Pathway: Structural and Biochemical Insights into Shape, Sugar, and Force. <i>Developmental Cell</i> , 2017, 41, 228-241.	3.1	291
53	Deletion of exons 9 and 10 of the Presenilin 1 gene in a patient with Early-onset Alzheimer Disease generates longer amyloid seeds. <i>Neurobiology of Disease</i> , 2017, 104, 97-103.	2.1	27
54	Structural Bases of Desensitization in AMPA Receptor-Auxiliary Subunit Complexes. <i>Neuron</i> , 2017, 94, 569-580.e5.	3.8	89
55	Single-Particle Electron Microscopy Analysis of DNA Repair Complexes. <i>Methods in Enzymology</i> , 2017, 592, 159-186.	0.4	2

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57	Î³-Secretase Modulators as AÎ²42-Lowering Pharmacological Agents to Treat Alzheimerâ€™s Disease. <i>Topics in Medicinal Chemistry</i> , 2017, , 87-118.	0.4	6
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61	Long-range allosteric regulation of the human 26S proteasome by 20S proteasome-targeting cancer drugs. <i>Nature Communications</i> , 2017, 8, 15578.	5.8	63
62	New approaches towards the understanding of integral membrane proteins: A structural perspective on G protein-coupled receptors. <i>Protein Science</i> , 2017, 26, 1493-1504.	3.1	41
63	Structures of RNA Polymerase Closed and Intermediate Complexes Reveal Mechanisms of DNA Opening and Transcription Initiation. <i>Molecular Cell</i> , 2017, 67, 106-116.e4.	4.5	44
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71	Structural insights into species-specific features of the ribosome from the human pathogen <i>Mycobacterium tuberculosis</i> . <i>Nucleic Acids Research</i> , 2017, 45, 10884-10894.	6.5	77
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75	Membrane Dynamics of Î³-Secretase Provides a Molecular Basis for Î²-Amyloid Binding and Processing. <i>ACS Chemical Neuroscience</i> , 2017, 8, 2424-2436.	1.7	54
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77	The cryo-electron microscopy structure of human transcription factor IIH. <i>Nature</i> , 2017, 549, 414-417.	13.7	89
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83	Structures of the calcium-activated, non-selective cation channel TRPM4. <i>Nature</i> , 2017, 552, 205-209.	13.7	158
84	Structural basis for the initiation of eukaryotic transcription-coupled DNA repair. <i>Nature</i> , 2017, 551, 653-657.	13.7	151
85	Activation of Î³-Secretase Trimming Activity by Topological Changes of Transmembrane Domain 1 of Presenilin 1. <i>Journal of Neuroscience</i> , 2017, 37, 12272-12280.	1.7	27
86	Cryo-EM: beyond the microscope. <i>Current Opinion in Structural Biology</i> , 2017, 46, 71-78.	2.6	76
87	Backbone Hydrogen Bond Strengths Can Vary Widely in Transmembrane Helices. <i>Journal of the American Chemical Society</i> , 2017, 139, 10742-10749.	6.6	36
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111	Cryo-EM structures of PRC2 simultaneously engaged with two functionally distinct nucleosomes. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 154-162.	3.6	170
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125	Likelihood-based structural analysis of electron microscopy images. <i>Current Opinion in Structural Biology</i> , 2018, 49, 162-168.	2.6	15
126	Rapid increase of near atomic resolution virus capsid structures determined by cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2018, 201, 1-4.	1.3	10
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148	Cryo-EM of ATP synthases. <i>Current Opinion in Structural Biology</i> , 2018, 52, 71-79.	2.6	46
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