

Cryo-EM structures of the autoinhibited E. coli ATP synthase

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Cryo-EM analysis of a domain antibody bound rotary ATPase complex. <i>Journal of Structural Biology</i> , 2017, 197, 350-353.	1.3	7
2	Conformational dynamics of the rotary subunit F in the A ₃ B ₃ DF complex of <i>Methanosarcina mazei</i> GÅ1 Aâ€ˆATP synthase monitored by single-molecule FRET. <i>FEBS Letters</i> , 2017, 591, 854-862.	1.3	8
3	Atomic model for the dimeric F _O region of mitochondrial ATP synthase. <i>Science</i> , 2017, 358, 936-940.	6.0	194
4	A Î³-subunit point mutation in <i>Chlamydomonas reinhardtii</i> chloroplast F ₁ F _o -ATP synthase confers tolerance to reactive oxygen species. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2017, 1858, 966-974.	0.5	13
5	Protonation-dependent stepped rotation of the F-type ATP synthase c-ring observed by single-molecule measurements. <i>Journal of Biological Chemistry</i> , 2017, 292, 17093-17100.	1.6	21
6	Catalytic robustness and torque generation of the F ₁ -ATPase. <i>Biophysical Reviews</i> , 2017, 9, 103-118.	1.5	48
7	Elastic strain and twist analysis of protein structural data and allostery of the transmembrane channel KcsA. <i>Physical Biology</i> , 2018, 15, 036004.	0.8	5
8	ATP synthase from <i>Trypanosoma brucei</i> has an elaborated canonical F ₁ -domain and conventional catalytic sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2102-2107.	3.3	27
9	The NMR solution structure of <i>Mycobacterium tuberculosis</i> F ₁ ATP synthase subunit Îµ provides new insight into energy coupling inside the rotary engine. <i>FEBS Journal</i> , 2018, 285, 1111-1128.	2.2	37
10	Cryo EM structure of intact rotary H ⁺ -ATPase/synthase from <i>Thermus thermophilus</i> . <i>Nature Communications</i> , 2018, 9, 89.	5.8	44
11	Crystallographic and enzymatic insights into the mechanisms of Mg-ADP inhibition in the A ₁ complex of the A ₁ A _o ATP synthase. <i>Journal of Structural Biology</i> , 2018, 201, 26-35.	1.3	4
12	Deleting the F ₁ -like Î¶ subunit from <i>Paracoccus denitrificans</i> ATP synthase is not sufficient to activate ATP hydrolysis. <i>Open Biology</i> , 2018, 8, 170206.	1.5	19
13	Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry. <i>Science</i> , 2018, 362, 829-834.	6.0	155
14	Control of rotation of the F ₁ F _o -ATP synthase nanomotor by an inhibitory Î±-helix from unfolded Îµ or intrinsically disordered Î¶ and IF ₁ proteins. <i>Journal of Bioenergetics and Biomembranes</i> , 2018, 50, 403-424.	1.0	17
15	ADP-Inhibition of H ⁺ -FOF ₁ -ATP Synthase. <i>Biochemistry (Moscow)</i> , 2018, 83, 1141-1160.	0.7	24
16	The Peripheral Stalk of Rotary ATPases. <i>Frontiers in Physiology</i> , 2018, 9, 1243.	1.3	24
17	Evidence for a Partially Stalled Î³ Rotor in F ₁ -ATPase from Hydrogenâ€ˆDeuterium Exchange Experiments and Molecular Dynamics Simulations. <i>Journal of the American Chemical Society</i> , 2018, 140, 14860-14869.	6.6	10
18	Structure and function of <i>Mycobacterium</i> -specific components of F-ATP synthase subunits Î± and Îµ. <i>Journal of Structural Biology</i> , 2018, 204, 420-434.	1.3	9

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19	Ectopic Neo-Formed Intracellular Membranes in Escherichia coli: A Response to Membrane Protein-Induced Stress Involving Membrane Curvature and Domains. <i>Biomolecules</i> , 2018, 8, 88.	1.8	13
20	Cryo-EM of ATP synthases. <i>Current Opinion in Structural Biology</i> , 2018, 52, 71-79.	2.6	46
21	Diffusion Measurements of Swimming Enzymes with Fluorescence Correlation Spectroscopy. <i>Accounts of Chemical Research</i> , 2018, 51, 1911-1920.	7.6	67
22	Insights into the regulatory function of the ϵ subunit from bacterial F-type ATP synthases: a comparison of structural, biochemical and biophysical data. <i>Open Biology</i> , 2018, 8, 170275.	1.5	21
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24	The regulatory subunit $\hat{\mu}$ in Escherichia coli FOF1-ATP synthase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, 775-788.	0.5	41
25	ATP Synthase Diseases of Mitochondrial Genetic Origin. <i>Frontiers in Physiology</i> , 2018, 9, 329.	1.3	88
26	Nucleus-Encoded Protein BFA1 Promotes Efficient Assembly of the Chloroplast ATP Synthase Coupling Factor 1. <i>Plant Cell</i> , 2018, 30, 1770-1788.	3.1	38
27	Structure, mechanism, and regulation of the chloroplast ATP synthase. <i>Science</i> , 2018, 360, .	6.0	308
28	Engineered Protein Model of the ATP synthase H ⁺ Channel Shows No Salt Bridge at the Rotor-Stator Interface. <i>Scientific Reports</i> , 2018, 8, 11361.	1.6	4
29	Interaction between \hat{I}^3C87 and \hat{I}^3R242 residues participates in energy coupling between catalysis and proton translocation in Escherichia coli ATP synthase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2019, 1860, 679-687.	0.5	5
30	Disrupting coupling within mycobacterial F-ATP synthases subunit $\hat{\mu}$ causes dysregulated energy production and cell wall biosynthesis. <i>Scientific Reports</i> , 2019, 9, 16759.	1.6	29
31	Cryo-EM studies of the rotary H ⁺ -ATPase/synthase from <i>Thermus thermophilus</i> . <i>Biophysics and Physicobiology</i> , 2019, 16, 140-146.	0.5	8
32	The structure of the catalytic domain of the ATP synthase from <i>Mycobacterium smegmatis</i> is a target for developing antitubercular drugs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4206-4211.	3.3	38
33	Amino Acid Residues \hat{I}^2139 , \hat{I}^2189 , and \hat{I}^2319 Modulate ADP-Inhibition in Escherichia coli H ⁺ -FOF1-ATP Synthase. <i>Biochemistry (Moscow)</i> , 2019, 84, 407-415.	0.7	4
34	Structure of F ₁ -ATPase from the obligate anaerobe <i>Fusobacterium nucleatum</i> . <i>Open Biology</i> , 2019, 9, 190066.	1.5	3
35	Structure and subunit arrangement of Mycobacterial F1FO ATP synthase and novel features of the unique mycobacterial subunit \hat{I} . <i>Journal of Structural Biology</i> , 2019, 207, 199-208.	1.3	22
36	Cryo-EM structure of the mammalian ATP synthase tetramer bound with inhibitory protein IF1. <i>Science</i> , 2019, 364, 1068-1075.	6.0	145

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38	Essay on Biomembrane Structure. Journal of Membrane Biology, 2019, 252, 115-130.	1.0	11
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42	Single-molecule analysis reveals rotational substeps and chemo-mechanical coupling scheme of <i>Enterococcus hirae</i> V1-ATPase. Journal of Biological Chemistry, 2019, 294, 17017-17030.	1.6	29
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46	The Unique C-Terminal Extension of Mycobacterial F-ATP Synthase Subunit ϵ Is the Major Contributor to Its Latent ATP Hydrolysis Activity. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	12
47	The 3 Å– 120 Å rotary mechanism of <i>Paracoccus denitrificans</i> F ₁ -ATPase is different from that of the bacterial and mitochondrial F ₁ -ATPases. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29647-29657.	3.3	19
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55	3D reconstruction and flexibility of the hybrid engine <i>Acetobacterium woodii</i> F-ATP synthase. <i>Biochemical and Biophysical Research Communications</i> , 2020, 527, 518-524.	1.0	1
56	Structural and functional properties of plant mitochondrial F-ATP synthase. <i>Mitochondrion</i> , 2020, 53, 178-193.	1.6	37
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79	Cryo-EM reveals distinct conformations of <i>E. coli</i> ATP synthase on exposure to ATP. <i>ELife</i> , 2019, 8, .	2.8	48
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89	A basic introduction to single particles cryo-electron microscopy. <i>AIMS Biophysics</i> , 2021, 9, 5-20.	0.3	1
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