

John L Rubinstein

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7451893/publications.pdf>

Version: 2024-02-01

109
papers

13,173
citations

57758

44
h-index

30922

102
g-index

152
all docs

152
docs citations

152
times ranked

16801
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Apoptolidin family glycomacrolides target leukemia through inhibition of ATP synthase. <i>Nature Chemical Biology</i> , 2022, 18, 360-367.	8.0	20
3	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
4	Structural basis of <i>Plasmodium vivax</i> inhibition by antibodies binding to the circumsporozoite protein repeats. <i>ELife</i> , 2022, 11, .	6.0	5
5	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
6	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
7	The respiratory supercomplex from <i>C.Âglutamicum</i> . <i>Structure</i> , 2022, 30, 338-349.e3.	3.3	7
8	Structure of ATP synthase under strain during catalysis. <i>Nature Communications</i> , 2022, 13, 2232.	12.8	20
9	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
10	Structure of mycobacterial ATP synthase bound to the tuberculosis drug bedaquiline. <i>Nature</i> , 2021, 589, 143-147.	27.8	110
11	Revised subunit order of mammalian septin complexes explains their in vitro polymerization properties. <i>Molecular Biology of the Cell</i> , 2021, 32, 289-300.	2.1	47
12	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
13	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
14	CryoEM map of <i>Pseudomonas aeruginosa</i> PilQ enables structural characterization of TsaP. <i>Structure</i> , 2021, 29, 457-466.e4.	3.3	9
15	Structural Characterization of Endogenous Tuberous Sclerosis Protein Complex Revealed Potential Polymeric Assembly. <i>Biochemistry</i> , 2021, 60, 1808-1821.	2.5	1
16	Multivalency transforms SARS-CoV-2 antibodies into ultrapotent neutralizers. <i>Nature Communications</i> , 2021, 12, 3661.	12.8	48
17	Through-grid wicking enables high-speed cryoEM specimen preparation. <i>Microscopy and Microanalysis</i> , 2021, 27, 526-528.	0.4	1
18	Structure of mycobacterial CIII2CIV2 respiratory supercomplex bound to the tuberculosis drug candidate telacebec (Q203). <i>ELife</i> , 2021, 10, .	6.0	19

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	Probing Cooperativity of N-Terminal Domain Orientations in the p97 Molecular Machine: Synergy Between NMR Spectroscopy and Cryo-EM. <i>Angewandte Chemie</i> , 2020, 132, 22609-22612.	2.0	1
22	Probing Cooperativity of N-Terminal Domain Orientations in the p97 Molecular Machine: Synergy Between NMR Spectroscopy and Cryo-EM. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 22423-22426.	13.8	4
23	Through-grid wicking enables high-speed cryoEM specimen preparation. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 1092-1103.	2.3	31
24	Structure of V-ATPase from the mammalian brain. <i>Science</i> , 2020, 367, 1240-1246.	12.6	153
25	Recognition of Semaphorin Proteins by Pseudomonas aeruginosa Lethal Toxin Reveals Principles of Receptor Specificity in Clostridial Toxins. <i>Cell</i> , 2020, 182, 345-356.e16.	28.9	29
26	An allosteric switch regulates Mycobacterium tuberculosis ClpP1P2 protease function as established by cryo-EM and methyl-TROSY NMR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 5895-5906.	7.1	47
27	Structure and Roles of V-type ATPases. <i>Trends in Biochemical Sciences</i> , 2020, 45, 295-307.	7.5	115
28	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
29	A processive rotary mechanism couples substrate unfolding and proteolysis in the ClpXP degradation machinery. <i>ELife</i> , 2020, 9, .	6.0	94
30	Structural ordering of the Plasmodium berghei circumsporozoite protein repeats by inhibitory antibody 3D11. <i>ELife</i> , 2020, 9, .	6.0	15
31	Structure of the Alternative Complex III from Flavobacterium johnsoniae in a Supercomplex with Cytochrome c Oxidase. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.5	0
32	Inhibition of mitochondrial translation overcomes venetoclax resistance in AML through activation of the integrated stress response. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	129
33	Structural comparison of the vacuolar and Golgi V-ATPases from Saccharomyces cerevisiae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7272-7277.	7.1	73
34	Multiple conformations facilitate PilT function in the type IV pilus. <i>Nature Communications</i> , 2019, 10, 5198.	12.8	16
35	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
36	Shake-it-off: a simple ultrasonic cryo-EM specimen-preparation device. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 1063-1070.	2.3	58

#	ARTICLE	IF	CITATIONS
37	Structure of a bacterial ATP synthase. <i>ELife</i> , 2019, 8, .	6.0	133
38	The human coronavirus HCoV-229E S-protein structure and receptor binding. <i>ELife</i> , 2019, 8, .	6.0	153
39	Structure of the alternative complex III in a supercomplex with cytochrome oxidase. <i>Nature</i> , 2018, 557, 123-126.	27.8	198
40	Band 3 function and dysfunction in a structural context. <i>Current Opinion in Hematology</i> , 2018, 25, 163-170.	2.5	8
41	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
42	Algorithmic Advances in Single Particle Cryo-EM Data Processing. <i>Microscopy and Microanalysis</i> , 2018, 24, 868-869.	0.4	0
43	Cryo-EM of ATP synthases. <i>Current Opinion in Structural Biology</i> , 2018, 52, 71-79.	5.7	46
44	Reversible inhibition of the ClpP protease via an N-terminal conformational switch. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6447-E6456.	7.1	56
45	Cryo-EM Captures the Dynamics of Ion Channel Opening. <i>Cell</i> , 2017, 168, 341-343.	28.9	8
46	cryoSPARC: algorithms for rapid unsupervised cryo-EM structure determination. <i>Nature Methods</i> , 2017, 14, 290-296.	19.0	5,371
47	Atomic model for the dimeric F _O region of mitochondrial ATP synthase. <i>Science</i> , 2017, 358, 936-940.	12.6	194
48	Molecular basis of human CD22 function and therapeutic targeting. <i>Nature Communications</i> , 2017, 8, 764.	12.8	114
49	Molecular basis for the binding and modulation of V-ATPase by a bacterial effector protein. <i>PLoS Pathogens</i> , 2017, 13, e1006394.	4.7	53
50	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
51	Structure of a AAA+ unfoldase in the process of unfolding substrate. <i>ELife</i> , 2017, 6, .	6.0	119
52	Cryo-EM studies of the structure and dynamics of vacuolar-type ATPases. <i>Science Advances</i> , 2016, 2, e1600725.	10.3	19
53	Processing of Cryo-EM Movie Data. <i>Methods in Enzymology</i> , 2016, 579, 103-124.	1.0	25
54	Structure of the <i>Pseudomonas aeruginosa</i> Type IVa Pilus Secretin at 7.4Å.... <i>Structure</i> , 2016, 24, 1778-1787.	3.3	47

#	ARTICLE	IF	CITATIONS
55	The structural basis of modified nucleosome recognition by 53BP1. <i>Nature</i> , 2016, 536, 100-103.	27.8	201
56	Unfolding the mechanism of the AAA+ unfoldase VAT by a combined cryo-EM, solution NMR study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4190-9.	7.1	55
57	Atomic model for the membrane-embedded VO motor of a eukaryotic V-ATPase. <i>Nature</i> , 2016, 539, 118-122.	27.8	141
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	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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3245-3250.	7.1	47
60	Structural Insights into KCTD Protein Assembly and Cullin3 Recognition. <i>Journal of Molecular Biology</i> , 2016, 428, 92-107.	4.2	47
61	Structure and conformational states of the bovine mitochondrial ATP synthase by cryo-EM. <i>ELife</i> , 2015, 4, e10180.	6.0	264
62	Validating maps from single particle electron cryomicroscopy. <i>Current Opinion in Structural Biology</i> , 2015, 34, 135-144.	5.7	50
63	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
64	Electron cryomicroscopy observation of rotational states in a eukaryotic V-ATPase. <i>Nature</i> , 2015, 521, 241-245.	27.8	261
65	Activity-Independent Discovery of Secondary Metabolites Using Chemical Elicitation and Cheminformatic Inference. <i>ACS Chemical Biology</i> , 2015, 10, 2616-2623.	3.4	43
66	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
67	Alignment of cryo-EM movies of individual particles by optimization of image translations. <i>Journal of Structural Biology</i> , 2015, 192, 188-195.	2.8	252
68	The study of vacuolar-type ATPases by single particle electron microscopy. <i>Biochemistry and Cell Biology</i> , 2014, 92, 460-466.	2.0	5
69	Automated particle picking for low-contrast macromolecules in cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2014, 186, 1-7.	2.8	52
70	Fabrication of carbon films with ~ 4500 nm holes for cryo-EM with a direct detector device. <i>Journal of Structural Biology</i> , 2014, 185, 42-47.	2.8	92
71	Eukaryotic V-ATPase: Novel structural findings and functional insights. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 857-879.	1.0	150
72	Flexibility leads to function. <i>Nature Chemistry</i> , 2014, 6, 170-171.	13.6	1

#	ARTICLE	IF	CITATIONS
73	Beyond blob-ology. <i>Science</i> , 2014, 345, 617-619.	12.6	40
74	Single Particle Electron Microscopy. <i>Methods in Molecular Biology</i> , 2013, 955, 401-426.	0.9	11
75	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
76	The N Termini of α -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
77	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
78	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
79	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
80	Subnanometre-resolution structure of the intact <i>Thermus thermophilus</i> H ⁺ -driven ATP synthase. <i>Nature</i> , 2012, 481, 214-218.	27.8	109
81	Adaptor Protein Self-Assembly Drives the Control of a Cullin-RING Ubiquitin Ligase. <i>Structure</i> , 2012, 20, 1141-1153.	3.3	127
82	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
83	Tilt-Pair Analysis of Images from a Range of Different Specimens in Single-Particle Electron Cryomicroscopy. <i>Journal of Molecular Biology</i> , 2011, 413, 1028-1046.	4.2	138
84	Porphysome nanovesicles generated by porphyrin bilayers for use as multimodal biophotonic contrast agents. <i>Nature Materials</i> , 2011, 10, 324-332.	27.5	1,219
85	Electron cryomicroscopy of membrane proteins: Specimen preparation for two-dimensional crystals and single particles. <i>Micron</i> , 2011, 42, 107-116.	2.2	31
86	The Polydispersity of β -Crystallin Is Rationalized by an Interconverting Polyhedral Architecture. <i>Structure</i> , 2011, 19, 1855-1863.	3.3	116
87	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
88	SINGLE PARTICLE ELECTRON MICROSCOPY OF THE MITOCHONDRIAL ATP SYNTHASE. <i>Biophysical Reviews and Letters</i> , 2010, 05, 59-71.	0.8	4
89	Structure of intact <i>Thermus thermophilus</i> V-ATPase by cryo-EM reveals organization of the membrane-bound V _O motor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 1367-1372.	7.1	69
90	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

#	ARTICLE	IF	CITATIONS
91	Triggered Instability of Liposomes Bound to Hydrophobically Modified Core-Shell PNIPAM Hydrogel Beads. <i>Langmuir</i> , 2010, 26, 1081-1089.	3.5	28
92	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
93	The Crystal Structure of Bacteriophage HK97 gp6: Defining a Large Family of Head-Tail Connector Proteins. <i>Journal of Molecular Biology</i> , 2010, 395, 754-768.	4.2	62
94	Radiation Damage in Electron Cryomicroscopy. <i>Methods in Enzymology</i> , 2010, 481, 371-388.	1.0	107
95	Phospholipid Association Is Essential for Dynamin-related Protein Mgm1 to Function in Mitochondrial Membrane Fusion. <i>Journal of Biological Chemistry</i> , 2009, 284, 28682-28686.	3.4	62
96	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
97	TROSY-Based NMR Evidence for a Novel Class of 20S Proteasome Inhibitors. <i>Biochemistry</i> , 2008, 47, 6727-6734.	2.5	74
98	Angle determination for side views in single particle electron microscopy. <i>Journal of Structural Biology</i> , 2008, 162, 260-270.	2.8	13
99	Cryo-EM Structure of the Yeast ATP Synthase. <i>Journal of Molecular Biology</i> , 2008, 382, 1256-1264.	4.2	62
100	Assembly and structural analysis of a covalently closed nano-scale DNA cage. <i>Nucleic Acids Research</i> , 2008, 36, 1113-1119.	14.5	112
101	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
102	Structural analysis of membrane protein complexes by single particle electron microscopy. <i>Methods</i> , 2007, 41, 409-416.	3.8	39
103	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
104	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
105	Structure of the mitochondrial ATP synthase by electron cryomicroscopy. <i>EMBO Journal</i> , 2003, 22, 6182-6192.	7.8	199
106	ATP Synthase from <i>Saccharomyces cerevisiae</i> : Location of the OSCP Subunit in the Peripheral Stalk Region. <i>Journal of Molecular Biology</i> , 2002, 321, 613-619.	4.2	54
107	Protocol for rapid unsupervised cryo-EM structure determination using cryoSPARC software. <i>Protocol Exchange</i> , 0, , .	0.3	16
108	Membrane Protein Structure Determination by Electron Cryo-Microscopy. , 0, , 29-54.		0

#	ARTICLE	IF	CITATIONS
109	CryoEM Reveals the Complexity and Diversity of ATP Synthases. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	13