

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	Structural determinants of water permeation through aquaporin-1. <i>Nature</i> , 2000, 407, 599-605.	13.7	1,584
2	Amyloid pores from pathogenic mutations. <i>Nature</i> , 2002, 418, 291-291.	13.7	1,182
3	Global Conformational Rearrangements in Integrin Extracellular Domains in Outside-In and Inside-Out Signaling. <i>Cell</i> , 2002, 110, 599-611.	13.5	1,050
4	A Virulence Locus of <i>Pseudomonas aeruginosa</i> Encodes a Protein Secretion Apparatus. <i>Science</i> , 2006, 312, 1526-1530.	6.0	984
5	The RIP1/RIP3 Necrosome Forms a Functional Amyloid Signaling Complex Required for Programmed Necrosis. <i>Cell</i> , 2012, 150, 339-350.	13.5	968
6	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
7	Latent TGF- β 2 structure and activation. <i>Nature</i> , 2011, 474, 343-349.	13.7	815
8	α -Synuclein, Especially the Parkinson's Disease-associated Mutants, Forms Pore-like Annular and Tubular Protofibrils. <i>Journal of Molecular Biology</i> , 2002, 322, 1089-1102.	2.0	772
9	Lipid-protein interactions in double-layered two-dimensional AQP0 crystals. <i>Nature</i> , 2005, 438, 633-638.	13.7	617
10	Negative staining and image classification – powerful tools in modern electron microscopy. <i>Biological Procedures Online</i> , 2004, 6, 23-34.	1.4	598
11	Multiple Associated Proteins Regulate Proteasome Structure and Function. <i>Molecular Cell</i> , 2002, 10, 495-507.	4.5	579
12	A Primer to Single-Particle Cryo-Electron Microscopy. <i>Cell</i> , 2015, 161, 438-449.	13.5	478
13	Structure of the Human Transferrin Receptor-Transferrin Complex. <i>Cell</i> , 2004, 116, 565-576.	13.5	475
14	Molecular model for a complete clathrin lattice from electron cryomicroscopy. <i>Nature</i> , 2004, 432, 573-579.	13.7	464
15	Structural Basis for dsRNA Recognition, Filament Formation, and Antiviral Signal Activation by MDA5. <i>Cell</i> , 2013, 152, 276-289.	13.5	447
16	The three-dimensional structure of aquaporin-1. <i>Nature</i> , 1997, 387, 624-627.	13.7	441
17	Implications of the Aquaporin-4 Structure on Array Formation and Cell Adhesion. <i>Journal of Molecular Biology</i> , 2006, 355, 628-639.	2.0	363
18	ATG2 transports lipids to promote autophagosome biogenesis. <i>Journal of Cell Biology</i> , 2019, 218, 1787-1798.	2.3	351

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19	Aquaporin-0 membrane junctions reveal the structure of a closed water pore. <i>Nature</i> , 2004, 429, 193-197.	13.7	347
20	Structure of the Human mTOR Complex I and Its Implications for Rapamycin Inhibition. <i>Molecular Cell</i> , 2010, 38, 768-774.	4.5	347
21	Cryo-EM structure of the insect olfactory receptor Orco. <i>Nature</i> , 2018, 560, 447-452.	13.7	322
22	Structure of integrin $\alpha 5 \beta 1$ in complex with fibronectin. <i>EMBO Journal</i> , 2003, 22, 4607-4615.	3.5	305
23	The structure of aquaporins. <i>Quarterly Reviews of Biophysics</i> , 2006, 39, 361-396.	2.4	291
24	Projection structures of three photosynthetic complexes from <i>Rhodobacter sphaeroides</i> : LH2 at 6 Å..., LH1 and RC-LH1 at 25 Å... 1 Edited by K. Nagai. <i>Journal of Molecular Biology</i> , 1998, 282, 833-845.	2.0	275
25	Sequence and structure relationships within von Willebrand factor. <i>Blood</i> , 2012, 120, 449-458.	0.6	251
26	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
27	Structure and different conformational states of native AMPA receptor complexes. <i>Nature</i> , 2005, 433, 545-549.	13.7	247
28	Death Domain Assembly Mechanism Revealed by Crystal Structure of the Oligomeric PIDDosome Core Complex. <i>Cell</i> , 2007, 128, 533-546.	13.5	244
29	Assembly of the SIR Complex and Its Regulation by O ⁶ -Acetyl-ADP-Ribose, a Product of NAD-Dependent Histone Deacetylation. <i>Cell</i> , 2005, 121, 515-527.	13.5	242
30	The Fas ^Δ 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
31	Activation of Leukocyte $\beta 2$ Integrins by Conversion from Bent to Extended Conformations. <i>Immunity</i> , 2006, 25, 583-594.	6.6	233
32	ATP Binding to PAN or the 26S ATPases Causes Association with the 20S Proteasome, Gate Opening, and Translocation of Unfolded Proteins. <i>Molecular Cell</i> , 2005, 20, 687-698.	4.5	230
33	Mixtures of Wild-type and a Pathogenic (E22G) Form of A β 40 in Vitro Accumulate Protofibrils, Including Amyloid Pores. <i>Journal of Molecular Biology</i> , 2003, 332, 795-808.	2.0	229
34	Quaternary Structure, Protein Dynamics, and Synaptic Function of SAP97 Controlled by L27 Domain Interactions. <i>Neuron</i> , 2004, 44, 453-467.	3.8	225
35	Covalently circularized nanodiscs for studying membrane proteins and viral entry. <i>Nature Methods</i> , 2017, 14, 49-52.	9.0	221
36	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

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37	Structural basis of MsbA-mediated lipopolysaccharide transport. <i>Nature</i> , 2017, 549, 233-237.	13.7	214
38	Î±-Smooth muscle actin is expressed in a subpopulation of cultured and cloned fibroblasts and is modulated by Î³-interferon. <i>Experimental Cell Research</i> , 1992, 201, 64-73.	1.2	208
39	Macromolecular Assemblies of the Mammalian Circadian Clock. <i>Molecular Cell</i> , 2017, 67, 770-782.e6.	4.5	198
40	Properties of the hybrid form of the 26S proteasome containing both 19S and PA28 complexes. <i>EMBO Journal</i> , 2002, 21, 2636-2645.	3.5	188
41	RIG-I Forms Signaling-Competent Filaments in an ATP-Dependent, Ubiquitin-Independent Manner. <i>Molecular Cell</i> , 2013, 51, 573-583.	4.5	188
42	Structure of the influenza virus A H5N1 nucleoprotein: implications for RNA binding, oligomerization, and vaccine design. <i>FASEB Journal</i> , 2008, 22, 3638-3647.	0.2	186
43	Structure and Dynamics of AMPA Receptor GluA2 in Resting, Pre-Open, and Desensitized States. <i>Cell</i> , 2014, 158, 778-792.	13.5	186
44	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
45	The HEAT repeat protein Bim10 regulates the yeast proteasome by capping the core particle. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 294-303.	3.6	176
46	Huntingtin facilitates polycomb repressive complex 2. <i>Human Molecular Genetics</i> , 2010, 19, 573-583.	1.4	169
47	The Architecture of the Multisubunit TRAPP I Complex Suggests a Model for Vesicle Tethering. <i>Cell</i> , 2006, 127, 817-830.	13.5	166
48	Structure of an auxilin-bound clathrin coat and its implications for the mechanism of uncoating. <i>Nature</i> , 2004, 432, 649-653.	13.7	159
49	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
50	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
51	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
52	Structural basis of Dscam isoform specificity. <i>Nature</i> , 2007, 449, 487-491.	13.7	146
53	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
54	A Structure-Based Mechanism for Vesicle Capture by the Multisubunit Tethering Complex Dsl1. <i>Cell</i> , 2009, 139, 1119-1129.	13.5	145

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55	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
56	The EM structure of the TRAPPIII 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
57	Rac1 GTPase activates the WAVE regulatory complex through two distinct binding sites. <i>ELife</i> , 2017, 6, .	2.8	129
58	Signaling conformations of the tall cytokine receptor gp130 when in complex with IL-6 and IL-6 receptor. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 545-551.	3.6	128
59	Structural transitions of complement component C3 and its activation products. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 19737-19742.	3.3	128
60	Î² ² Protofibrils Possess a Stable Core Structure Resistant to Hydrogen Exchangeâ€“. <i>Biochemistry</i> , 2003, 42, 14092-14098.	1.2	127
61	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
62	The Structure of Aquaporin-1 at 4.5-Å... Resolution Reveals Short Î±-Helices in the Center of the Monomer. <i>Journal of Structural Biology</i> , 1999, 128, 34-43.	1.3	122
63	Molecular basis for the recognition of the human AALUAAA polyadenylation signal. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E1419-E1428.	3.3	121
64	Aquaporin-0 Membrane Junctions Form Upon Proteolytic Cleavage. <i>Journal of Molecular Biology</i> , 2004, 342, 1337-1345.	2.0	119
65	The Monopolin Complex Crosslinks Kinetochores to Regulate Chromosome-Microtubule Attachments. <i>Cell</i> , 2010, 142, 556-567.	13.5	119
66	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
67	Discovery and characterization of stable and toxic Tau/phospholipid oligomeric complexes. <i>Nature Communications</i> , 2017, 8, 1678.	5.8	117
68	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
69	Requirement of open headpiece conformation for activation of leukocyte integrin Î± _X Î² ₂ . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14727-14732.	3.3	113
70	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
71	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
72	An Intersubunit Disulfide Bond Prevents in Vitro Aggregation of a Superoxide Dismutase-1 Mutant Linked to Familial Amyotrophic Lateral Sclerosis. <i>Biochemistry</i> , 2004, 43, 4899-4905.	1.2	110

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73	Production and characterization of astrocyte-derived human apolipoprotein E isoforms from immortalized astrocytes and their interactions with amyloid- β . <i>Neurobiology of Disease</i> , 2005, 19, 66-76.	2.1	110
74	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
75	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
76	Molecular architecture of the $\alpha \beta$ 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
77	Cryo-electron microscopy structure of the Slo2.2 Na ⁺ -activated K ⁺ channel. <i>Nature</i> , 2015, 527, 198-203.	13.7	107
78	Towards the Molecular Architecture of the Asymmetric Unit Membrane of the Mammalian Urinary Bladder Epithelium: A Closed α -Twisted Ribbon-Structure. <i>Journal of Molecular Biology</i> , 1995, 248, 887-900.	2.0	104
79	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
80	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
81	Cell-free Expressed Bacteriorhodopsin in Different Soluble Membrane Mimetics: Biophysical Properties and NMR Accessibility. <i>Structure</i> , 2013, 21, 394-401.	1.6	103
82	A pH-regulated dimeric bouquet in the structure of von Willebrand factor. <i>EMBO Journal</i> , 2011, 30, 4098-4111.	3.5	102
83	Two-dimensional crystallization of the light-harvesting I - reaction centre photounit from <i>Rhodospirillum rubrum</i> . <i>Journal of Molecular Biology</i> , 1997, 265, 107-111.	2.0	101
84	Structural Insight into Pre-B Cell Receptor Function. <i>Science</i> , 2007, 316, 291-294.	6.0	101
85	The supramolecular architecture of junctional microdomains in native lens membranes. <i>EMBO Reports</i> , 2007, 8, 51-55.	2.0	100
86	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
87	A Structural Model of the Endogenous Human BAF Complex Informs Disease Mechanisms. <i>Cell</i> , 2020, 183, 802-817.e24.	13.5	100
88	2D Crystallization of Membrane Proteins: Rationales and Examples. <i>Journal of Structural Biology</i> , 1998, 121, 162-171.	1.3	98
89	Structural specializations of $\alpha 4 \beta 7$, an integrin that mediates rolling adhesion. <i>Journal of Cell Biology</i> , 2012, 196, 131-146.	2.3	97
90	Structural Organization of a Full-Length gp130/LIF-R Cytokine Receptor Transmembrane Complex. <i>Molecular Cell</i> , 2008, 31, 737-748.	4.5	94

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91	Surface Topographies at Subnanometer-resolution Reveal Asymmetry and Sidedness of Aquaporin-1. <i>Journal of Molecular Biology</i> , 1996, 264, 907-918.	2.0	93
92	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
93	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
94	Functional and Structural Stability of the Epidermal Growth Factor Receptor in Detergent Micelles and Phospholipid Nanodiscs. <i>Biochemistry</i> , 2008, 47, 10314-10323.	1.2	89
95	Projection map of aquaporin-1 determined by electron crystallography. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 730-732.	3.6	88
96	Electron Crystallography of Two-Dimensional Crystals of Membrane Proteins. <i>Journal of Structural Biology</i> , 1998, 121, 142-161.	1.3	87
97	Transglutaminase Induces Protofibril-like Amyloid β -Protein Assemblies That Are Protease-resistant and Inhibit Long-term Potentiation. <i>Journal of Biological Chemistry</i> , 2008, 283, 16790-16800.	1.6	86
98	Purified lens major intrinsic protein (MIP) forms highly ordered tetragonal two-dimensional arrays by reconstitution. <i>Journal of Molecular Biology</i> , 1998, 279, 855-864.	2.0	84
99	CATCHR, HOPS and CORVET tethering complexes share a similar architecture. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 761-763.	3.6	84
100	Junction-forming aquaporins. <i>Current Opinion in Structural Biology</i> , 2008, 18, 229-235.	2.6	83
101	Structure of the Cdc48 ATPase with its ubiquitin-binding cofactor Ufd1-Npl4. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 616-622.	3.6	82
102	Molecular Mechanism for p202-Mediated Specific Inhibition of AIM2 Inflammasome Activation. <i>Cell Reports</i> , 2013, 4, 327-339.	2.9	81
103	Molecular organization of the COG vesicle tethering complex. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1292-1297.	3.6	79
104	Structural and Functional Analysis of Essential pre-mRNA Splicing Factor Prp19p. <i>Molecular and Cellular Biology</i> , 2005, 25, 451-460.	1.1	78
105	Structural Snapshots of Full-Length Jak1, a Transmembrane gp130/IL-6/IL-6R α Cytokine Receptor Complex, and the Receptor-Jak1 Holocomplex. <i>Structure</i> , 2011, 19, 45-55.	1.6	78
106	Visualization of the mechanosensitive ion channel MscS under membrane tension. <i>Nature</i> , 2021, 590, 509-514.	18.7	77
107	Structure of an active human histone pre-mRNA 3'-end processing machinery. <i>Science</i> , 2020, 367, 700-703.	6.0	76
108	Murine apolipoprotein serum amyloid A in solution forms a hexamer containing a central channel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 15947-15952.	3.3	73

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109	The AQP Structure and Functional Implications. Handbook of Experimental Pharmacology, 2009, , 31-56.	0.9	72
110	Unique double-ring structure of the peroxisomal Pex1/Pex6 ATPase complex revealed by cryo-electron microscopy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4017-25.	3.3	72
111	The Affinity Grid: A Pre-fabricated EM Grid for Monolayer Purification. Journal of Molecular Biology, 2008, 382, 423-433.	2.0	71
112	Molecular architecture of the TRAPP II complex and implications for vesicle tethering. Nature Structural and Molecular Biology, 2010, 17, 1298-1304.	3.6	70
113	Mechanisms for Kinase-mediated Dimerization of the Epidermal Growth Factor Receptor. Journal of Biological Chemistry, 2012, 287, 38244-38253.	1.6	70
114	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
115	Allosteric α 21 Integrin Antibodies That Stabilize the Low Affinity State by Preventing the Swing-out of the Hybrid Domain. Journal of Biological Chemistry, 2004, 279, 27466-27471.	1.6	67
116	Electron Crystallography as a Technique to Study the Structure on Membrane Proteins in a Lipidic Environment. Annual Review of Biophysics, 2009, 38, 89-105.	4.5	66
117	Molecular Electron Microscopy: State of the Art and Current Challenges. ACS Chemical Biology, 2008, 3, 268-281.	1.6	65
118	6S RNA Mimics B-Form DNA to Regulate Escherichia coli RNA Polymerase. Molecular Cell, 2017, 68, 388-397.e6.	4.5	65
119	Assembly of a functional Machupo virus polymerase complex. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20069-20074.	3.3	64
120	UtpA and UtpB chaperone nascent pre-ribosomal RNA and U3 snoRNA to initiate eukaryotic ribosome assembly. Nature Communications, 2016, 7, 12090.	5.8	63
121	The aquaporin family of membrane water channels. Current Opinion in Structural Biology, 1994, 4, 545-553.	2.6	62
122	Intact α 23 Integrin Is Extended after Activation as Measured by Solution X-ray Scattering and Electron Microscopy. Journal of Biological Chemistry, 2011, 286, 35218-35226.	1.6	62
123	Pre-termination Transcription Complex: Structure and Function. Molecular Cell, 2021, 81, 281-292.e8.	4.5	62
124	Structural analyses of the chromatin remodelling enzymes INO80-C and SWR-C. Nature Communications, 2015, 6, 7108.	5.8	61
125	Molecular driving forces defining lipid positions around aquaporin-0. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9887-9892.	3.3	60
126	Structural Basis of the Activation of Heterotrimeric Gs-Protein by Isoproterenol-Bound α 21-Adrenergic Receptor. Molecular Cell, 2020, 80, 59-71.e4.	4.5	60

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127	Extracellular Architecture of the SYG-1/SYG-2 Adhesion Complex Instructs Synaptogenesis. <i>Cell</i> , 2014, 156, 482-494.	13.5	59
128	Single Particle Reconstructions of the Transferrinâ€“Transferrin Receptor Complex Obtained with Different Specimen Preparation Techniques. <i>Journal of Molecular Biology</i> , 2006, 355, 1048-1065.	2.0	57
129	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
130	New approach for membrane protein reconstitution into peptidiscs and basis for their adaptability to different proteins. <i>ELife</i> , 2020, 9, .	2.8	57
131	Oligomeric States of Bacteriophage T7 Gene 4 Primase/Helicase. <i>Journal of Molecular Biology</i> , 2006, 360, 667-677.	2.0	56
132	Structural Organization of the Anaphase-Promoting Complex Bound to the Mitotic Activator Slp1. <i>Molecular Cell</i> , 2007, 28, 871-885.	4.5	54
133	Architecture of the human PI4KIII β 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
134	Structures of monomeric and dimeric PRC2:EZH1 reveal flexible modules involved in chromatin compaction. <i>Nature Communications</i> , 2021, 12, 714.	5.8	54
135	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
136	Structural Insights into the Human Pre-mRNA 3â€²-End Processing Machinery. <i>Molecular Cell</i> , 2020, 77, 800-809.e6.	4.5	53
137	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
138	The Molecular Architecture of Native BBSome Obtained by an Integrated Structural Approach. <i>Structure</i> , 2019, 27, 1384-1394.e4.	1.6	51
139	Tubular Crystals of a Photosystem II Core Complex. <i>Journal of Molecular Biology</i> , 1996, 259, 241-248.	2.0	50
140	Domain structure of separase and its binding to securin as determined by EM. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 552-553.	3.6	50
141	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
142	Molecular basis for complement recognition by integrin α _X β ₂ . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4586-4591.	3.3	49
143	Structural characterization of the fission yeast U5.U2/U6 spliceosome complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3195-3200.	3.3	48
144	Structural models of the supramolecular organization of AQPO and connexons in junctional microdomains. <i>Journal of Structural Biology</i> , 2007, 160, 385-394.	1.3	48

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145	Revival of electron crystallography. <i>Current Opinion in Structural Biology</i> , 2007, 17, 389-395.	2.6	48
146	Ligand Binding Induces a Conformational Change in ifnar1 that Is Propagated to Its Membrane-Proximal Domain. <i>Journal of Molecular Biology</i> , 2008, 377, 725-739.	2.0	48
147	Molecular architecture of the complete COG tethering complex. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 758-760.	3.6	47
148	The Advent of Near-Atomic Resolution in Single-Particle Electron Microscopy. <i>Annual Review of Biochemistry</i> , 2009, 78, 723-742.	5.0	46
149	Human Erythrocyte Band 3. <i>Journal of Molecular Biology</i> , 1993, 231, 119-132.	2.0	44
150	Three-dimensional structure of an AMPA receptor without associated stargazin/TARP proteins. <i>Biological Chemistry</i> , 2006, 387, 179-87.	1.2	42
151	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
152	Factor XI Homodimer Structure Is Essential for Normal Proteolytic Activation by Factor XIIa, Thrombin, and Factor XIa. <i>Journal of Biological Chemistry</i> , 2008, 283, 18655-18664.	1.6	42
153	Structural Insights into Mdn1, an Essential AAA Protein Required for Ribosome Biogenesis. <i>Cell</i> , 2018, 175, 822-834.e18.	13.5	42
154	Single-molecule and in silico dissection of the interaction between Polycomb repressive complex 2 and chromatin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30465-30475.	3.3	41
155	Cryo-EM structure of the human CST±/primase complex in a recruitment state. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 813-819.	3.6	40
156	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
157	The EM Structure of a Type I Interferon Receptor Complex Reveals a Novel Mechanism for Cytokine Signaling. <i>Journal of Molecular Biology</i> , 2008, 377, 715-724.	2.0	37
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