

Eva Nogales

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230
papers

22,040
citations

77
h-index

146
g-index

260
ext. papers

25,355
ext. citations

14
avg, IF

7.16
L-index

#	Paper	IF	Citations
230	Structure of the alpha beta tubulin dimer by electron crystallography. <i>Nature</i> , 1998 , 391, 199-203	50.4	1772
229	Refined structure of alpha beta-tubulin at 3.5 A resolution. <i>Journal of Molecular Biology</i> , 2001 , 313, 1045-57	56.2	977
228	High-resolution model of the microtubule. <i>Cell</i> , 1999 , 96, 79-88	56.2	946
227	Structures of Cas9 endonucleases reveal RNA-mediated conformational activation. <i>Science</i> , 2014 , 343, 1247-997	33.3	701
226	Structural insights into microtubule function. <i>Annual Review of Biochemistry</i> , 2000 , 69, 277-302	29.1	519
225	Complete subunit architecture of the proteasome regulatory particle. <i>Nature</i> , 2012 , 482, 186-91	50.4	465
224	A common pharmacophore for epothilone and taxanes: molecular basis for drug resistance conferred by tubulin mutations in human cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 2904-9	11.5	428
223	Tubulin and FtsZ form a distinct family of GTPases. <i>Nature Structural Biology</i> , 1998 , 5, 451-8		425
222	High-resolution microtubule structures reveal the structural transitions in β -tubulin upon GTP hydrolysis. <i>Cell</i> , 2014 , 157, 1117-29	56.2	422
221	Structural visualization of key steps in human transcription initiation. <i>Nature</i> , 2013 , 495, 481-6	50.4	403
220	Structures of a CRISPR-Cas9 R-loop complex primed for DNA cleavage. <i>Science</i> , 2016 , 351, 867-71	33.3	359
219	Microtubule structure at 8 A resolution. <i>Structure</i> , 2002 , 10, 1317-28	5.2	334
218	The binding conformation of Taxol in beta-tubulin: a model based on electron crystallographic density. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001 , 98, 5312-6	11.5	322
217	Structure of tubulin at 6.5 A and location of the taxol-binding site. <i>Nature</i> , 1995 , 375, 424-7	50.4	313
216	Structures of the RNA-guided surveillance complex from a bacterial immune system. <i>Nature</i> , 2011 , 477, 486-489	50.4	299
215	Mechanistic Origin of Microtubule Dynamic Instability and Its Modulation by EB Proteins. <i>Cell</i> , 2015 , 162, 849-59	56.2	277
214	Structural insight into microtubule function. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2001 , 30, 397-420		267

213	The structural basis for MCM2-7 helicase activation by GINS and Cdc45. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 471-7	17.6	255
212	Formation of a dynamic kinetochore- microtubule interface through assembly of the Dam1 ring complex. <i>Molecular Cell</i> , 2005 , 17, 277-90	17.6	248
211	Nucleotide-dependent bending flexibility of tubulin regulates microtubule assembly. <i>Nature</i> , 2005 , 435, 911-5	50.4	243
210	The development of cryo-EM into a mainstream structural biology technique. <i>Nature Methods</i> , 2016 , 13, 24-7	21.6	241
209	Structural roles for human translation factor eIF3 in initiation of protein synthesis. <i>Science</i> , 2005 , 310, 1513-5	33.3	236
208	The Dam1 kinetochore ring complex moves processively on depolymerizing microtubule ends. <i>Nature</i> , 2006 , 440, 565-9	50.4	236
207	The Ndc80 kinetochore complex forms oligomeric arrays along microtubules. <i>Nature</i> , 2010 , 467, 805-10	50.4	223
206	<i>Saccharomyces cerevisiae</i> septins: supramolecular organization of heterooligomers and the mechanism of filament assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 8274-9	11.5	222
205	Backtracking determines the force sensitivity of RNAP II in a factor-dependent manner. <i>Nature</i> , 2007 , 446, 820-3	50.4	221
204	Structure, function, and activator-induced conformations of the CRSP coactivator. <i>Science</i> , 2002 , 295, 1058-62	33.3	219
203	Cryo-EM: A Unique Tool for the Visualization of Macromolecular Complexity. <i>Molecular Cell</i> , 2015 , 58, 677-89	17.6	218
202	Disabling Cas9 by an anti-CRISPR DNA mimic. <i>Science Advances</i> , 2017 , 3, e1701620	14.3	216
201	CasX enzymes comprise a distinct family of RNA-guided genome editors. <i>Nature</i> , 2019 , 566, 218-223	50.4	203
200	RNA targeting by the type III-A CRISPR-Cas Csm complex of <i>Thermus thermophilus</i> . <i>Molecular Cell</i> , 2014 , 56, 518-30	17.6	202
199	Direct binding of Cenp-C to the Mis12 complex joins the inner and outer kinetochore. <i>Current Biology</i> , 2011 , 21, 391-8	6.3	202
198	Near-atomic resolution visualization of human transcription promoter opening. <i>Nature</i> , 2016 , 533, 359-65	50.4	197
197	Tubulin and microtubule structure. <i>Current Opinion in Cell Biology</i> , 1998 , 10, 16-22	9	192
196	Molecular architecture of human polycomb repressive complex 2. <i>ELife</i> , 2012 , 1, e00005	8.9	186

195	Structural insights into RNA processing by the human RISC-loading complex. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 1148-53	17.6	183
194	Recognition of RNA polymerase II and transcription bubbles by XPG, CSB, and TFIIH: insights for transcription-coupled repair and Cockayne Syndrome. <i>Molecular Cell</i> , 2005 , 20, 187-98	17.6	176
193	Near-atomic model of microtubule-tau interactions. <i>Science</i> , 2018 , 360, 1242-1246	33.3	175
192	Enhanced FIB-SEM systems for large-volume 3D imaging. <i>ELife</i> , 2017 , 6,	8.9	167
191	Phosphatidylinositol-4,5-bisphosphate promotes budding yeast septin filament assembly and organization. <i>Journal of Molecular Biology</i> , 2010 , 404, 711-31	6.5	163
190	Tubulin structure: insights into microtubule properties and functions. <i>Current Opinion in Structural Biology</i> , 1998 , 8, 785-91	8.1	162
189	CasA mediates Cas3-catalyzed target degradation during CRISPR RNA-guided interference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 6618-23	11.5	153
188	Structural intermediates in microtubule assembly and disassembly: how and why?. <i>Current Opinion in Cell Biology</i> , 2006 , 18, 179-84	9	151
187	Structure of promoter-bound TFIID and model of human pre-initiation complex assembly. <i>Nature</i> , 2016 , 531, 604-9	50.4	141
186	Structure and function of SWI/SNF chromatin remodeling complexes and mechanistic implications for transcription. <i>Progress in Biophysics and Molecular Biology</i> , 2010 , 102, 122-8	4.7	136
185	Mutations in TUBB8 and Human Oocyte Meiotic Arrest. <i>New England Journal of Medicine</i> , 2016 , 374, 223-32	5.2	132
184	Synthesis of heterobifunctional protein fusions using copper-free click chemistry and the aldehyde tag. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 4161-5	16.4	131
183	Low resolution structure of microtubules in solution. Synchrotron X-ray scattering and electron microscopy of taxol-induced microtubules assembled from purified tubulin in comparison with glycerol and MAP-induced microtubules. <i>Journal of Molecular Biology</i> , 1992 , 226, 169-84	6.5	129
182	In vitro system capable of differentiating fast Ca ²⁺ -triggered content mixing from lipid exchange for mechanistic studies of neurotransmitter release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, E304-13	11.5	127
181	Structural mechanisms underlying nucleotide-dependent self-assembly of tubulin and its relatives. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 221-9	8.1	125
180	Human CRSP interacts with RNA polymerase II CTD and adopts a specific CTD-bound conformation. <i>Genes and Development</i> , 2002 , 16, 1339-44	12.6	125
179	The structural basis of flagellin detection by NAIP5: A strategy to limit pathogen immune evasion. <i>Science</i> , 2017 , 358, 888-893	33.3	123
178	Subunit-dependent modulation of septin assembly: budding yeast septin Shs1 promotes ring and gauze formation. <i>Journal of Cell Biology</i> , 2011 , 195, 993-1004	7.3	123

177	Three-dimensional structure of the human TFIID-IIA-IIB complex. <i>Science</i> , 1999 , 286, 2153-6	33.3	120
176	Effects of tubulin acetylation on microtubule structure and stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 10366-10371	11.5	117
175	Cryo-EM structures of PRC2 simultaneously engaged with two functionally distinct nucleosomes. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 154-162	17.6	114
174	A mutation in gamma-tubulin alters microtubule dynamics and organization and is synthetically lethal with the kinesin-like protein pkl1p. <i>Molecular Biology of the Cell</i> , 2000 , 11, 1225-39	3.5	114
173	Effects of tubulin acetylation and tubulin acetyltransferase binding on microtubule structure. <i>Molecular Biology of the Cell</i> , 2014 , 25, 257-66	3.5	112
172	Septin filament formation is essential in budding yeast. <i>Developmental Cell</i> , 2011 , 20, 540-9	10.2	111
171	Cryo-EM structure of substrate-bound human telomerase holoenzyme. <i>Nature</i> , 2018 , 557, 190-195	50.4	109
170	Structures of human PRC2 with its cofactors AEBP2 and JARID2. <i>Science</i> , 2018 , 359, 940-944	33.3	109
169	Cold adaptation of microtubule assembly and dynamics. Structural interpretation of primary sequence changes present in the alpha- and beta-tubulins of Antarctic fishes. <i>Journal of Biological Chemistry</i> , 2000 , 275, 37038-47	5.4	109
168	Insights into the Distinct Mechanisms of Action of Taxane and Non-Taxane Microtubule Stabilizers from Cryo-EM Structures. <i>Journal of Molecular Biology</i> , 2017 , 429, 633-646	6.5	107
167	Architecture and dynamics of the autophagic phosphatidylinositol 3-kinase complex. <i>ELife</i> , 2014 , 3,	8.9	106
166	Structure-function relationships in yeast tubulins. <i>Molecular Biology of the Cell</i> , 2000 , 11, 1887-903	3.5	103
165	The structural basis for regulated assembly and function of the transcriptional activator NtrC. <i>Genes and Development</i> , 2006 , 20, 1485-95	12.6	97
164	Microtubule dynamics. <i>Journal of Cell Science</i> , 2002 , 115, 3-4	5.3	96
163	Structural biology. Structures of the CRISPR-Cmr complex reveal mode of RNA target positioning. <i>Science</i> , 2015 , 348, 581-5	33.3	94
162	Architecture of the yeast Rrp44 exosome complex suggests routes of RNA recruitment for 3' end processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 16844-9	11.5	92
161	Structure of the activated ROQ1 resistosome directly recognizing the pathogen effector XopQ. <i>Science</i> , 2020 , 370,	33.3	91
160	Human TFIID binds to core promoter DNA in a reorganized structural state. <i>Cell</i> , 2013 , 152, 120-31	56.2	89

159	Functional reconstitution of human eukaryotic translation initiation factor 3 (eIF3). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 20473-8	11.5	88
158	Structures of the CRISPR genome integration complex. <i>Science</i> , 2017 , 357, 1113-1118	33.3	86
157	Architecture and flexibility of the yeast Ndc80 kinetochore complex. <i>Journal of Molecular Biology</i> , 2008 , 383, 894-903	6.5	86
156	Visualizing flexibility at molecular resolution: analysis of heterogeneity in single-particle electron microscopy reconstructions. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2007 , 36, 43-62		83
155	Conformational flexibility in the chromatin remodeler RSC observed by electron microscopy and the orthogonal tilt reconstruction method. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 4913-8	11.5	79
154	The orthogonal tilt reconstruction method: an approach to generating single-class volumes with no missing cone for ab initio reconstruction of asymmetric particles. <i>Journal of Structural Biology</i> , 2006 , 153, 284-99	3.4	79
153	Molecular architecture of the human Mediator-RNA polymerase II-TFIIF assembly. <i>PLoS Biology</i> , 2011 , 9, e1000603	9.7	77
152	Three-dimensional ultrastructure of the septin filament network in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2012 , 23, 423-32	3.5	77
151	Architecture of the Dam1 kinetochore ring complex and implications for microtubule-driven assembly and force-coupling mechanisms. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 721-6	17.6	77
150	Structure of human TFIID and mechanism of TBP loading onto promoter DNA. <i>Science</i> , 2018 , 362,	33.3	77
149	Structural Insights into the Eukaryotic Transcription Initiation Machinery. <i>Annual Review of Biophysics</i> , 2017 , 46, 59-83	21.1	74
148	Separating the effects of nucleotide and EB binding on microtubule structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E6191-E6200	11.5	73
147	Substrate-specific structural rearrangements of human Dicer. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 662-70	17.6	72
146	Nucleotide-dependent conformational changes in the DnaA-like core of the origin recognition complex. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 684-90	17.6	71
145	Tubulin rings: which way do they curve?. <i>Current Opinion in Structural Biology</i> , 2003 , 13, 256-61	8.1	71
144	Mutations in Human Tubulin Proximal to the Kinesin-Binding Site Alter Dynamic Instability at Microtubule Plus- and Minus-Ends. <i>Developmental Cell</i> , 2016 , 37, 72-84	10.2	70
143	A structural view of microtubule dynamics. <i>Cellular and Molecular Life Sciences</i> , 1999 , 56, 133-42	10.3	69
142	Multimodal microtubule binding by the Ndc80 kinetochore complex. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1161-7	17.6	68

141	Structural models for the self-assembly and microtubule interactions of gamma-, delta- and epsilon-tubulin. <i>Journal of Cell Science</i> , 2001 , 114, 413-422	5.3	66
140	Remote control of myosin and kinesin motors using light-activated gearshifting. <i>Nature Nanotechnology</i> , 2014 , 9, 693-7	28.7	64
139	XKCM1 acts on a single protofilament and requires the C terminus of tubulin. <i>Journal of Molecular Biology</i> , 2002 , 316, 817-28	6.5	64
138	ATP ground- and transition states of bacterial enhancer binding AAA+ ATPases support complex formation with their target protein, sigma54. <i>Structure</i> , 2007 , 15, 429-40	5.2	62
137	Cryo-electron microscopy studies of human TFIID: conformational breathing in the integration of gene regulatory cues. <i>Structure</i> , 2006 , 14, 511-20	5.2	61
136	The cryo-electron microscopy structure of human transcription factor IIH. <i>Nature</i> , 2017 , 549, 414-417	50.4	60
135	Tumor cells resistant to a microtubule-depolymerizing hemisterlin analogue, HTI-286, have mutations in alpha- or beta-tubulin and increased microtubule stability. <i>Biochemistry</i> , 2004 , 43, 13944-54 ^{3,2}		59
134	Structural insight into TPX2-stimulated microtubule assembly. <i>ELife</i> , 2017 , 6,	8.9	59
133	Structural models for the self-assembly and microtubule interactions of gamma-, delta- and epsilon-tubulin. <i>Journal of Cell Science</i> , 2001 , 114, 413-22	5.3	59
132	New insights into microtubule structure and function from the atomic model of tubulin. <i>European Biophysics Journal</i> , 1998 , 27, 431-6	1.9	58
131	Molecular requirements for the formation of a kinetochore-microtubule interface by Dam1 and Ndc80 complexes. <i>Journal of Cell Biology</i> , 2013 , 200, 21-30	7.3	56
130	Architecture of human translation initiation factor 3. <i>Structure</i> , 2013 , 21, 920-8	5.2	55
129	Structures of three distinct activator-TFIID complexes. <i>Genes and Development</i> , 2009 , 23, 1510-21	12.6	54
128	Alanine-scanning mutagenesis of Aspergillus gamma-tubulin yields diverse and novel phenotypes. <i>Molecular Biology of the Cell</i> , 2001 , 12, 2119-36	3.5	54
127	Crystallographic structure of tubulin: implications for dynamics and drug binding. <i>Cell Structure and Function</i> , 1999 , 24, 269-75	2.2	54
126	The complete structure of the human TFIH core complex. <i>ELife</i> , 2019 , 8,	8.9	53
125	Two RNA-binding motifs in eIF3 direct HCV IRES-dependent translation. <i>Nucleic Acids Research</i> , 2013 , 41, 7512-21	20.1	52
124	Structural changes in TAF4b-TFIID correlate with promoter selectivity. <i>Molecular Cell</i> , 2008 , 29, 81-91	17.6	52

123	Molecular architecture and connectivity of the budding yeast Mtw1 kinetochore complex. <i>Journal of Molecular Biology</i> , 2011 , 405, 548-59	6.5	51
122	Flexible tethering of primase and DNA Pol δ in the eukaryotic primosome. <i>Nucleic Acids Research</i> , 2011 , 39, 8187-99	20.1	51
121	A revised nomenclature for the human and rodent alpha-tubulin gene family. <i>Genomics</i> , 2007 , 90, 285-9	4.3	50
120	Microtubules: 50 years on from the discovery of tubulin. <i>Nature Reviews Molecular Cell Biology</i> , 2016 , 17, 322-8	48.7	50
119	Near-atomic cryo-EM structure of PRC1 bound to the microtubule. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 9430-9	11.5	50
118	Temperature-Responsive Competitive Inhibition of CRISPR-Cas9. <i>Molecular Cell</i> , 2019 , 73, 601-610.e5	17.6	50
117	DNA Targeting by a Minimal CRISPR RNA-Guided Cascade. <i>Molecular Cell</i> , 2016 , 63, 840-51	17.6	49
116	Molecular Machines: putting the pieces together. <i>Journal of Cell Biology</i> , 2001 , 152, F1-10	7.3	49
115	Alf1p, a CLIP-170 domain-containing protein, is functionally and physically associated with alpha-tubulin. <i>Journal of Cell Biology</i> , 1999 , 144, 113-24	7.3	46
114	A new protocol to accurately determine microtubule lattice seam location. <i>Journal of Structural Biology</i> , 2015 , 192, 245-54	3.4	42
113	Structural differences between yeast and mammalian microtubules revealed by cryo-EM. <i>Journal of Cell Biology</i> , 2017 , 216, 2669-2677	7.3	42
112	JARID2 and AEBP2 regulate PRC2 in the presence of H2AK119ub1 and other histone modifications. <i>Science</i> , 2021 , 371,	33.3	41
111	Visualizing microtubule structural transitions and interactions with associated proteins. <i>Current Opinion in Structural Biology</i> , 2016 , 37, 90-6	8.1	39
110	How Cryo-EM Became so Hot. <i>Cell</i> , 2017 , 171, 1229-1231	56.2	39
109	Molecular architecture and conformational flexibility of human RNA polymerase II. <i>Structure</i> , 2006 , 14, 1691-700	5.2	38
108	A Meier-Gorlin syndrome mutation in a conserved C-terminal helix of Orc6 impedes origin recognition complex formation. <i>ELife</i> , 2013 , 2, e00882	8.9	37
107	The Dam1 ring binds to the E-hook of tubulin and diffuses along the microtubule. <i>Molecular Biology of the Cell</i> , 2011 , 22, 457-66	3.5	36
106	Structural studies of the human PBAF chromatin-remodeling complex. <i>Structure</i> , 2005 , 13, 267-75	5.2	36

105	Multiple domains of human CLASP contribute to microtubule dynamics and organization in vitro and in <i>Xenopus</i> egg extracts. <i>Cytoskeleton</i> , 2012 , 69, 155-65	2.4	35
104	Repair complexes of FEN1 endonuclease, DNA, and Rad9-Hus1-Rad1 are distinguished from their PCNA counterparts by functionally important stability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 8528-33	11.5	34
103	Architecture of the chromatin remodeler RSC and insights into its nucleosome engagement. <i>ELife</i> , 2019 , 8,	8.9	33
102	Preservation of 2-D crystals of tubulin for electron crystallography. <i>Journal of Structural Biology</i> , 1995 , 115, 199-208	3.4	32
101	Structure-function insights into the yeast Dam1 kinetochore complex. <i>Journal of Cell Science</i> , 2009 , 122, 3831-6	5.3	29
100	Synthesis of Heterobifunctional Protein Fusions Using Copper-Free Click Chemistry and the Aldehyde Tag. <i>Angewandte Chemie</i> , 2012 , 124, 4237-4241	3.6	28
99	Visualizing the secondary structure of tubulin: three-dimensional map at 4 Å. <i>Journal of Structural Biology</i> , 1997 , 118, 119-27	3.4	27
98	Assembly of GMPCPP-bound tubulin into helical ribbons and tubes and effect of colchicine. <i>Cell Cycle</i> , 2005 , 4, 1157-60	4.7	27
97	A unique supramolecular organization of photosystem I in the moss <i>Physcomitrella patens</i> . <i>Nature Plants</i> , 2018 , 4, 904-909	11.5	27
96	Cryo-electron microscopy of GDP-tubulin rings. <i>Cell Biochemistry and Biophysics</i> , 1999 , 31, 175-83	3.2	26
95	The microtubule binding properties of CENP-E _B C-terminus and CENP-F. <i>Journal of Molecular Biology</i> , 2013 , 425, 4427-41	6.5	25
94	Structural mimicry in transcription regulation of human RNA polymerase II by the DNA helicase RECQL5. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 892-9	17.6	25
93	Subunit organization in the Dam1 kinetochore complex and its ring around microtubules. <i>Molecular Biology of the Cell</i> , 2011 , 22, 4335-42	3.5	24
92	The effect of temperature on the structure of vinblastine-induced polymers of purified tubulin: detection of a reversible conformational change. <i>Journal of Molecular Biology</i> , 1995 , 254, 416-30	6.5	24
91	The cryoelectron microscopy structure of the human CDK-activating kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 22849-22857	11.5	24
90	Discovery and characterization of a novel family of prokaryotic nanocompartments involved in sulfur metabolism. <i>ELife</i> , 2021 , 10,	8.9	23
89	Target preference of Type III-A CRISPR-Cas complexes at the transcription bubble. <i>Nature Communications</i> , 2019 , 10, 3001	17.4	22
88	Architecture of the human XPC DNA repair and stem cell coactivator complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 14817-22	11.5	20

87	Comparative studies of microtubule mechanics with two competing models suggest functional roles of alternative tubulin lateral interactions. <i>Biophysical Journal</i> , 2012 , 102, 2687-96	2.9	20
86	Current outcomes when optimizing standard sample preparation for single-particle cryo-EM. <i>Journal of Microscopy</i> , 2019 , 276, 39-45	1.9	19
85	Ranking TEM cameras by their response to electron shot noise. <i>Ultramicroscopy</i> , 2013 , 133, 1-7	3.1	19
84	Visualizing kinetochore architecture. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 661-9	8.1	19
83	Simulations of tubulin sheet polymers as possible structural intermediates in microtubule assembly. <i>PLoS ONE</i> , 2009 , 4, e7291	3.7	19
82	Interpreting a medium-resolution model of tubulin: comparison of zinc-sheet and microtubule structure. <i>Journal of Molecular Biology</i> , 1996 , 262, 485-501	6.5	19
81	Recent insights into the structure of TFIID, its assembly, and its binding to core promoter. <i>Current Opinion in Structural Biology</i> , 2020 , 61, 17-24	8.1	19
80	Electron microscopy visualization of DNA-protein complexes formed by Ku and DNA ligase IV. <i>DNA Repair</i> , 2012 , 11, 74-81	4.3	18
79	An electron microscopy journey in the study of microtubule structure and dynamics. <i>Protein Science</i> , 2015 , 24, 1912-9	6.3	18
78	Atomic force microscopy of photosystem II and its unit cell clustering quantitatively delineate the mesoscale variability in Arabidopsis thylakoids. <i>PLoS ONE</i> , 2014 , 9, e101470	3.7	18
77	Next-generation electron microscopy in autophagy research. <i>Current Opinion in Structural Biology</i> , 2016 , 41, 211-216	8.1	18
76	Cryo-EM in the study of challenging systems: the human transcription pre-initiation complex. <i>Current Opinion in Structural Biology</i> , 2016 , 40, 120-127	8.1	18
75	Assembly, molecular organization, and membrane-binding properties of development-specific septins. <i>Journal of Cell Biology</i> , 2016 , 212, 515-29	7.3	17
74	Structural basis for dimerization quality control. <i>Nature</i> , 2020 , 586, 452-456	50.4	17
73	Structural and functional differences between porcine brain and budding yeast microtubules. <i>Cell Cycle</i> , 2018 , 17, 278-287	4.7	16
72	Structural insights into transcriptional repression by noncoding RNAs that bind to human Pol II. <i>Journal of Molecular Biology</i> , 2013 , 425, 3639-48	6.5	16
71	Coordinate action of distinct sequence elements localizes checkpoint kinase Hsl1 to the septin collar at the bud neck in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2016 , 27, 2213-33	3.5	14
70	Protein domain mapping by internal labeling and single particle electron microscopy. <i>Journal of Structural Biology</i> , 2015 , 192, 159-62	3.4	14

69	Ab initio reconstruction of helical samples with heterogeneity, disorder and coexisting symmetries. <i>Journal of Structural Biology</i> , 2009 , 167, 97-105	3.4	14
68	Structure of a P element transposase-DNA complex reveals unusual DNA structures and GTP-DNA contacts. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 1013-1022	17.6	13
67	Towards a mechanistic understanding of core promoter recognition from cryo-EM studies of human TFIID. <i>Current Opinion in Structural Biology</i> , 2017 , 47, 60-66	8.1	13
66	An iterative Fourier-Bessel algorithm for reconstruction of helical structures with severe Bessel overlap. <i>Journal of Structural Biology</i> , 2005 , 149, 65-78	3.4	13
65	Recent Structural Insights into Polycomb Repressive Complex 2 Regulation and Substrate Binding. <i>Biochemistry</i> , 2019 , 58, 346-354	3.2	13
64	Challenges and opportunities in the high-resolution cryo-EM visualization of microtubules and their binding partners. <i>Current Opinion in Structural Biology</i> , 2017 , 46, 65-70	8.1	12
63	Septin filament organization in <i>Saccharomyces cerevisiae</i> . <i>Communicative and Integrative Biology</i> , 2012 , 5, 503-5	1.7	12
62	The Structures of Eukaryotic Transcription Pre-initiation Complexes and Their Functional Implications. <i>Sub-Cellular Biochemistry</i> , 2019 , 93, 143-192	5.5	12
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