

# Sriram Subramaniam

## List of Publications by Year in descending order

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Version: 2024-02-01

162  
papers

13,522  
citations

18482

62  
h-index

26613

107  
g-index

194  
all docs

194  
docs citations

194  
times ranked

15309  
citing authors

#	ARTICLE	IF	CITATIONS
1	A paradigm shift in structural biology. <i>Nature Methods</i> , 2022, 19, 20-23.	19.0	27
2	SARS-CoV-2 Omicron variant: Antibody evasion and cryo-EM structure of spike protein-ACE2 complex. <i>Science</i> , 2022, 375, 760-764.	12.6	488
3	Structural and biochemical rationale for enhanced spike protein fitness in delta and kappa SARS-CoV-2 variants. <i>Nature Communications</i> , 2022, 13, 742.	12.8	71
4	Comparison of side-chain dispersion in protein structures determined by cryo-EM and X-ray crystallography. <i>IUCr</i> , 2022, 9, 98-103.	2.2	4
5	Malaria parasites use a soluble RhopH complex for erythrocyte invasion and an integral form for nutrient uptake. <i>ELife</i> , 2021, 10, .	6.0	35
6	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.	5.6	171
7	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.	3.3	22
8	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.	3.4	13
9	New insights into Raf regulation from structural analyses. <i>Current Opinion in Structural Biology</i> , 2021, 71, 223-231.	5.7	4
10	A molecular mechanism for the generation of ligand-dependent differential outputs by the epidermal growth factor receptor. <i>ELife</i> , 2021, 10, .	6.0	44
11	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.	6.4	67
12	High Potency of a Bivalent Human VH Domain in SARS-CoV-2 Animal Models. <i>Cell</i> , 2020, 183, 429-441.e16.	28.9	100
13	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.	7.1	20
14	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.	3.4	25
15	<i>Plasmodium vivax</i> and human hexokinases share similar active sites but display distinct quaternary architectures. <i>IUCr</i> , 2020, 7, 453-461.	2.2	6
16	1.8 Å resolution structure of Î²-galactosidase with a 200 kV CRYO ARM electron microscope. <i>IUCr</i> , 2020, 7, 639-643.	2.2	26
17	COVID-19 and cryo-EM. <i>IUCr</i> , 2020, 7, 575-576.	2.2	9
18	Cryo-EM structures reveal coordinated domain motions that govern DNA cleavage by Cas9. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 679-685.	8.2	97

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19	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.	14.5	30
20	Cryo-EM structure of a dimeric B-Raf:14-3-3 complex reveals asymmetry in the active sites of B-Raf kinases. <i>Science</i> , 2019, 366, 109-115.	12.6	127
21	Frontiers in Cryo Electron Microscopy of Complex Macromolecular Assemblies. <i>Annual Review of Biomedical Engineering</i> , 2019, 21, 395-415.	12.3	44
22	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.	2.8	18
23	The cryo-EM revolution: fueling the next phase. <i>IUCr</i> , 2019, 6, 1-2.	2.2	32
24	A Tail-Based Mechanism Drives Nucleosome Demethylation by the LSD2/NPAC Multimeric Complex. <i>Cell Reports</i> , 2019, 27, 387-399.e7.	6.4	31
25	Cryo-electron microscopy instrumentation and techniques for life sciences and materials science. <i>MRS Bulletin</i> , 2019, 44, 929-934.	3.5	7
26	Deep-Learning-Assisted Volume Visualization. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2019, 25, 1378-1391.	4.4	24
27	Microbiology catches the cryo-EM bug. <i>Current Opinion in Microbiology</i> , 2018, 43, 199-207.	5.1	9
28	Structural mechanisms of centromeric nucleosome recognition by the kinetochore protein CENP-N. <i>Science</i> , 2018, 359, 339-343.	12.6	98
29	Atomic Resolution Cryo-EM Structure of $\beta$ -Galactosidase. <i>Structure</i> , 2018, 26, 848-856.e3.	3.3	115
30	Cryo-EM structure of human rhodopsin bound to an inhibitory G protein. <i>Nature</i> , 2018, 558, 553-558.	27.8	230
31	Single-particle cryo-EM structure of a voltage-activated potassium channel in lipid nanodiscs. <i>ELife</i> , 2018, 7, .	6.0	80
32	Power Grid Protection of the Muscle Mitochondrial Reticulum. <i>Cell Reports</i> , 2017, 19, 487-496.	6.4	155
33	Cryo-EM Structures Reveal Mechanism and Inhibition of DNA Targeting by a CRISPR-Cas Surveillance Complex. <i>Cell</i> , 2017, 171, 414-426.e12.	28.9	158
34	Broadly protective murine monoclonal antibodies against influenza B virus target highly conserved neuraminidase epitopes. <i>Nature Microbiology</i> , 2017, 2, 1415-1424.	13.3	96
35	Cryo-EM: beyond the microscope. <i>Current Opinion in Structural Biology</i> , 2017, 46, 71-78.	5.7	76
36	CryoEM at <i>IUCr</i> : a new era. <i>IUCr</i> , 2016, 3, 3-7.	2.2	54

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37	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.	3.4	32
38	Structural basis for early-onset neurological disorders caused by mutations in human selenocysteine synthase. <i>Scientific Reports</i> , 2016, 6, 32563.	3.3	13
39	Cryo-electron Microscopy Structures of Chimeric Hemagglutinin Displayed on a Universal Influenza Vaccine Candidate. <i>MBio</i> , 2016, 7, e00257.	4.1	26
40	Breaking Cryo-EM Resolution Barriers to Facilitate Drug Discovery. <i>Cell</i> , 2016, 165, 1698-1707.	28.9	458
41	Cryo-EM Analysis of the Conformational Landscape of Human P-glycoprotein (ABCB1) During its Catalytic Cycle. <i>Molecular Pharmacology</i> , 2016, 90, 35-41.	2.3	75
42	The crystal structure of human GlnRS provides basis for the development of neurological disorders. <i>Nucleic Acids Research</i> , 2016, 44, 3420-3431.	14.5	14
43	Using Cryo-EM to Map Small Ligands on Dynamic Metabolic Enzymes: Studies with Glutamate Dehydrogenase. <i>Molecular Pharmacology</i> , 2016, 89, 645-651.	2.3	41
44	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.	7.1	16
45	The democratization of cryo-EM. <i>Nature Methods</i> , 2016, 13, 607-608.	19.0	35
46	Resolution advances in cryo-EM enable application to drug discovery. <i>Current Opinion in Structural Biology</i> , 2016, 41, 194-202.	5.7	95
47	Structural basis of kainate subtype glutamate receptor desensitization. <i>Nature</i> , 2016, 537, 567-571.	27.8	78
48	2.3 Å... resolution cryo-EM structure of human p97 and mechanism of allosteric inhibition. <i>Science</i> , 2016, 351, 871-875.	12.6	305
49	Cryo-EM Structures of the Magnesium Channel CorA Reveal Symmetry Break upon Gating. <i>Cell</i> , 2016, 164, 747-756.	28.9	111
50	A versatile nano display platform from bacterial spore coat proteins. <i>Nature Communications</i> , 2015, 6, 6777.	12.8	35
51	Griffithsin tandemers: flexible and potent lectin inhibitors of the human immunodeficiency virus. <i>Retrovirology</i> , 2015, 12, 6.	2.0	34
52	Maturation of the HIV-1 core by a non-diffusional phase transition. <i>Nature Communications</i> , 2015, 6, 5854.	12.8	49
53	Mitochondrial reticulum for cellular energy distribution in muscle. <i>Nature</i> , 2015, 523, 617-620.	27.8	355
54	Cryo-EM structure of the bacteriophage T4 portal protein assembly at near-atomic resolution. <i>Nature Communications</i> , 2015, 6, 7548.	12.8	88

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55	2.2 Å... resolution cryo-EM structure of Î²-galactosidase in complex with a cell-permeant inhibitor. Science, 2015, 348, 1147-1151.	12.6	440
56	Focused ion beams in biology. Nature Methods, 2015, 12, 1021-1031.	19.0	184
57	Three-Dimensional Imaging of HIV-1 Virological Synapses Reveals Membrane Architectures Involved in Virus Transmission. Journal of Virology, 2014, 88, 10327-10339.	3.4	61
58	A 3D cellular context for the macromolecular world. Nature Structural and Molecular Biology, 2014, 21, 841-845.	8.2	47
59	Spatial Localization of the Ebola Virus Glycoprotein Mucin-Like Domain Determined by Cryo-Electron Tomography. Journal of Virology, 2014, 88, 10958-10962.	3.4	53
60	Structure of Î²-galactosidase at 3.2-Å... resolution obtained by cryo-electron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11709-11714.	7.1	184
61	Multi-resolution correlative focused ion beam scanning electron microscopy: Applications to cell biology. Journal of Structural Biology, 2014, 185, 278-284.	2.8	99
62	Three-Dimensional Imaging of Viral Infections. Annual Review of Virology, 2014, 1, 453-473.	6.7	49
63	Structural mechanism of glutamate receptor activation and desensitization. Nature, 2014, 514, 328-334.	27.8	207
64	Single-Particle Cryo-Electron Microscopy (Cryo-EM). Advances in Imaging and Electron Physics, 2014, , 113-137.	0.2	20
65	Accelerating Discovery in 3D Microanalysis: Leveraging Open Source Software and Deskside High Performance Computing. Microscopy and Microanalysis, 2014, 20, 774-775.	0.4	0
66	Self-assembled monolayers improve protein distribution on holey carbon cryo-EM supports. Scientific Reports, 2014, 4, 7084.	3.3	88
67	Targeted conformational search with map-restrained self-guided Langevin dynamics: Application to flexible fitting into electron microscopic density maps. Journal of Structural Biology, 2013, 183, 429-440.	2.8	50
68	HIV-1 envelope glycoprotein structure. Current Opinion in Structural Biology, 2013, 23, 268-276.	5.7	73
69	Cryo-electron microscopy " a primer for the non-microscopist. FEBS Journal, 2013, 280, 28-45.	4.7	194
70	A collaborative framework for 3D alignment and classification of heterogeneous subvolumes in cryo-electron tomography. Journal of Structural Biology, 2013, 181, 116-127.	2.8	524
71	Catching HIV "in the act" with 3D electron microscopy. Trends in Microbiology, 2013, 21, 397-404.	7.7	21
72	Prefusion structure of trimeric HIV-1 envelope glycoprotein determined by cryo-electron microscopy. Nature Structural and Molecular Biology, 2013, 20, 1352-1357.	8.2	152

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73	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.	3.4	27
74	Molecular structures of trimeric HIV-1 Env in complex with small antibody derivatives. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 513-518.	7.1	44
75	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.	7.1	53
76	Structure and accessibility of HA trimers on intact 2009 H1N1 pandemic influenza virus to stem region-specific neutralizing antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4592-4597.	7.1	99
77	Structure of trimeric HIV-1 envelope glycoproteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4172-4.	7.1	39
78	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.	2.5	17
79	Derivation of Neural Stem Cells from Human Adult Peripheral CD34+ Cells for an Autologous Model of Neuroinflammation. <i>PLoS ONE</i> , 2013, 8, e81720.	2.5	26
80	Structural Mechanism of Trimeric HIV-1 Envelope Glycoprotein Activation. <i>PLoS Pathogens</i> , 2012, 8, e1002797.	4.7	182
81	Data management challenges in three-dimensional EM. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1203-1207.	8.2	49
82	Shape-Based Regularization of Electron Tomographic Reconstruction. <i>IEEE Transactions on Medical Imaging</i> , 2012, 31, 2241-2252.	8.9	10
83	Chemical mapping of mammalian cells by atom probe tomography. <i>Journal of Structural Biology</i> , 2012, 178, 98-107.	2.8	41
84	Computational separation of conformational heterogeneity using cryo-electron tomography and 3D sub-volume averaging. <i>Journal of Structural Biology</i> , 2012, 178, 165-176.	2.8	19
85	Protein Secondary Structure Determination by Constrained Single-Particle Cryo-Electron Tomography. <i>Structure</i> , 2012, 20, 2003-2013.	3.3	90
86	There is no overkill in biochemistry. <i>Resonance</i> , 2012, 17, 1157-1164.	0.3	0
87	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.	1.2	4
88	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.	7.1	45
89	Compositional Mapping of the Surface and Interior of Mammalian Cells at Submicrometer Resolution. <i>Analytical Chemistry</i> , 2011, 83, 1207-1213.	6.5	42
90	Correlative 3D imaging of whole mammalian cells with light and electron microscopy. <i>Journal of Structural Biology</i> , 2011, 176, 268-278.	2.8	81

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91	HIV-1 activates Cdc42 and induces membrane extensions in immature dendritic cells to facilitate cell-to-cell virus propagation. <i>Blood</i> , 2011, 118, 4841-4852.	1.4	79
92	Determination of Molecular Structures of HIV Envelope Glycoproteins using Cryo-Electron Tomography and Automated Sub-tomogram Averaging. <i>Journal of Visualized Experiments</i> , 2011, , .	0.3	14
93	Chemotaxis kinase CheA is activated by three neighbouring chemoreceptor dimers as effectively as by receptor clusters. <i>Molecular Microbiology</i> , 2011, 79, 677-685.	2.5	38
94	Lateral density of receptor arrays in the membrane plane influences sensitivity of the E. coli chemotaxis response. <i>EMBO Journal</i> , 2011, 30, 1719-1729.	7.8	37
95	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.	3.4	46
96	Spiral Architecture of the Nucleoid in <i>Bdellovibrio bacteriovorus</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1341-1350.	2.2	47
97	Trimeric HIV-1 glycoprotein gp140 immunogens and native HIV-1 envelope glycoproteins display the same closed and open quaternary molecular architectures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11440-11445.	7.1	149
98	A coiled-coil-repeat protein $\alpha$ -Ccrp <sup>TM</sup> 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.	1.8	11
99	3D visualization of HIV transfer at the virological synapse between dendritic cells and T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13336-13341.	7.1	169
100	Molecular Architectures of Trimeric SIV and HIV-1 Envelope Glycoproteins on Intact Viruses: Strain-Dependent Variation in Quaternary Structure. <i>PLoS Pathogens</i> , 2010, 6, e1001249.	4.7	161
101	Ion-abrasion scanning electron microscopy reveals distorted liver mitochondrial morphology in murine methylmalonic acidemia. <i>Journal of Structural Biology</i> , 2010, 171, 125-132.	2.8	31
102	Protein Conformational Changes in the Bacteriorhodopsin Photocycle: Comparison of Findings from Electron and X-Ray Crystallographic Analyses. <i>PLoS ONE</i> , 2009, 4, e5769.	2.5	38
103	Ion-Abrasion Scanning Electron Microscopy Reveals Surface-Connected Tubular Conduits in HIV-Infected Macrophages. <i>PLoS Pathogens</i> , 2009, 5, e1000591.	4.7	151
104	Membrane protein structure determination using cryo-electron tomography and 3D image averaging. <i>Current Opinion in Structural Biology</i> , 2009, 19, 402-407.	5.7	65
105	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.	5.7	64
106	Cryo-electron tomography of bacteria: progress, challenges and future prospects. <i>Nature Reviews Microbiology</i> , 2009, 7, 666-675.	28.6	144
107	Automatic joint classification and segmentation of whole cell 3D images. <i>Pattern Recognition</i> , 2009, 42, 1067-1079.	8.1	42
108	3D Imaging of mammalian cells with ion-abrasion scanning electron microscopy. <i>Journal of Structural Biology</i> , 2009, 166, 1-7.	2.8	113

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109	3D imaging of diatoms with ion-abrasion scanning electron microscopy. <i>Journal of Structural Biology</i> , 2009, 166, 316-328.	2.8	71
110	Staphylococcal Enterotoxin A Induces Small Clusters of HLA-DR1 on B Cells. <i>PLoS ONE</i> , 2009, 4, e6188.	2.5	5
111	Molecular architecture of native HIV-1 gp120 trimers. <i>Nature</i> , 2008, 455, 109-113.	27.8	720
112	Extended Polypeptide Linkers Establish the Spatial Architecture of a Pyruvate Dehydrogenase Multienzyme Complex. <i>Structure</i> , 2008, 16, 93-103.	3.3	22
113	Evaluation of denoising algorithms for biological electron tomography. <i>Journal of Structural Biology</i> , 2008, 164, 7-17.	2.8	38
114	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.	2.2	55
115	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.	2.2	72
116	Electron tomography in nanoparticle imaging and analysis. <i>Nanomedicine</i> , 2008, 3, 125-131.	3.3	70
117	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.	7.1	72
118	Stoichiometry and Absolute Quantification of Proteins with Mass Spectrometry Using Fluorescent and Isotope-labeled Concatenated Peptide Standards. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 442-447.	3.8	42
119	Cell Surface Filaments of the Gliding Bacterium <i>Flavobacterium johnsoniae</i> Revealed by Cryo-Electron Tomography. <i>Journal of Bacteriology</i> , 2007, 189, 7503-7506.	2.2	76
120	Direct visualization of <i>Escherichia coli</i> 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.	7.1	176
121	Cryoelectron Tomographic Analysis of an HIV-neutralizing Protein and Its Complex with Native Viral gp120*. <i>Journal of Biological Chemistry</i> , 2007, 282, 27754-27759.	3.4	35
122	FROM GIGABYTES TO BYTES: AUTOMATED DENOISING AND FEATURE IDENTIFICATION IN ELECTRON TOMOGRAMS OF INTACT BACTERIAL CELLS. , 2007, , .		1
123	Electron Tomography of the Contact between T Cells and SIV/HIV-1: Implications for Viral Entry. <i>PLoS Pathogens</i> , 2007, 3, e63.	4.7	165
124	Gigabytes to Bytes: Automated Denoising and Feature Extraction as Applied to the Analysis of HIV Architecture and Variability using Electron Tomography. , 2007, , .		0
125	Electron Tomography of Bacterial Chemotaxis Receptor Assemblies. <i>Methods in Cell Biology</i> , 2007, 79, 373-384.	1.1	9
126	DETERMINATION OF PROTEIN STRUCTURES IN SITU: ELECTRON TOMOGRAPHY OF INTACT VIRUSES AND CELLS. , 2007, , .		0



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127	Automated 100-position specimen loader and image acquisition system for transmission electron microscopy. <i>Journal of Structural Biology</i> , 2007, 158, 318-326.	2.8	30
128	Electron tomography of viruses. <i>Current Opinion in Structural Biology</i> , 2007, 17, 596-602.	5.7	54
129	Site-specific 3D imaging of cells and tissues with a dual beam microscope. <i>Journal of Structural Biology</i> , 2006, 155, 63-73.	2.8	311
130	The SIV Surface Spike Imaged by Electron Tomography: One Leg or Three?. <i>PLoS Pathogens</i> , 2006, 2, e91.	4.7	21
131	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.	3.4	72
132	Bridging the imaging gap in nanobiology with three-dimensional electron microscopy. , 2006, , .		0
133	An energy-based three-dimensional segmentation approach for the quantitative interpretation of electron tomograms. <i>IEEE Transactions on Image Processing</i> , 2005, 14, 1314-1323.	9.8	38
134	Bridging the imaging gap: visualizing subcellular architecture with electron tomography. <i>Current Opinion in Microbiology</i> , 2005, 8, 316-322.	5.1	68
135	Electron tomography of degenerating neurons in mice with abnormal regulation of iron metabolism. <i>Journal of Structural Biology</i> , 2005, 150, 144-153.	2.8	55
136	Three-Dimensional Electron Microscopy at Molecular Resolution. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2004, 33, 141-155.	18.3	65
137	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.	2.2	70
138	Structure and Transport Mechanism of the Bacterial Oxalate Transporter OxIT. <i>Biophysical Journal</i> , 2004, 87, 3600-3607.	0.5	59
139	Site-specific 3D Imaging of Cells and Tissues Using DualBeam Technology. <i>Microscopy and Microanalysis</i> , 2004, 10, 1124-1125.	0.4	7
140	Projection structure of the bacterial oxalate transporter OxIT at 3.4Å... resolution. <i>Journal of Structural Biology</i> , 2003, 144, 320-326.	2.8	25
141	Structural insights into the mechanism of proton pumping by bacteriorhodopsin. <i>FEBS Letters</i> , 2003, 545, 2-8.	2.8	35
142	A core-weighted fitting method for docking atomic structures into low-resolution maps: Application to cryo-electron microscopy. <i>Journal of Structural Biology</i> , 2003, 141, 63-76.	2.8	77
143	Automated image acquisition and processing using a new generation of 4KÅ—4K CCD cameras for cryo electron microscopic studies of macromolecular assemblies. <i>Journal of Structural Biology</i> , 2003, 143, 135-144.	2.8	57
144	Electron Microscopic Analysis of Membrane Assemblies Formed by the Bacterial Chemotaxis Receptor Tsr. <i>Journal of Bacteriology</i> , 2003, 185, 3636-3643.	2.2	62

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145	Structural Model for 12-Helix Transporters Belonging to the Major Facilitator Superfamily. <i>Journal of Bacteriology</i> , 2003, 185, 1712-1718.	2.2	103
146	The Pyruvate Dehydrogenase Multienzyme Complex. <i>Oxidative Stress and Disease</i> , 2003, , .	0.3	0
147	From structure to mechanism: electron crystallographic studies of bacteriorhodopsin. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2002, 360, 859-874.	3.4	36
148	Molecular Structure of an Icosahedral Pyruvate Dehydrogenase Complex. <i>Microscopy and Microanalysis</i> , 2002, 8, 214-215.	0.4	0
149	Three-dimensional structure of a bacterial oxalate transporter. <i>Nature Structural Biology</i> , 2002, 9, 597-600.	9.7	114
150	Molecular architecture and mechanism of an icosahedral pyruvate dehydrogenase complex: a multifunctional catalytic machine. <i>EMBO Journal</i> , 2002, 21, 5587-5598.	7.8	115
151	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.	2.8	47
152	CCD detectors in high-resolution biological electron microscopy. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 1-27.	5.7	61
153	Molecular mechanism of vectorial proton translocation by bacteriorhodopsin. <i>Nature</i> , 2000, 406, 653-657.	27.8	451
154	Crystallographic analysis of protein conformational changes in the bacteriorhodopsin photocycle. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2000, 1460, 157-165.	1.0	44
155	The structure of bacteriorhodopsin: an emerging consensus. <i>Current Opinion in Structural Biology</i> , 1999, 9, 462-468.	5.7	45
156	Protein conformational changes in the bacteriorhodopsin photocycle 1 1Edited by B. Honig. <i>Journal of Molecular Biology</i> , 1999, 287, 145-161.	4.2	244
157	Electron Crystallography of Bacteriorhodopsin with Millisecond Time Resolution. <i>Journal of Structural Biology</i> , 1999, 128, 19-25.	2.8	49
158	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.	2.5	16
159	Expression of bacteriorhodopsin in Sf9 and COS-1 cells. <i>Journal of Bioenergetics and Biomembranes</i> , 1997, 29, 55-59.	2.3	4
160	Modulation of Arrestin Release in the Light-Driven Regeneration of Rh1 <i>Drosophila</i> Rhodopsin. <i>Biochemistry</i> , 1996, 35, 1848-1855.	2.5	9
161	Critical mixing in monolayer mixtures of phospholipid and cholesterol. <i>The Journal of Physical Chemistry</i> , 1987, 91, 1715-1718.	2.9	132
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