

# Thomas Walz

## List of Publications by Year in descending order

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213  
papers

29,955  
citations

3721

89  
h-index

5227

165  
g-index

224  
all docs

224  
docs citations

224  
times ranked

35956  
citing authors

#	ARTICLE	IF	CITATIONS
1	Native-like environments afford novel mechanistic insights into membrane proteins. Trends in Biochemical Sciences, 2022, 47, 561-569.	3.7	6
2	Cryo-EM structure of the human CST $\alpha$ -Pol $\delta$ /primase complex in a recruitment state. Nature Structural and Molecular Biology, 2022, 29, 813-819.	3.6	40
3	Pre-termination Transcription Complex: Structure and Function. Molecular Cell, 2021, 81, 281-292.e8.	4.5	62
4	Structures of monomeric and dimeric PRC2:EZH1 reveal flexible modules involved in chromatin compaction. Nature Communications, 2021, 12, 714.	5.8	54
5	Visualization of the mechanosensitive ion channel MscS under membrane tension. Nature, 2021, 590, 509-514.	13.7	77
6	Electron microscopy shows that binding of monoclonal antibody PT25-2 primes integrin $\alpha$ IIb $\beta$ 3 for ligand binding. Blood Advances, 2021, 5, 1781-1790.	2.5	2
7	Characterization of the multidrug efflux transporter <i>MdtM</i> from <i>Salmonella enterica</i> serovar Typhi. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1193-1204.	1.5	2
8	Cyclodextrins increase membrane tension and are universal activators of mechanosensitive channels. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	21
9	Cyclodextrins for structural and functional studies of mechanosensitive channels. Journal of Structural Biology: X, 2021, 5, 100053.	0.7	1
10	Mutational Diversity in the Quinolone Resistance-Determining Regions of Type-II Topoisomerases of Salmonella Serovars. Antibiotics, 2021, 10, 1455.	1.5	13
11	Structural Insights into the Human Pre-mRNA 3 $\alpha$ -End Processing Machinery. Molecular Cell, 2020, 77, 800-809.e6.	4.5	53
12	A Structural Model of the Endogenous Human BAF Complex Informs Disease Mechanisms. Cell, 2020, 183, 802-817.e24.	13.5	100
13	Long-range intramolecular allostery and regulation in the dynein-like AAA protein Mdn1. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18459-18469.	3.3	6
14	Dominant role of $\alpha$ IIb $\beta$ 3 in platelet interactions with cross-linked fibrin fragment D-dimer. Blood Advances, 2020, 4, 2939-2949.	2.5	6
15	Single-molecule and in silico dissection of the interaction between Polycomb repressive complex 2 and chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30465-30475.	3.3	41
16	Structural asymmetry governs the assembly and GTPase activity of McrBC restriction complexes. Nature Communications, 2020, 11, 5907.	5.8	7
17	Structural Basis of the Activation of Heterotrimeric Gs-Protein by Isoproterenol-Bound $\beta$ 2-Adrenergic Receptor. Molecular Cell, 2020, 80, 59-71.e4.	4.5	60
18	Structure of an active human histone pre-mRNA 3 $\alpha$ -end processing machinery. Science, 2020, 367, 700-703.	6.0	76

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19	Cryo-Electron Microscopy Structure of the Î±IIbÎ²3-Abciximab Complex. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 40, 624-637.	1.1	12
20	New approach for membrane protein reconstitution into peptidiscs and basis for their adaptability to different proteins. <i>ELife</i> , 2020, 9, .	2.8	57
21	Near-atomic structures of the BBSome reveal the basis for BBSome activation and binding to GPCR cargoes. <i>ELife</i> , 2020, 9, .	2.8	38
22	Novel Pure Î±VÎ²3 Integrin Antagonists That Do Not Induce Receptor Extension, Prime the Receptor, or Enhance Angiogenesis at Low Concentrations. <i>ACS Pharmacology and Translational Science</i> , 2019, 2, 387-401.	2.5	21
23	The Molecular Architecture of Native BBSome Obtained by an Integrated Structural Approach. <i>Structure</i> , 2019, 27, 1384-1394.e4.	1.6	51
24	An ensemble of flexible conformations underlies mechanotransduction by the cadherinâ€“catenin adhesion complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 21545-21555.	3.3	33
25	ATG2 transports lipids to promote autophagosome biogenesis. <i>Journal of Cell Biology</i> , 2019, 218, 1787-1798.	2.3	351
26	Visualization of ligand-induced transmembrane signaling in the full-length human insulin receptor. <i>Journal of Cell Biology</i> , 2018, 217, 1643-1649.	2.3	104
27	Structural and kinetic basis for the selectivity of aducanumab for aggregated forms of amyloid-Î². <i>Scientific Reports</i> , 2018, 8, 6412.	1.6	182
28	Molecular basis for the recognition of the human AAUAAA polyadenylation signal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1419-E1428.	3.3	121
29	Structural Insights into Mdn1, an Essential AAA Protein Required for Ribosome Biogenesis. <i>Cell</i> , 2018, 175, 822-834.e18.	13.5	42
30	Structure of the Cdc48 ATPase with its ubiquitin-binding cofactor Ufd1â€“Npl4. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 616-622.	3.6	82
31	Cryo-EM structure of the insect olfactory receptor Orco. <i>Nature</i> , 2018, 560, 447-452.	13.7	322
32	Electron crystallography reveals that substrate release from the PTS IIC glucose transporter is coupled to a subtle conformational change. <i>Journal of Structural Biology</i> , 2017, 199, 39-45.	1.3	5
33	Role of Pore-Lining Residues in Defining the Rate of Water Conduction by Aquaporin-0. <i>Biophysical Journal</i> , 2017, 112, 953-965.	0.2	14
34	6S RNA Mimics B-Form DNA to Regulate Escherichia coli RNA Polymerase. <i>Molecular Cell</i> , 2017, 68, 388-397.e6.	4.5	65
35	Macromolecular Assemblies of the Mammalian Circadian Clock. <i>Molecular Cell</i> , 2017, 67, 770-782.e6.	4.5	198
36	Structural basis of MsbA-mediated lipopolysaccharide transport. <i>Nature</i> , 2017, 549, 233-237.	13.7	214

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37	A Prodomain Fragment from the Proteolytic Activation of Growth Differentiation Factor 11 Remains Associated with the Mature Growth Factor and Keeps It Soluble. <i>Biochemistry</i> , 2017, 56, 4405-4418.	1.2	13
38	Architecture of the human PI4KIII $\alpha$ lipid kinase complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 13720-13725.	3.3	54
39	Discovery and characterization of stable and toxic Tau/phospholipid oligomeric complexes. <i>Nature Communications</i> , 2017, 8, 1678.	5.8	117
40	Covalently circularized nanodiscs for studying membrane proteins and viral entry. <i>Nature Methods</i> , 2017, 14, 49-52.	9.0	221
41	Rac1 GTPase activates the WAVE regulatory complex through two distinct binding sites. <i>ELife</i> , 2017, 6, .	2.8	129
42	UtpA and UtpB chaperone nascent pre-ribosomal RNA and U3 snoRNA to initiate eukaryotic ribosome assembly. <i>Nature Communications</i> , 2016, 7, 12090.	5.8	63
43	A unified molecular mechanism for the regulation of acetyl-CoA carboxylase by phosphorylation. <i>Cell Discovery</i> , 2016, 2, 16044.	3.1	29
44	Molecular architecture of the complete COG tethering complex. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 758-760.	3.6	47
45	CATCHR, HOPS and CORVET tethering complexes share a similar architecture. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 761-763.	3.6	84
46	Relating conformation to function in integrin $\alpha 5 \beta 1$ . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3872-81.	3.3	110
47	A mechanism of viral immune evasion revealed by cryo-EM analysis of the TAP transporter. <i>Nature</i> , 2016, 529, 537-540.	13.7	104
48	Structures of the double-ring AAA ATPase Pex1-Pex6 involved in peroxisome biogenesis. <i>FEBS Journal</i> , 2016, 283, 986-992.	2.2	19
49	The Special Issue of Microscopy on single-particle cryo-electron microscopy. <i>Microscopy (Oxford)</i> Tj ETQq1 1 0.784314 rgBT /Overlock 0.7 4		
50	Single-particle electron microscopy in the study of membrane protein structure. <i>Microscopy (Oxford)</i> Tj ETQq0 0 0 rgBT /Overlock 0.7 34 10 Tf		
51	Magnetically Directed Two-Dimensional Crystallization of OmpF Membrane Proteins in Block Copolymers. <i>Journal of the American Chemical Society</i> , 2016, 138, 28-31.	6.6	27
52	Evaluation of super-resolution performance of the K2 electron-counting camera using 2D crystals of aquaporin-0. <i>Journal of Structural Biology</i> , 2015, 192, 163-173.	1.3	26
53	Characterization of putative multidrug resistance transporters of the major facilitator-superfamily expressed in <i>Salmonella Typhi</i> . <i>Journal of Infection and Chemotherapy</i> , 2015, 21, 357-362.	0.8	17
54	Mapping the interaction between factor VIII and von Willebrand factor by electron microscopy and mass spectrometry. <i>Blood</i> , 2015, 126, 935-938.	0.6	53

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55	Highly permeable artificial water channels that can self-assemble into two-dimensional arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9810-9815.	3.3	152
56	Unique double-ring structure of the peroxisomal Pex1/Pex6 ATPase complex revealed by cryo-electron microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4017-25.	3.3	72
57	A Primer to Single-Particle Cryo-Electron Microscopy. <i>Cell</i> , 2015, 161, 438-449.	13.5	478
58	Structural analyses of the chromatin remodelling enzymes INO80-C and SWR-C. <i>Nature Communications</i> , 2015, 6, 7108.	5.8	61
59	Structure of bone morphogenetic protein 9 procomplex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3710-3715.	3.3	100
60	Cryo-electron microscopy structure of the Slo2.2 Na <sup>+</sup> -activated K <sup>+</sup> channel. <i>Nature</i> , 2015, 527, 198-203.	13.7	107
61	2D and 3D crystallization of the wild-type IIC domain of the glucose PTS transporter from <i>Escherichia coli</i> . <i>Journal of Structural Biology</i> , 2015, 191, 376-380.	1.3	5
62	Structure and function of a single-chain, multi-domain long-chain acyl-CoA carboxylase. <i>Nature</i> , 2015, 518, 120-124.	13.7	36
63	Effect of Lipid Head Groups on Double-Layered Two-Dimensional Crystals Formed by Aquaporin-0. <i>PLoS ONE</i> , 2015, 10, e0117371.	1.1	9
64	A requirement for ER-derived COPII vesicles in phagophore initiation. <i>Autophagy</i> , 2014, 10, 708-709.	4.3	27
65	Molecular architecture of the $\hat{I}\pm\hat{I}^2$ T cell receptor-CD3 complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17576-17581.	3.3	107
66	Molecular Imprinting as a Signal-Activation Mechanism of the Viral RNA Sensor RIG-I. <i>Molecular Cell</i> , 2014, 55, 511-523.	4.5	214
67	Structure and Dynamics of AMPA Receptor GluA2 in Resting, Pre-Open, and Desensitized States. <i>Cell</i> , 2014, 158, 778-792.	13.5	186
68	Structural Study of the RIPoptosome Core Reveals a Helical Assembly for Kinase Recruitment. <i>Biochemistry</i> , 2014, 53, 5424-5431.	1.2	25
69	Extracellular Architecture of the SYG-1/SYG-2 Adhesion Complex Instructs Synaptogenesis. <i>Cell</i> , 2014, 156, 482-494.	13.5	59
70	Assessing Structure-Activity Relationships in FVIII By Integration of Structural, Biophysical, and Biochemical Data Obtained with Anti-FVIII Antibodies. <i>Blood</i> , 2014, 124, 4223-4223.	0.6	1
71	Molecular Mechanism for p202-Mediated Specific Inhibition of AIM2 Inflammasome Activation. <i>Cell Reports</i> , 2013, 4, 327-339.	2.9	81
72	Cell-free Expressed Bacteriorhodopsin in Different Soluble Membrane Mimetics: Biophysical Properties and NMR Accessibility. <i>Structure</i> , 2013, 21, 394-401.	1.6	103

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73	RIG-I Forms Signaling-Competent Filaments in an ATP-Dependent, Ubiquitin-Independent Manner. <i>Molecular Cell</i> , 2013, 51, 573-583.	4.5	188
74	Structural Basis for dsRNA Recognition, Filament Formation, and Antiviral Signal Activation by MDA5. <i>Cell</i> , 2013, 152, 276-289.	13.5	447
75	A pipeline for comprehensive and automated processing of electron diffraction data in IPLT. <i>Journal of Structural Biology</i> , 2013, 182, 173-185.	1.3	9
76	The EM structure of the TRAPP3 complex leads to the identification of a requirement for COPII vesicles on the macroautophagy pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19432-19437.	3.3	135
77	Ypt1 recruits the Atg1 kinase to the preautophagosomal structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9800-9805.	3.3	112
78	Evidence For Flexible Tethering Of Fc To FVIII In Recombinant FVIII-Fc Fusion Protein rFVIII-Fc. <i>Blood</i> , 2013, 122, 1102-1102.	0.6	0
79	Critical phosphoprotein elements that regulate polymerase architecture and function in vesicular stomatitis virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14628-14633.	3.3	57
80	Molecular basis for complement recognition by integrin $\alpha$ <sub>X</sub> $\beta$ <sub>2</sub> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4586-4591.	3.3	49
81	Molecular driving forces defining lipid positions around aquaporin-0. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9887-9892.	3.3	60
82	Mechanisms for Kinase-mediated Dimerization of the Epidermal Growth Factor Receptor. <i>Journal of Biological Chemistry</i> , 2012, 287, 38244-38253.	1.6	70
83	Kinetic mechanism for viral dsRNA length discrimination by MDA5 filaments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E3340-9.	3.3	118
84	Structural specializations of $\alpha$ <sub>4</sub> $\beta$ <sub>7</sub> , an integrin that mediates rolling adhesion. <i>Journal of Cell Biology</i> , 2012, 196, 131-146.	2.3	97
85	High-Density Reconstitution of Functional Water Channels into Vesicular and Planar Block Copolymer Membranes. <i>Journal of the American Chemical Society</i> , 2012, 134, 18631-18637.	6.6	107
86	The RIP1/RIP3 Necrosome Forms a Functional Amyloid Signaling Complex Required for Programmed Necrosis. <i>Cell</i> , 2012, 150, 339-350.	13.5	968
87	Sequence and structure relationships within von Willebrand factor. <i>Blood</i> , 2012, 120, 449-458.	0.6	251
88	Chromatin affinity-precipitation using a small metabolic molecule: its application to analysis of O-acetyl-ADP-ribose. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 641-650.	2.4	11
89	Simultaneous visualization of the extracellular and cytoplasmic domains of the epidermal growth factor receptor. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 984-989.	3.6	126
90	Latent TGF- $\beta$ <sub>2</sub> structure and activation. <i>Nature</i> , 2011, 474, 343-349.	13.7	815

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91	A pH-regulated dimeric bouquet in the structure of von Willebrand factor. <i>EMBO Journal</i> , 2011, 30, 4098-4111.	3.5	102
92	Molecular Structure and Flexibility of the Yeast Coatmer as Revealed by Electron Microscopy. <i>Journal of Molecular Biology</i> , 2011, 408, 825-831.	2.0	17
93	Structural basis for allosteric regulation of human ribonucleotide reductase by nucleotide-induced oligomerization. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 316-322.	3.6	147
94	Structural Snapshots of Full-Length Jak1, a Transmembrane gp130/IL-6/IL-6R $\alpha$ Cytokine Receptor Complex, and the Receptor-Jak1 Holocomplex. <i>Structure</i> , 2011, 19, 45-55.	1.6	78
95	Intact $\beta$ 23 Integrin Is Extended after Activation as Measured by Solution X-ray Scattering and Electron Microscopy. <i>Journal of Biological Chemistry</i> , 2011, 286, 35218-35226.	1.6	62
96	Fast and easy protocol for the purification of recombinant S-layer protein for synthetic biology applications. <i>Biotechnology Journal</i> , 2011, 6, 807-811.	1.8	5
97	The use of trehalose in the preparation of specimens for molecular electron microscopy. <i>Micron</i> , 2011, 42, 762-772.	1.1	20
98	Cooperative assembly and dynamic disassembly of MDA5 filaments for viral dsRNA recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 21010-21015.	3.3	248
99	The Hexamer Structure of the Rift Valley Fever Virus Nucleoprotein Suggests a Mechanism for its Assembly into Ribonucleoprotein Complexes. <i>PLoS Pathogens</i> , 2011, 7, e1002030.	2.1	93
100	Molecular architecture of the TRAPP II complex and implications for vesicle tethering. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1298-1304.	3.6	70
101	Molecular organization of the COG vesicle tethering complex. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1292-1297.	3.6	79
102	The Fas-FADD death domain complex structure reveals the basis of DISC assembly and disease mutations. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1324-1329.	3.6	236
103	Principles of membrane protein interactions with annular lipids deduced from aquaporin-0 2D crystals. <i>EMBO Journal</i> , 2010, 29, 1652-1658.	3.5	111
104	Huntingtin facilitates polycomb repressive complex 2. <i>Human Molecular Genetics</i> , 2010, 19, 573-583.	1.4	169
105	Assembly of a functional Machupo virus polymerase complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20069-20074.	3.3	64
106	The Structure of the Trimer of Human 4-1BB Ligand Is Unique among Members of the Tumor Necrosis Factor Superfamily. <i>Journal of Biological Chemistry</i> , 2010, 285, 9202-9210.	1.6	49
107	Requirement of open headpiece conformation for activation of leukocyte integrin $\alpha$ X $\beta$ 2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14727-14732.	3.3	113
108	Molecular architecture of the vesicular stomatitis virus RNA polymerase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 20075-20080.	3.3	91

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109	Evaluation of imaging plates as recording medium for images of negatively stained single particles and electron diffraction patterns of two-dimensional crystals. <i>Microscopy (Oxford, England)</i> , 2010, 59, 53-63.	0.7	10
110	Structure of the Human mTOR Complex I and Its Implications for Rapamycin Inhibition. <i>Molecular Cell</i> , 2010, 38, 768-774.	4.5	347
111	Strategy for the Use of Affinity Grids to Prepare Non-His-Tagged Macromolecular Complexes for Single-Particle Electron Microscopy. <i>Journal of Molecular Biology</i> , 2010, 400, 675-681.	2.0	52
112	The Monopolin Complex Crosslinks Kinetochore Components to Regulate Chromosome-Microtubule Attachments. <i>Cell</i> , 2010, 142, 556-567.	13.5	119
113	Collecting Electron Crystallographic Data of Two-Dimensional Protein Crystals. <i>Methods in Enzymology</i> , 2010, 481, 251-282.	0.4	12
114	A Practical Guide to the Use of Monolayer Purification and Affinity Grids. <i>Methods in Enzymology</i> , 2010, 481, 83-107.	0.4	32
115	Electron Crystallography and Aquaporins. <i>Methods in Enzymology</i> , 2010, 483, 91-119.	0.4	10
116	Molecular Structure and Dimeric Organization of the Notch Extracellular Domain as Revealed by Electron Microscopy. <i>PLoS ONE</i> , 2010, 5, e10532.	1.1	35
117	The AQP Structure and Functional Implications. <i>Handbook of Experimental Pharmacology</i> , 2009, , 31-56.	0.9	72
118	Rubisco in complex with Rubisco large subunit methyltransferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 3160-3165.	3.3	27
119	STIM1 Clusters and Activates CRAC Channels via Direct Binding of a Cytosolic Domain to Orai1. <i>Cell</i> , 2009, 136, 876-890.	13.5	839
120	A Structure-Based Mechanism for Vesicle Capture by the Multisubunit Tethering Complex Dsl1. <i>Cell</i> , 2009, 139, 1119-1129.	13.5	145
121	Structural and functional studies on the stalk of the transferrin receptor. <i>Biochemical and Biophysical Research Communications</i> , 2009, 381, 712-716.	1.0	9
122	Oligomeric Structure and Functional Characterization of the Urea Transporter from <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Molecular Biology</i> , 2009, 387, 619-627.	2.0	22
123	An Alpha Motif at Tas3 C Terminus Mediates RITS cis Spreading and Promotes Heterochromatic Gene Silencing. <i>Molecular Cell</i> , 2009, 34, 155-167.	4.5	31
124	The Advent of Near-Atomic Resolution in Single-Particle Electron Microscopy. <i>Annual Review of Biochemistry</i> , 2009, 78, 723-742.	5.0	46
125	Structural and Functional Characterization of the Integral Membrane Protein VDAC-1 in Lipid Bilayer Nanodiscs. <i>Journal of the American Chemical Society</i> , 2009, 131, 17777-17779.	6.6	158
126	Electron Crystallography as a Technique to Study the Structure on Membrane Proteins in a Lipidic Environment. <i>Annual Review of Biophysics</i> , 2009, 38, 89-105.	4.5	66



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127	Interactions of lipids with aquaporin-0 and other membrane proteins. Pflugers Archiv European Journal of Physiology, 2008, 456, 651-661.	1.3	35
128	Polymorphic Assemblies and Crystalline Arrays of Lens Tetraspanin MP20. Journal of Molecular Biology, 2008, 376, 380-392.	2.0	8
129	The EM Structure of a Type I Interferon Receptor Complex Reveals a Novel Mechanism for Cytokine Signaling. Journal of Molecular Biology, 2008, 377, 715-724.	2.0	37
130	Ligand Binding Induces a Conformational Change in ifnar1 that Is Propagated to Its Membrane-Proximal Domain. Journal of Molecular Biology, 2008, 377, 725-739.	2.0	48
131	The Affinity Grid: A Pre-fabricated EM Grid for Monolayer Purification. Journal of Molecular Biology, 2008, 382, 423-433.	2.0	71
132	Structural Organization of a Full-Length gp130/LIF-R Cytokine Receptor Transmembrane Complex. Molecular Cell, 2008, 31, 737-748.	4.5	94
133	Junction-forming aquaporins. Current Opinion in Structural Biology, 2008, 18, 229-235.	2.6	83
134	Molecular Electron Microscopy: State of the Art and Current Challenges. ACS Chemical Biology, 2008, 3, 268-281.	1.6	65
135	Functional and Structural Stability of the Epidermal Growth Factor Receptor in Detergent Micelles and Phospholipid Nanodiscs. Biochemistry, 2008, 47, 10314-10323.	1.2	89
136	Monolayer purification: A rapid method for isolating protein complexes for single-particle electron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4703-4708.	3.3	68
137	Factor XI Homodimer Structure Is Essential for Normal Proteolytic Activation by Factor XIIa, Thrombin, and Factor XIa. Journal of Biological Chemistry, 2008, 283, 18655-18664.	1.6	42
138	Transglutaminase Induces Protofibril-like Amyloid $\beta$ -Protein Assemblies That Are Protease-resistant and Inhibit Long-term Potentiation. Journal of Biological Chemistry, 2008, 283, 16790-16800.	1.6	86
139	Structure of the influenza virus A H5N1 nucleoprotein: implications for RNA binding, oligomerization, and vaccine design. FASEB Journal, 2008, 22, 3638-3647.	0.2	186
140	Conformational variability of the intracellular domain of Drosophila Notch and its interaction with Suppressor of Hairless. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 9591-9596.	3.3	13
141	Reconstructing the Endocytotic Machinery. Methods in Cell Biology, 2007, 79, 463-487.	0.5	3
142	Acetylated Histone Tail Peptides Induce Structural Rearrangements in the RSC Chromatin Remodeling Complex*. Journal of Biological Chemistry, 2007, 282, 20804-20808.	1.6	35
143	Structural characterization of the fission yeast U5.U2/U6 spliceosome complex. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3195-3200.	3.3	48
144	Death Domain Assembly Mechanism Revealed by Crystal Structure of the Oligomeric PIDDosome Core Complex. Cell, 2007, 128, 533-546.	13.5	244

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145	7Å... projection map of the S-layer protein sbpA obtained with trehalose-embedded monolayer crystals. <i>Journal of Structural Biology</i> , 2007, 160, 313-323.	1.3	42
146	Structural models of the supramolecular organization of AQP0 and connexons in junctional microdomains. <i>Journal of Structural Biology</i> , 2007, 160, 385-394.	1.3	48
147	Cryo-electron Tomography of Clathrin-coated Vesicles: Structural Implications for Coat Assembly. <i>Journal of Molecular Biology</i> , 2007, 365, 892-899.	2.0	116
148	Projection Map of Aquaporin-9 at 7Å... Resolution. <i>Journal of Molecular Biology</i> , 2007, 367, 80-88.	2.0	35
149	Structural Organization of the Anaphase-Promoting Complex Bound to the Mitotic Activator Slp1. <i>Molecular Cell</i> , 2007, 28, 871-885.	4.5	54
150	Role of the Conserved Sir3-BAH Domain in Nucleosome Binding and Silent Chromatin Assembly. <i>Molecular Cell</i> , 2007, 28, 1015-1028.	4.5	145
151	The supramolecular architecture of junctional microdomains in native lens membranes. <i>EMBO Reports</i> , 2007, 8, 51-55.	2.0	100
152	Structure of a VEGFâ€“VEGF receptor complex determined by electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 249-250.	3.6	137
153	Structural basis of Dscam isoform specificity. <i>Nature</i> , 2007, 449, 487-491.	13.7	146
154	Revival of electron crystallography. <i>Current Opinion in Structural Biology</i> , 2007, 17, 389-395.	2.6	48
155	Structural Insight into Pre-B Cell Receptor Function. <i>Science</i> , 2007, 316, 291-294.	6.0	101
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