

John L Rubinstein

List of Publications by Year in descending order

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109
papers

13,173
citations

57758

44
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30922

102
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152
all docs

152
docs citations

152
times ranked

16801
citing authors

#	ARTICLE	IF	CITATIONS
1	cryoSPARC: algorithms for rapid unsupervised cryo-EM structure determination. Nature Methods, 2017, 14, 290-296.	19.0	5,371
2	Porphyosome nanovesicles generated by porphyrin bilayers for use as multimodal biophotonic contrast agents. Nature Materials, 2011, 10, 324-332.	27.5	1,219
3	Structure and conformational states of the bovine mitochondrial ATP synthase by cryo-EM. ELife, 2015, 4, e10180.	6.0	264
4	Electron cryomicroscopy observation of rotational states in a eukaryotic V-ATPase. Nature, 2015, 521, 241-245.	27.8	261
5	Alignment of cryo-EM movies of individual particles by optimization of image translations. Journal of Structural Biology, 2015, 192, 188-195.	2.8	252
6	The structural basis of modified nucleosome recognition by 53BP1. Nature, 2016, 536, 100-103.	27.8	201
7	Structure of the mitochondrial ATP synthase by electron cryomicroscopy. EMBO Journal, 2003, 22, 6182-6192.	7.8	199
8	Structure of the alternative complex III in a supercomplex with cytochrome oxidase. Nature, 2018, 557, 123-126.	27.8	198
9	Atomic model for the dimeric F _O region of mitochondrial ATP synthase. Science, 2017, 358, 936-940.	12.6	194
10	Structure of V-ATPase from the mammalian brain. Science, 2020, 367, 1240-1246.	12.6	153
11	The human coronavirus HCoV-229E S-protein structure and receptor binding. ELife, 2019, 8, .	6.0	153
12	Eukaryotic V-ATPase: Novel structural findings and functional insights. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 857-879.	1.0	150
13	Atomic model for the membrane-embedded VO motor of a eukaryotic V-ATPase. Nature, 2016, 539, 118-122.	27.8	141
14	Tilt-Pair Analysis of Images from a Range of Different Specimens in Single-Particle Electron Cryomicroscopy. Journal of Molecular Biology, 2011, 413, 1028-1046.	4.2	138
15	Structure of a bacterial ATP synthase. ELife, 2019, 8, .	6.0	133
16	Inhibition of mitochondrial translation overcomes venetoclax resistance in AML through activation of the integrated stress response. Science Translational Medicine, 2019, 11, .	12.4	129
17	Adaptor Protein Self-Assembly Drives the Control of a Cullin-RING Ubiquitin Ligase. Structure, 2012, 20, 1141-1153.	3.3	127
18	Structure of a AAA+ unfoldase in the process of unfolding substrate. ELife, 2017, 6, .	6.0	119

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19	The Polydispersity of β -Crystallin Is Rationalized by an Interconverting Polyhedral Architecture. <i>Structure</i> , 2011, 19, 1855-1863.	3.3	116
20	Structure and Roles of V-type ATPases. <i>Trends in Biochemical Sciences</i> , 2020, 45, 295-307.	7.5	115
21	Molecular basis of human CD22 function and therapeutic targeting. <i>Nature Communications</i> , 2017, 8, 764.	12.8	114
22	Assembly and structural analysis of a covalently closed nano-scale DNA cage. <i>Nucleic Acids Research</i> , 2008, 36, 1113-1119.	14.5	112
23	Arrangement of subunits in intact mammalian mitochondrial ATP synthase determined by cryo-EM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11675-11680.	7.1	112
24	An Autoinhibited Structure of β -Catenin and Its Implications for Vinculin Recruitment to Adherens Junctions. <i>Journal of Biological Chemistry</i> , 2013, 288, 15913-15925.	3.4	110
25	Structure of mycobacterial ATP synthase bound to the tuberculosis drug bedaquiline. <i>Nature</i> , 2021, 589, 143-147.	27.8	110
26	Subnanometre-resolution structure of the intact <i>Thermus thermophilus</i> H ⁺ -driven ATP synthase. <i>Nature</i> , 2012, 481, 214-218.	27.8	109
27	Radiation Damage in Electron Cryomicroscopy. <i>Methods in Enzymology</i> , 2010, 481, 371-388.	1.0	107
28	Bacterial polysaccharide co-polymerases share a common framework for control of polymer length. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 130-138.	8.2	103
29	Structure of a functional obligate complex III ₂ IV ₂ respiratory supercomplex from <i>Mycobacterium smegmatis</i> . <i>Nature Structural and Molecular Biology</i> , 2018, 25, 1128-1136.	8.2	95
30	A processive rotary mechanism couples substrate unfolding and proteolysis in the ClpXP degradation machinery. <i>ELife</i> , 2020, 9, .	6.0	94
31	Fabrication of carbon films with \sim 450nm holes for cryo-EM with a direct detector device. <i>Journal of Structural Biology</i> , 2014, 185, 42-47.	2.8	92
32	Structure of the vacuolar-type ATPase from <i>Saccharomyces cerevisiae</i> at 11-Å... resolution. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1356-1362.	8.2	90
33	TROSY-Based NMR Evidence for a Novel Class of 20S Proteasome Inhibitors. <i>Biochemistry</i> , 2008, 47, 6727-6734.	2.5	74
34	The resolution dependence of optimal exposures in liquid nitrogen temperature electron cryomicroscopy of catalase crystals. <i>Journal of Structural Biology</i> , 2010, 169, 431-437.	2.8	73
35	Structural comparison of the vacuolar and Golgi V-ATPases from <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7272-7277.	7.1	73
36	Electron-event representation data enable efficient cryoEM file storage with full preservation of spatial and temporal resolution. <i>IUCr</i> , 2020, 7, 860-869.	2.2	71

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37	Structure of intact <i>Thermus thermophilus</i> V-ATPase by cryo-EM reveals organization of the membrane-bound V _O motor. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1367-1372.	7.1	69
38	Cryo-EM Structure of the Yeast ATP Synthase. Journal of Molecular Biology, 2008, 382, 1256-1264.	4.2	62
39	Phospholipid Association Is Essential for Dynamin-related Protein Mgm1 to Function in Mitochondrial Membrane Fusion. Journal of Biological Chemistry, 2009, 284, 28682-28686.	3.4	62
40	The Crystal Structure of Bacteriophage HK97 gp6: Defining a Large Family of Head-Tail Connector Proteins. Journal of Molecular Biology, 2010, 395, 754-768.	4.2	62
41	Shake-it-off: a simple ultrasonic cryo-EM specimen-preparation device. Acta Crystallographica Section D: Structural Biology, 2019, 75, 1063-1070.	2.3	58
42	Reversible inhibition of the ClpP protease via an N-terminal conformational switch. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6447-E6456.	7.1	56
43	Unfolding the mechanism of the AAA+ unfoldase VAT by a combined cryo-EM, solution NMR study. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E4190-9.	7.1	55
44	ATP Synthase from <i>Saccharomyces cerevisiae</i> : Location of the OSCP Subunit in the Peripheral Stalk Region. Journal of Molecular Biology, 2002, 321, 613-619.	4.2	54
45	Molecular basis for the binding and modulation of V-ATPase by a bacterial effector protein. PLoS Pathogens, 2017, 13, e1006394.	4.7	53
46	Automated particle picking for low-contrast macromolecules in cryo-electron microscopy. Journal of Structural Biology, 2014, 186, 1-7.	2.8	52
47	Validating maps from single particle electron cryomicroscopy. Current Opinion in Structural Biology, 2015, 34, 135-144.	5.7	50
48	Multivalency transforms SARS-CoV-2 antibodies into ultrapotent neutralizers. Nature Communications, 2021, 12, 3661.	12.8	48
49	Structure of the <i>Pseudomonas aeruginosa</i> Type IVa Pilus Secretin at 7.4 Å. Structure, 2016, 24, 1778-1787.	3.3	47
50	Models for the a subunits of the <i>Thermus thermophilus</i> V/A-ATPase and <i>Saccharomyces cerevisiae</i> V-ATPase enzymes by cryo-EM and evolutionary covariance. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3245-3250.	7.1	47
51	Structural Insights into KCTD Protein Assembly and Cullin3 Recognition. Journal of Molecular Biology, 2016, 428, 92-107.	4.2	47
52	An allosteric switch regulates <i>Mycobacterium tuberculosis</i> ClpP1P2 protease function as established by cryo-EM and methyl-TROSY NMR. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 5895-5906.	7.1	47
53	Revised subunit order of mammalian septin complexes explains their in vitro polymerization properties. Molecular Biology of the Cell, 2021, 32, 289-300.	2.1	47
54	Cryo-EM of ATP synthases. Current Opinion in Structural Biology, 2018, 52, 71-79.	5.7	46

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55	The RNF168 paralog RNF169 defines a new class of ubiquitylated histone reader involved in the response to DNA damage. <i>ELife</i> , 2017, 6, .	6.0	44
56	Activity-Independent Discovery of Secondary Metabolites Using Chemical Elicitation and Cheminformatic Inference. <i>ACS Chemical Biology</i> , 2015, 10, 2616-2623.	3.4	43
57	The N Termini of a-Subunit Isoforms Are Involved in Signaling between Vacuolar H ⁺ -ATPase (V-ATPase) and Cytohesin-2*. <i>Journal of Biological Chemistry</i> , 2013, 288, 5896-5913.	3.4	42
58	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.	14.5	42
59	Beyond blob-ology. <i>Science</i> , 2014, 345, 617-619.	12.6	40
60	Structural analysis of membrane protein complexes by single particle electron microscopy. <i>Methods</i> , 2007, 41, 409-416.	3.8	39
61	ATP Synthase from <i>Saccharomyces cerevisiae</i> : Location of Subunit h in the Peripheral Stalk Region. <i>Journal of Molecular Biology</i> , 2005, 345, 513-520.	4.2	38
62	Phages have adapted the same protein fold to fulfill multiple functions in virion assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14384-14389.	7.1	37
63	Cryo-EM structure and kinetics reveal electron transfer by 2D diffusion of cytochrome <i>c</i> in the yeast III-IV respiratory supercomplex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	33
64	Electron cryomicroscopy of membrane proteins: Specimen preparation for two-dimensional crystals and single particles. <i>Micron</i> , 2011, 42, 107-116.	2.2	31
65	Cooperative subunit dynamics modulate p97 function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 158-167.	7.1	31
66	Through-grid wicking enables high-speed cryoEM specimen preparation. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1092-1103.	2.3	31
67	Recognition of Semaphorin Proteins by P.Âsordellii Lethal Toxin Reveals Principles of Receptor Specificity in Clostridial Toxins. <i>Cell</i> , 2020, 182, 345-356.e16.	28.9	29
68	Triggered Instability of Liposomes Bound to Hydrophobically Modified Coreâˆ”Shell PNIPAM Hydrogel Beads. <i>Langmuir</i> , 2010, 26, 1081-1089.	3.5	28
69	Description and comparison of algorithms for correcting anisotropic magnification in cryo-EM images. <i>Journal of Structural Biology</i> , 2015, 192, 209-215.	2.8	27
70	TMaCS: A hybrid template matching and classification system for partially-automated particle selection. <i>Journal of Structural Biology</i> , 2013, 181, 234-242.	2.8	25
71	Processing of Cryo-EM Movie Data. <i>Methods in Enzymology</i> , 2016, 579, 103-124.	1.0	25
72	Structure of Ycf1p reveals the transmembrane domain TMD0 and the regulatory region of ABCC transporters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	24

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73	A Bayesian method for 3D macromolecular structure inference using class average images from single particle electron microscopy. <i>Bioinformatics</i> , 2010, 26, 2406-2415.	4.1	20
74	Apoptolidin family glycomacrolides target leukemia through inhibition of ATP synthase. <i>Nature Chemical Biology</i> , 2022, 18, 360-367.	8.0	20
75	Structure of ATP synthase under strain during catalysis. <i>Nature Communications</i> , 2022, 13, 2232.	12.8	20
76	Cryo-EM studies of the structure and dynamics of vacuolar-type ATPases. <i>Science Advances</i> , 2016, 2, e1600725.	10.3	19
77	An intrinsically disordered motif regulates the interaction between the p47 adaptor and the p97 AAA+ ATPase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 26226-26236.	7.1	19
78	Structure of mycobacterial CIII2CIV2 respiratory supercomplex bound to the tuberculosis drug candidate telacebec (Q203). <i>ELife</i> , 2021, 10, .	6.0	19
79	Vma9p Need Not Be Associated with the Yeast V-ATPase for Fully-Coupled Proton Pumping Activity in Vitro. <i>Biochemistry</i> , 2015, 54, 853-858.	2.5	16
80	Multiple conformations facilitate PilT function in the type IV pilus. <i>Nature Communications</i> , 2019, 10, 5198.	12.8	16
81	Protocol for rapid unsupervised cryo-EM structure determination using cryoSPARC software. <i>Protocol Exchange</i> , 0, , .	0.3	16
82	Detection and quantification of the vacuolar H ⁺ -ATPase using the <i>Legionella</i> effector protein SidK. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	16
83	Coordinated conformational changes in the V1 complex during V-ATPase reversible dissociation. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 430-439.	8.2	16
84	Rieske head domain dynamics and indazole-derivative inhibition of <i>Candida albicans</i> complex III. <i>Structure</i> , 2022, 30, 129-138.e4.	3.3	15
85	Structural ordering of the <i>Plasmodium berghei</i> circumsporozoite protein repeats by inhibitory antibody 3D11. <i>ELife</i> , 2020, 9, .	6.0	15
86	Angle determination for side views in single particle electron microscopy. <i>Journal of Structural Biology</i> , 2008, 162, 260-270.	2.8	13
87	CryoEM Reveals the Complexity and Diversity of ATP Synthases. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	13
88	A pH-Dependent Conformational Switch Controls <i>N. meningitidis</i> ClpP Protease Function. <i>Journal of the American Chemical Society</i> , 2020, 142, 20519-20523.	13.7	12
89	Toosendanin, a novel potent vacuolar-type H ⁺ -translocating ATPase inhibitor, sensitizes cancer cells to chemotherapy by blocking protective autophagy. <i>International Journal of Biological Sciences</i> , 2022, 18, 2684-2702.	6.4	12
90	Use of phage display and high-density screening for the isolation of an antibody against the 51-kDa subunit of complex I. <i>Analytical Biochemistry</i> , 2003, 314, 294-300.	2.4	11

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91	Location of Subunit d in the Peripheral Stalk of the ATP Synthase from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2008, 47, 11804-11810.	2.5	11
92	Single Particle Electron Microscopy. <i>Methods in Molecular Biology</i> , 2013, 955, 401-426.	0.9	11
93	CryoEM map of <i>Pseudomonas aeruginosa</i> PilQ enables structural characterization of TsaP. <i>Structure</i> , 2021, 29, 457-466.e4.	3.3	9
94	Cryo-EM Captures the Dynamics of Ion Channel Opening. <i>Cell</i> , 2017, 168, 341-343.	28.9	8
95	Band 3 function and dysfunction in a structural context. <i>Current Opinion in Hematology</i> , 2018, 25, 163-170.	2.5	8
96	The respiratory supercomplex from <i>C.Âglutamicum</i> . <i>Structure</i> , 2022, 30, 338-349.e3.	3.3	7
97	Edged watershed segmentation: A semi-interactive algorithm for segmentation of low-resolution maps from electron cryomicroscopy. <i>Journal of Structural Biology</i> , 2011, 176, 127-132.	2.8	6
98	The study of vacuolar-type ATPases by single particle electron microscopy. <i>Biochemistry and Cell Biology</i> , 2014, 92, 460-466.	2.0	5
99	Structural basis of <i>Plasmodium vivax</i> inhibition by antibodies binding to the circumsporozoite protein repeats. <i>ELife</i> , 2022, 11, .	6.0	5
100	SINGLE PARTICLE ELECTRON MICROSCOPY OF THE MITOCHONDRIAL ATP SYNTHASE. <i>Biophysical Reviews and Letters</i> , 2010, 05, 59-71.	0.8	4
101	Probing Cooperativity of Nâ€œTerminal Domain Orientations in the p97 Molecular Machine: Synergy Between NMR Spectroscopy and Cryoâ€œEM. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 22423-22426.	13.8	4
102	Cryo-EM of the Yeast V_O Complex Reveals Distinct Binding Sites for Macrolide V-ATPase Inhibitors. <i>ACS Chemical Biology</i> , 2022, 17, 619-628.	3.4	4
103	Flexibility leads to function. <i>Nature Chemistry</i> , 2014, 6, 170-171.	13.6	1
104	Probing Cooperativity of Nâ€œTerminal Domain Orientations in the p97 Molecular Machine: Synergy Between NMR Spectroscopy and Cryoâ€œEM. <i>Angewandte Chemie</i> , 2020, 132, 22609-22612.	2.0	1
105	Structural Characterization of Endogenous Tuberous Sclerosis Protein Complex Revealed Potential Polymeric Assembly. <i>Biochemistry</i> , 2021, 60, 1808-1821.	2.5	1
106	Through-grid wicking enables high-speed cryoEM specimen preparation. <i>Microscopy and Microanalysis</i> , 2021, 27, 526-528.	0.4	1
107	Algorithmic Advances in Single Particle Cryo-EM Data Processing. <i>Microscopy and Microanalysis</i> , 2018, 24, 868-869.	0.4	0
108	Structure of the Alternative Complex III from <i>Flavobacterium johnsoniae</i> in a Supercomplex with Cytochrome <i>c</i> Oxidase. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.5	0

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109	Membrane Protein Structure Determination by Electron Cryo-Microscopy. , 0, , 29-54.		0