

Sriram Subramaniam

List of Publications by Year in descending order

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162
papers

13,522
citations

18436

62
h-index

26548

107
g-index

194
all docs

194
docs citations

194
times ranked

15309
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular architecture of native HIV-1 gp120 trimers. <i>Nature</i> , 2008, 455, 109-113.	13.7	720
2	A collaborative framework for 3D alignment and classification of heterogeneous subvolumes in cryo-electron tomography. <i>Journal of Structural Biology</i> , 2013, 181, 116-127.	1.3	524
3	SARS-CoV-2 Omicron variant: Antibody evasion and cryo-EM structure of spike protein-ACE2 complex. <i>Science</i> , 2022, 375, 760-764.	6.0	488
4	Breaking Cryo-EM Resolution Barriers to Facilitate Drug Discovery. <i>Cell</i> , 2016, 165, 1698-1707.	13.5	458
5	Molecular mechanism of vectorial proton translocation by bacteriorhodopsin. <i>Nature</i> , 2000, 406, 653-657.	13.7	451
6	2.2 Å... resolution cryo-EM structure of Î²-galactosidase in complex with a cell-permeant inhibitor. <i>Science</i> , 2015, 348, 1147-1151.	6.0	440
7	Mitochondrial reticulum for cellular energy distribution in muscle. <i>Nature</i> , 2015, 523, 617-620.	13.7	355
8	Site-specific 3D imaging of cells and tissues with a dual beam microscope. <i>Journal of Structural Biology</i> , 2006, 155, 63-73.	1.3	311
9	2.3 Å... resolution cryo-EM structure of human p97 and mechanism of allosteric inhibition. <i>Science</i> , 2016, 351, 871-875.	6.0	305
10	Protein conformational changes in the bacteriorhodopsin photocycle 1 Edited by B. Honig. <i>Journal of Molecular Biology</i> , 1999, 287, 145-161.	2.0	244
11	Cryo-EM structure of human rhodopsin bound to an inhibitory G protein. <i>Nature</i> , 2018, 558, 553-558.	13.7	230
12	Structural mechanism of glutamate receptor activation and desensitization. <i>Nature</i> , 2014, 514, 328-334.	13.7	207
13	Cryo-electron microscopy – a primer for the non-microscopist. <i>FEBS Journal</i> , 2013, 280, 28-45.	2.2	194
14	Structure of Î²-galactosidase at 3.2-Å... resolution obtained by cryo-electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11709-11714.	3.3	184
15	Focused ion beams in biology. <i>Nature Methods</i> , 2015, 12, 1021-1031.	9.0	184
16	Structural Mechanism of Trimeric HIV-1 Envelope Glycoprotein Activation. <i>PLoS Pathogens</i> , 2012, 8, e1002797.	2.1	182
17	Direct visualization of Escherichia coli chemotaxis receptor arrays using cryo-electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3777-3781.	3.3	176
18	Cryo-electron microscopy structures of the N501Y SARS-CoV-2 spike protein in complex with ACE2 and 2 potent neutralizing antibodies. <i>PLoS Biology</i> , 2021, 19, e3001237.	2.6	171

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19	3D visualization of HIV transfer at the virological synapse between dendritic cells and T cells. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 13336-13341.	3.3	169
20	Electron Tomography of the Contact between T Cells and SIV/HIV-1: Implications for Viral Entry. PLoS Pathogens, 2007, 3, e63.	2.1	165
21	Molecular Architectures of Trimeric SIV and HIV-1 Envelope Glycoproteins on Intact Viruses: Strain-Dependent Variation in Quaternary Structure. PLoS Pathogens, 2010, 6, e1001249.	2.1	161
22	Cryo-EM Structures Reveal Mechanism and Inhibition of DNA Targeting by a CRISPR-Cas Surveillance Complex. Cell, 2017, 171, 414-426.e12.	13.5	158
23	Power Grid Protection of the Muscle Mitochondrial Reticulum. Cell Reports, 2017, 19, 487-496.	2.9	155
24	Prefusion structure of trimeric HIV-1 envelope glycoprotein determined by cryo-electron microscopy. Nature Structural and Molecular Biology, 2013, 20, 1352-1357.	3.6	152
25	Ion-Abrasion Scanning Electron Microscopy Reveals Surface-Connected Tubular Conduits in HIV-Infected Macrophages. PLoS Pathogens, 2009, 5, e1000591.	2.1	151
26	Trimeric HIV-1 glycoprotein gp140 immunogens and native HIV-1 envelope glycoproteins display the same closed and open quaternary molecular architectures. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 11440-11445.	3.3	149
27	Cryo-electron tomography of bacteria: progress, challenges and future prospects. Nature Reviews Microbiology, 2009, 7, 666-675.	13.6	144
28	Critical mixing in monolayer mixtures of phospholipid and cholesterol. The Journal of Physical Chemistry, 1987, 91, 1715-1718.	2.9	132
29	Cryo-EM structure of a dimeric B-Raf:14-3-3 complex reveals asymmetry in the active sites of B-Raf kinases. Science, 2019, 366, 109-115.	6.0	127
30	Molecular architecture and mechanism of an icosahedral pyruvate dehydrogenase complex: a multifunctional catalytic machine. EMBO Journal, 2002, 21, 5587-5598.	3.5	115
31	Atomic Resolution Cryo-EM Structure of β -Galactosidase. Structure, 2018, 26, 848-856.e3.	1.6	115
32	Three-dimensional structure of a bacterial oxalate transporter. Nature Structural Biology, 2002, 9, 597-600.	9.7	114
33	3D Imaging of mammalian cells with ion-abrasion scanning electron microscopy. Journal of Structural Biology, 2009, 166, 1-7.	1.3	113
34	Cryo-EM Structures of the Magnesium Channel CorA Reveal Symmetry Break upon Gating. Cell, 2016, 164, 747-756.	13.5	111
35	Structural Model for 12-Helix Transporters Belonging to the Major Facilitator Superfamily. Journal of Bacteriology, 2003, 185, 1712-1718.	1.0	103
36	High Potency of a Bivalent Human VH Domain in SARS-CoV-2 Animal Models. Cell, 2020, 183, 429-441.e16.	13.5	100

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37	Structure and accessibility of HA trimers on intact 2009 H1N1 pandemic influenza virus to stem region-specific neutralizing antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4592-4597.	3.3	99
38	Multi-resolution correlative focused ion beam scanning electron microscopy: Applications to cell biology. Journal of Structural Biology, 2014, 185, 278-284.	1.3	99
39	Structural mechanisms of centromeric nucleosome recognition by the kinetochore protein CENP-N. Science, 2018, 359, 339-343.	6.0	98
40	Cryo-EM structures reveal coordinated domain motions that govern DNA cleavage by Cas9. Nature Structural and Molecular Biology, 2019, 26, 679-685.	3.6	97
41	Broadly protective murine monoclonal antibodies against influenza B virus target highly conserved neuraminidase epitopes. Nature Microbiology, 2017, 2, 1415-1424.	5.9	96
42	Resolution advances in cryo-EM enable application to drug discovery. Current Opinion in Structural Biology, 2016, 41, 194-202.	2.6	95
43	Protein Secondary Structure Determination by Constrained Single-Particle Cryo-Electron Tomography. Structure, 2012, 20, 2003-2013.	1.6	90
44	Self-assembled monolayers improve protein distribution on holey carbon cryo-EM supports. Scientific Reports, 2014, 4, 7084.	1.6	88
45	Cryo-EM structure of the bacteriophage T4 portal protein assembly at near-atomic resolution. Nature Communications, 2015, 6, 7548.	5.8	88
46	Correlative 3D imaging of whole mammalian cells with light and electron microscopy. Journal of Structural Biology, 2011, 176, 268-278.	1.3	81
47	Single-particle cryo-EM structure of a voltage-activated potassium channel in lipid nanodiscs. ELife, 2018, 7, .	2.8	80
48	HIV-1 activates Cdc42 and induces membrane extensions in immature dendritic cells to facilitate cell-to-cell virus propagation. Blood, 2011, 118, 4841-4852.	0.6	79
49	Structural basis of kainate subtype glutamate receptor desensitization. Nature, 2016, 537, 567-571.	13.7	78
50	A core-weighted fitting method for docking atomic structures into low-resolution maps: Application to cryo-electron microscopy. Journal of Structural Biology, 2003, 141, 63-76.	1.3	77
51	Cell Surface Filaments of the Gliding Bacterium <i>Flavobacterium johnsoniae</i> Revealed by Cryo-Electron Tomography. Journal of Bacteriology, 2007, 189, 7503-7506.	1.0	76
52	Cryo-EM: beyond the microscope. Current Opinion in Structural Biology, 2017, 46, 71-78.	2.6	76
53	Cryo-EM Analysis of the Conformational Landscape of Human P-glycoprotein (ABCB1) During its Catalytic Cycle. Molecular Pharmacology, 2016, 90, 35-41.	1.0	75
54	HIV-1 envelope glycoprotein structure. Current Opinion in Structural Biology, 2013, 23, 268-276.	2.6	73

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55	Molecular Structure of a 9-MDa Icosahedral Pyruvate Dehydrogenase Subcomplex Containing the E2 and E3 Enzymes Using Cryoelectron Microscopy. <i>Journal of Biological Chemistry</i> , 2006, 281, 4364-4370.	1.6	72
56	Chemoreceptors in <i>Caulobacter crescentus</i> : Trimers of Receptor Dimers in a Partially Ordered Hexagonally Packed Array. <i>Journal of Bacteriology</i> , 2008, 190, 6805-6810.	1.0	72
57	Role of HAMP domains in chemotaxis signaling by bacterial chemoreceptors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16555-16560.	3.3	72
58	3D imaging of diatoms with ion-abrasion scanning electron microscopy. <i>Journal of Structural Biology</i> , 2009, 166, 316-328.	1.3	71
59	Structural and biochemical rationale for enhanced spike protein fitness in delta and kappa SARS-CoV-2 variants. <i>Nature Communications</i> , 2022, 13, 742.	5.8	71
60	Three-Dimensional Electron Microscopic Imaging of Membrane Invaginations in <i>Escherichia coli</i> Overproducing the Chemotaxis Receptor Tsr. <i>Journal of Bacteriology</i> , 2004, 186, 5052-5061.	1.0	70
61	Electron tomography in nanoparticle imaging and analysis. <i>Nanomedicine</i> , 2008, 3, 125-131.	1.7	70
62	Bridging the imaging gap: visualizing subcellular architecture with electron tomography. <i>Current Opinion in Microbiology</i> , 2005, 8, 316-322.	2.3	68
63	Structural analysis of receptor binding domain mutations in SARS-CoV-2 variants of concern that modulate ACE2 and antibody binding. <i>Cell Reports</i> , 2021, 37, 110156.	2.9	67
64	Three-Dimensional Electron Microscopy at Molecular Resolution. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2004, 33, 141-155.	18.3	65
65	Membrane protein structure determination using cryo-electron tomography and 3D image averaging. <i>Current Opinion in Structural Biology</i> , 2009, 19, 402-407.	2.6	65
66	Structural snapshots of conformational changes in a seven-helix membrane protein: lessons from bacteriorhodopsin. <i>Current Opinion in Structural Biology</i> , 2009, 19, 433-439.	2.6	64
67	Electron Microscopic Analysis of Membrane Assemblies Formed by the Bacterial Chemotaxis Receptor Tsr. <i>Journal of Bacteriology</i> , 2003, 185, 3636-3643.	1.0	62
68	CCD detectors in high-resolution biological electron microscopy. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 1-27.	2.4	61
69	Three-Dimensional Imaging of HIV-1 Virological Synapses Reveals Membrane Architectures Involved in Virus Transmission. <i>Journal of Virology</i> , 2014, 88, 10327-10339.	1.5	61
70	Structure and Transport Mechanism of the Bacterial Oxalate Transporter OxIT. <i>Biophysical Journal</i> , 2004, 87, 3600-3607.	0.2	59
71	Automated image acquisition and processing using a new generation of 4K \times 4K CCD cameras for cryo electron microscopic studies of macromolecular assemblies. <i>Journal of Structural Biology</i> , 2003, 143, 135-144.	1.3	57
72	Electron tomography of degenerating neurons in mice with abnormal regulation of iron metabolism. <i>Journal of Structural Biology</i> , 2005, 150, 144-153.	1.3	55

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73	Three-Dimensional Imaging of the Highly Bent Architecture of <i>Bdellovibrio bacteriovorus</i> by Using Cryo-Electron Tomography. <i>Journal of Bacteriology</i> , 2008, 190, 2588-2596.	1.0	55
74	Electron tomography of viruses. <i>Current Opinion in Structural Biology</i> , 2007, 17, 596-602.	2.6	54
75	CryoEM at IUCr: a new era. <i>IUCr</i> , 2016, 3, 3-7.	1.0	54
76	Glutamate receptor desensitization is mediated by changes in quaternary structure of the ligand binding domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5921-5926.	3.3	53
77	Spatial Localization of the Ebola Virus Glycoprotein Mucin-Like Domain Determined by Cryo-Electron Tomography. <i>Journal of Virology</i> , 2014, 88, 10958-10962.	1.5	53
78	Targeted conformational search with map-restrained self-guided Langevin dynamics: Application to flexible fitting into electron microscopic density maps. <i>Journal of Structural Biology</i> , 2013, 183, 429-440.	1.3	50
79	Electron Crystallography of Bacteriorhodopsin with Millisecond Time Resolution. <i>Journal of Structural Biology</i> , 1999, 128, 19-25.	1.3	49
80	Data management challenges in three-dimensional EM. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1203-1207.	3.6	49
81	Three-Dimensional Imaging of Viral Infections. <i>Annual Review of Virology</i> , 2014, 1, 453-473.	3.0	49
82	Maturation of the HIV-1 core by a non-diffusional phase transition. <i>Nature Communications</i> , 2015, 6, 5854.	5.8	49
83	Mono- and bilayers of phospholipids at interfaces: interlayer coupling and phase stability. <i>The Journal of Physical Chemistry</i> , 1985, 89, 3592-3595.	2.9	48
84	Automated Data Collection with a Tecnai 12 Electron Microscope: Applications for Molecular Imaging by Cryomicroscopy. <i>Journal of Structural Biology</i> , 2001, 135, 251-261.	1.3	47
85	Spiral Architecture of the Nucleoid in <i>Bdellovibrio bacteriovorus</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1341-1350.	1.0	47
86	A 3D cellular context for the macromolecular world. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 841-845.	3.6	47
87	Three-Dimensional Structures of Soluble CD4-Bound States of Trimeric Simian Immunodeficiency Virus Envelope Glycoproteins Determined by Using Cryo-Electron Tomography. <i>Journal of Virology</i> , 2011, 85, 12114-12123.	1.5	46
88	The structure of bacteriorhodopsin: an emerging consensus. <i>Current Opinion in Structural Biology</i> , 1999, 9, 462-468.	2.6	45
89	Structural plasticity of a transmembrane peptide allows self-assembly into biologically active nanoparticles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9798-9803.	3.3	45
90	Crystallographic analysis of protein conformational changes in the bacteriorhodopsin photocycle. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2000, 1460, 157-165.	0.5	44

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91	Molecular structures of trimeric HIV-1 Env in complex with small antibody derivatives. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 513-518.	3.3	44
92	Frontiers in Cryo Electron Microscopy of Complex Macromolecular Assemblies. Annual Review of Biomedical Engineering, 2019, 21, 395-415.	5.7	44
93	A molecular mechanism for the generation of ligand-dependent differential outputs by the epidermal growth factor receptor. ELife, 2021, 10, .	2.8	44
94	Stoichiometry and Absolute Quantification of Proteins with Mass Spectrometry Using Fluorescent and Isotope-labeled Concatenated Peptide Standards. Molecular and Cellular Proteomics, 2008, 7, 442-447.	2.5	42
95	Automatic joint classification and segmentation of whole cell 3D images. Pattern Recognition, 2009, 42, 1067-1079.	5.1	42
96	Compositional Mapping of the Surface and Interior of Mammalian Cells at Submicrometer Resolution. Analytical Chemistry, 2011, 83, 1207-1213.	3.2	42
97	Chemical mapping of mammalian cells by atom probe tomography. Journal of Structural Biology, 2012, 178, 98-107.	1.3	41
98	Using Cryo-EM to Map Small Ligands on Dynamic Metabolic Enzymes: Studies with Glutamate Dehydrogenase. Molecular Pharmacology, 2016, 89, 645-651.	1.0	41
99	Structure of trimeric HIV-1 envelope glycoproteins. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4172-4.	3.3	39
100	An energy-based three-dimensional segmentation approach for the quantitative interpretation of electron tomograms. IEEE Transactions on Image Processing, 2005, 14, 1314-1323.	6.0	38
101	Evaluation of denoising algorithms for biological electron tomography. Journal of Structural Biology, 2008, 164, 7-17.	1.3	38
102	Protein Conformational Changes in the Bacteriorhodopsin Photocycle: Comparison of Findings from Electron and X-Ray Crystallographic Analyses. PLoS ONE, 2009, 4, e5769.	1.1	38
103	Chemotaxis kinase CheA is activated by three neighbouring chemoreceptor dimers as effectively as by receptor clusters. Molecular Microbiology, 2011, 79, 677-685.	1.2	38
104	Lateral density of receptor arrays in the membrane plane influences sensitivity of the E. coli chemotaxis response. EMBO Journal, 2011, 30, 1719-1729.	3.5	37
105	From structure to mechanism: electron crystallographic studies of bacteriorhodopsin. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2002, 360, 859-874.	1.6	36
106	Structural insights into the mechanism of proton pumping by bacteriorhodopsin. FEBS Letters, 2003, 545, 2-8.	1.3	35
107	Cryoelectron Tomographic Analysis of an HIV-neutralizing Protein and Its Complex with Native Viral gp120*. Journal of Biological Chemistry, 2007, 282, 27754-27759.	1.6	35
108	A versatile nano display platform from bacterial spore coat proteins. Nature Communications, 2015, 6, 6777.	5.8	35

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109	The democratization of cryo-EM. <i>Nature Methods</i> , 2016, 13, 607-608.	9.0	35
110	Malaria parasites use a soluble RhopH complex for erythrocyte invasion and an integral form for nutrient uptake. <i>ELife</i> , 2021, 10, .	2.8	35
111	Griffithsin tandemers: flexible and potent lectin inhibitors of the human immunodeficiency virus. <i>Retrovirology</i> , 2015, 12, 6.	0.9	34
112	Mapping of Ebolavirus Neutralization by Monoclonal Antibodies in the ZMapp Cocktail Using Cryo-Electron Tomography and Studies of Cellular Entry. <i>Journal of Virology</i> , 2016, 90, 7618-7627.	1.5	32
113	The cryo-EM revolution: fueling the next phase. <i>IUCrJ</i> , 2019, 6, 1-2.	1.0	32
114	Ion-abrasion scanning electron microscopy reveals distorted liver mitochondrial morphology in murine methylmalonic acidemia. <i>Journal of Structural Biology</i> , 2010, 171, 125-132.	1.3	31
115	A Tail-Based Mechanism Drives Nucleosome Demethylation by the LSD2/NPAC Multimeric Complex. <i>Cell Reports</i> , 2019, 27, 387-399.e7.	2.9	31
116	Automated 100-position specimen loader and image acquisition system for transmission electron microscopy. <i>Journal of Structural Biology</i> , 2007, 158, 318-326.	1.3	30
117	Structure of the primed state of the ATPase domain of chromatin remodeling factor ISWI bound to the nucleosome. <i>Nucleic Acids Research</i> , 2019, 47, 9400-9409.	6.5	30
118	HIV-1 Envelope Glycoprotein Trimers Display Open Quaternary Conformation When Bound to the gp41 Membrane-Proximal External-Region-Directed Broadly Neutralizing Antibody Z13e1. <i>Journal of Virology</i> , 2013, 87, 7191-7196.	1.5	27
119	A paradigm shift in structural biology. <i>Nature Methods</i> , 2022, 19, 20-23.	9.0	27
120	Derivation of Neural Stem Cells from Human Adult Peripheral CD34+ Cells for an Autologous Model of Neuroinflammation. <i>PLoS ONE</i> , 2013, 8, e81720.	1.1	26
121	Cryo-electron Microscopy Structures of Chimeric Hemagglutinin Displayed on a Universal Influenza Vaccine Candidate. <i>MBio</i> , 2016, 7, e00257.	1.8	26
122	1.8 Å... resolution structure of Î²-galactosidase with a 200 kV CRYO ARM electron microscope. <i>IUCrJ</i> , 2020, 7, 639-643.	1.0	26
123	Projection structure of the bacterial oxalate transporter OxIT at 3.4 Å... resolution. <i>Journal of Structural Biology</i> , 2003, 144, 320-326.	1.3	25
124	Biochemical and structural analyses reveal that the tumor suppressor neurofibromin (NF1) forms a high-affinity dimer. <i>Journal of Biological Chemistry</i> , 2020, 295, 1105-1119.	1.6	25
125	Deep-Learning-Assisted Volume Visualization. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2019, 25, 1378-1391.	2.9	24
126	Extended Polypeptide Linkers Establish the Spatial Architecture of a Pyruvate Dehydrogenase Multienzyme Complex. <i>Structure</i> , 2008, 16, 93-103.	1.6	22

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127	Glycan reactive anti-HIV-1 antibodies bind the SARS-CoV-2 spike protein but do not block viral entry. <i>Scientific Reports</i> , 2021, 11, 12448.	1.6	22
128	The SIV Surface Spike Imaged by Electron Tomography: One Leg or Three?. <i>PLoS Pathogens</i> , 2006, 2, e91.	2.1	21
129	Catching HIV in the act™ with 3D electron microscopy. <i>Trends in Microbiology</i> , 2013, 21, 397-404.	3.5	21
130	Single-Particle Cryo-Electron Microscopy (Cryo-EM). <i>Advances in Imaging and Electron Physics</i> , 2014, , 113-137.	0.1	20
131	Host membrane lipids are trafficked to membranes of intravacuolar bacterium <i>Ehrlichia chaffeensis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8032-8043.	3.3	20
132	Computational separation of conformational heterogeneity using cryo-electron tomography and 3D sub-volume averaging. <i>Journal of Structural Biology</i> , 2012, 178, 165-176.	1.3	19
133	Semi-automated 3D segmentation of human skeletal muscle using Focused Ion Beam-Scanning Electron Microscopic images. <i>Journal of Structural Biology</i> , 2019, 207, 1-11.	1.3	18
134	Complexes of Neutralizing and Non-Neutralizing Affinity Matured Fabs with a Mimetic of the Internal Trimeric Coiled-Coil of HIV-1 gp41. <i>PLoS ONE</i> , 2013, 8, e78187.	1.1	17
135	Studies of Rh1 Metarhodopsin Stabilization in Wild-Type <i>Drosophila</i> and in Mutants Lacking One or Both Arrestins. <i>Biochemistry</i> , 1997, 36, 2188-2196.	1.2	16
136	Cryo-EM of viruses and vaccine design. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8903-8905.	3.3	16
137	Determination of Molecular Structures of HIV Envelope Glycoproteins using Cryo-Electron Tomography and Automated Sub-tomogram Averaging. <i>Journal of Visualized Experiments</i> , 2011, , .	0.2	14
138	The crystal structure of human GlnRS provides basis for the development of neurological disorders. <i>Nucleic Acids Research</i> , 2016, 44, 3420-3431.	6.5	14
139	Structural basis for early-onset neurological disorders caused by mutations in human selenocysteine synthase. <i>Scientific Reports</i> , 2016, 6, 32563.	1.6	13
140	AAA+ ATPase p97/VCP mutants and inhibitor binding disrupt inter-domain coupling and subsequent allosteric activation. <i>Journal of Biological Chemistry</i> , 2021, 297, 101187.	1.6	13
141	A coiled-coil-repeat protein Ccrp™ in <i>Bdellovibrio bacteriovorus</i> prevents cellular indentation, but is not essential for vibroid cell morphology. <i>FEMS Microbiology Letters</i> , 2010, 313, 89-95.	0.7	11
142	Shape-Based Regularization of Electron Tomographic Reconstruction. <i>IEEE Transactions on Medical Imaging</i> , 2012, 31, 2241-2252.	5.4	10
143	Modulation of Arrestin Release in the Light-Driven Regeneration of Rh1 <i>Drosophila</i> Rhodopsin. <i>Biochemistry</i> , 1996, 35, 1848-1855.	1.2	9
144	Electron Tomography of Bacterial Chemotaxis Receptor Assemblies. <i>Methods in Cell Biology</i> , 2007, 79, 373-384.	0.5	9

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145	Microbiology catches the cryo-EM bug. <i>Current Opinion in Microbiology</i> , 2018, 43, 199-207.	2.3	9
146	COVID-19 and cryo-EM. <i>IUCr</i> , 2020, 7, 575-576.	1.0	9
147	Site-specific 3D Imaging of Cells and Tissues Using DualBeam Technology. <i>Microscopy and Microanalysis</i> , 2004, 10, 1124-1125.	0.2	7
148	Cryo-electron microscopy instrumentation and techniques for life sciences and materials science. <i>MRS Bulletin</i> , 2019, 44, 929-934.	1.7	7
149	<i>Plasmodium vivax</i> and human hexokinases share similar active sites but display distinct quaternary architectures. <i>IUCr</i> , 2020, 7, 453-461.	1.0	6
150	Staphylococcal Enterotoxin A Induces Small Clusters of HLA-DR1 on B Cells. <i>PLoS ONE</i> , 2009, 4, e6188.	1.1	5
151	Expression of bacteriorhodopsin in Sf9 and COS-1 cells. <i>Journal of Bioenergetics and Biomembranes</i> , 1997, 29, 55-59.	1.0	4
152	Visualizing Cells and Humans in 3D: Biomedical Image Analysis at Nanometer and Meter Scales. <i>IEEE Computer Graphics and Applications</i> , 2012, 32, 39-49.	1.0	4
153	New insights into Raf regulation from structural analyses. <i>Current Opinion in Structural Biology</i> , 2021, 71, 223-231.	2.6	4
154	Comparison of side-chain dispersion in protein structures determined by cryo-EM and X-ray crystallography. <i>IUCr</i> , 2022, 9, 98-103.	1.0	4
155	FROM GIGABYTES TO BYTES: AUTOMATED DENOISING AND FEATURE IDENTIFICATION IN ELECTRON TOMOGRAMS OF INTACT BACTERIAL CELLS. , 2007, , .		1
156	Molecular Structure of an Icosahedral Pyruvate Dehydrogenase Complex. <i>Microscopy and Microanalysis</i> , 2002, 8, 214-215.	0.2	0
157	Bridging the imaging gap in nanobiology with three-dimensional electron microscopy. , 2006, , .		0
158	Gigabytes to Bytes: Automated Denoising and Feature Extraction as Applied to the Analysis of HIV Architecture and Variability using Electron Tomography. , 2007, , .		0
159	DETERMINATION OF PROTEIN STRUCTURES IN SITU: ELECTRON TOMOGRAPHY OF INTACT VIRUSES AND CELLS. , 2007, , .		0
160	There is no overkill in biochemistry. <i>Resonance</i> , 2012, 17, 1157-1164.	0.2	0
161	Accelerating Discovery in 3D Microanalysis: Leveraging Open Source Software and Deskside High Performance Computing. <i>Microscopy and Microanalysis</i> , 2014, 20, 774-775.	0.2	0
162	The Pyruvate Dehydrogenase Multienzyme Complex. <i>Oxidative Stress and Disease</i> , 2003, , .	0.3	0