

Eva Nogales

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Structural and functional insight into regulation of kinesin-1 by microtubule-associated protein MAP7.. <i>Science</i> , 2022 , 375, 326-331	33.3	8
229	Structural transitions in the GTP cap visualized by cryo-electron microscopy of catalytically inactive microtubules.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119,	11.5	8
228	Chimeric CRISPR-CasX enzymes and guide RNAs for improved genome editing activity.. <i>Molecular Cell</i> , 2022 ,	17.6	2
227	CRISPR-Cas9 bends and twists DNA to read its sequence.. <i>Nature Structural and Molecular Biology</i> , 2022 , 29, 395-402	17.6	4
226	Structure of the human SAGA coactivator complex. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 989-996	17.6	4
225	The encapsulin from <i>Thermotoga maritima</i> is a flavoprotein with a symmetry matched ferritin-like cargo protein. <i>Scientific Reports</i> , 2021 , 11, 22810	4.9	4
224	Discovery and characterization of a novel family of prokaryotic nanocompartments involved in sulfur metabolism. <i>ELife</i> , 2021 , 10,	8.9	23
223	JARID2 and AEBP2 regulate PRC2 in the presence of H2AK119ub1 and other histone modifications. <i>Science</i> , 2021 , 371,	33.3	41
222	2.5Å resolution structure of human CDK-activating kinase bound to the clinical inhibitor ICEC0942. <i>Biophysical Journal</i> , 2021 , 120, 677-686	2.9	7
221	DNA interference states of the hypercompact CRISPR-Cas5 effector. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 652-661	17.6	7
220	Chloroplast Sec14-like 1 (CPSFL1) is essential for normal chloroplast development and affects carotenoid accumulation in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 12452-12463	11.5	8
219	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
218	Structure of the activated ROQ1 resistosome directly recognizing the pathogen effector XopQ. <i>Science</i> , 2020 , 370,	33.3	91
217	The gammaherpesviral TATA-box-binding protein directly interacts with the CTD of host RNA Pol II to direct late gene transcription. <i>PLoS Pathogens</i> , 2020 , 16, e1008843	7.6	4
216	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
215	Structural basis for dimerization quality control. <i>Nature</i> , 2020 , 586, 452-456	50.4	17
214	The gammaherpesviral TATA-box-binding protein directly interacts with the CTD of host RNA Pol II to direct late gene transcription 2020 , 16, e1008843		

213	The gammaherpesviral TATA-box-binding protein directly interacts with the CTD of host RNA Pol II to direct late gene transcription 2020 , 16, e1008843		
212	The gammaherpesviral TATA-box-binding protein directly interacts with the CTD of host RNA Pol II to direct late gene transcription 2020 , 16, e1008843		
211	The gammaherpesviral TATA-box-binding protein directly interacts with the CTD of host RNA Pol II to direct late gene transcription 2020 , 16, e1008843		
210	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
209	Telomerase structures and regulation: shedding light on the chromosome end. <i>Current Opinion in Structural Biology</i> , 2019 , 55, 185-193	8.1	7
208	Cryo-EM studies of NAIP-NLRC4 inflammasomes. <i>Methods in Enzymology</i> , 2019 , 625, 177-204	1.7	4
207	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
206	Target preference of Type III-A CRISPR-Cas complexes at the transcription bubble. <i>Nature Communications</i> , 2019 , 10, 3001	17.4	22
205	High-resolution cryo-EM structures of TFIIH and their functional implications. <i>Current Opinion in Structural Biology</i> , 2019 , 59, 188-194	8.1	7
204	Towards a Mechanistic Understanding of P element Transposition Using Single-Particle Cryo-EM. <i>Microscopy and Microanalysis</i> , 2019 , 25, 1288-1289	0.5	
203	Current outcomes when optimizing standard sample preparation for single-particle cryo-EM. <i>Journal of Microscopy</i> , 2019 , 276, 39-45	1.9	19
202	The complete structure of the human TFIIH core complex. <i>ELife</i> , 2019 , 8,	8.9	53
201	Architecture of the chromatin remodeler RSC and insights into its nucleosome engagement. <i>ELife</i> , 2019 , 8,	8.9	33
200	Cryo-EM Structure of the P Element Transposase Strand Transfer Complex. <i>FASEB Journal</i> , 2019 , 33, 89.3	0.9	
199	The Structures of Eukaryotic Transcription Pre-initiation Complexes and Their Functional Implications. <i>Sub-Cellular Biochemistry</i> , 2019 , 93, 143-192	5.5	12
198	CasX enzymes comprise a distinct family of RNA-guided genome editors. <i>Nature</i> , 2019 , 566, 218-223	50.4	203
197	Temperature-Responsive Competitive Inhibition of CRISPR-Cas9. <i>Molecular Cell</i> , 2019 , 73, 601-610.e5	17.6	50
196	Recent Structural Insights into Polycomb Repressive Complex 2 Regulation and Substrate Binding. <i>Biochemistry</i> , 2019 , 58, 346-354	3.2	13

195	Cryo-EM structure of substrate-bound human telomerase holoenzyme. <i>Nature</i> , 2018 , 557, 190-195	50.4	109
194	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
193	Structures of human PRC2 with its cofactors AEBP2 and JARID2. <i>Science</i> , 2018 , 359, 940-944	33.3	109
192	Structural and functional differences between porcine brain and budding yeast microtubules. <i>Cell Cycle</i> , 2018 , 17, 278-287	4.7	16
191	Near-atomic model of microtubule-tau interactions. <i>Science</i> , 2018 , 360, 1242-1246	33.3	175
190	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
189	Profile of Joachim Frank, Richard Henderson, and Jacques Dubochet, 2017 Nobel Laureates in Chemistry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 441-444	11.5	5
188	Structure of human TFIID and mechanism of TBP loading onto promoter DNA. <i>Science</i> , 2018 , 362,	33.3	77
187	Cryo-EM. <i>Current Biology</i> , 2018 , 28, R1127-R1128	6.3	4
186	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
185	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
184	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
183	Structural Insights into the Eukaryotic Transcription Initiation Machinery. <i>Annual Review of Biophysics</i> , 2017 , 46, 59-83	21.1	74
182	Structural dynamics and DNA interaction of human TFIID. <i>Transcription</i> , 2017 , 8, 55-60	4.8	6
181	Enhanced FIB-SEM systems for large-volume 3D imaging. <i>ELife</i> , 2017 , 6,	8.9	167
180	The cryo-electron microscopy structure of human transcription factor IIH. <i>Nature</i> , 2017 , 549, 414-417	50.4	60
179	Disabling Cas9 by an anti-CRISPR DNA mimic. <i>Science Advances</i> , 2017 , 3, e1701620	14.3	216
178	Structures of the CRISPR genome integration complex. <i>Science</i> , 2017 , 357, 1113-1118	33.3	86

177	How Cryo-EM Became so Hot. <i>Cell</i> , 2017 , 171, 1229-1231	56.2	39
176	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
175	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
174	Structural differences between yeast and mammalian microtubules revealed by cryo-EM. <i>Journal of Cell Biology</i> , 2017 , 216, 2669-2677	7.3	42
173	Tubulin and Microtubule Structure: Mechanistic Insights Into Dynamic Instability and Its Biological Relevance 2017 ,		0
172	Author response: Enhanced FIB-SEM systems for large-volume 3D imaging 2017 ,		4
171	Structural insight into TPX2-stimulated microtubule assembly. <i>ELife</i> , 2017 , 6,	8.9	59
170	DNA Targeting by a Minimal CRISPR RNA-Guided Cascade. <i>Molecular Cell</i> , 2016 , 63, 840-51	17.6	49
169	Preparing recombinant yeast septins and their analysis by electron microscopy. <i>Methods in Cell Biology</i> , 2016 , 136, 21-34	1.8	2
168	Effects of Bni5 Binding on Septin Filament Organization. <i>Journal of Molecular Biology</i> , 2016 , 428, 4962-4980	3.0	4
167	Dear microtubule, I see you. <i>Molecular Biology of the Cell</i> , 2016 , 27, 3202-3204	3.5	
166	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
165	Visualizing microtubule structural transitions and interactions with associated proteins. <i>Current Opinion in Structural Biology</i> , 2016 , 37, 90-6	8.1	39
164	Mutations in TUBB8 and Human Oocyte Meiotic Arrest. <i>New England Journal of Medicine</i> , 2016 , 374, 223-32	5.2	132
163	The development of cryo-EM into a mainstream structural biology technique. <i>Nature Methods</i> , 2016 , 13, 24-7	21.6	241
162	Structures of a CRISPR-Cas9 R-loop complex primed for DNA cleavage. <i>Science</i> , 2016 , 351, 867-71	33.3	359
161	Structure of promoter-bound TFIID and model of human pre-initiation complex assembly. <i>Nature</i> , 2016 , 531, 604-9	50.4	141
160	Assembly, molecular organization, and membrane-binding properties of development-specific septins. <i>Journal of Cell Biology</i> , 2016 , 212, 515-29	7.3	17

159	Characterization of Septin Ultrastructure in Budding Yeast Using Electron Tomography. <i>Methods in Molecular Biology</i> , 2016 , 1369, 113-23	1.4	3
158	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
157	Microtubules: 50 years on from the discovery of tubulin. <i>Nature Reviews Molecular Cell Biology</i> , 2016 , 17, 322-8	48.7	50
156	Near-atomic resolution visualization of human transcription promoter opening. <i>Nature</i> , 2016 , 533, 359-65	50.4	197
155	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
154	Next-generation electron microscopy in autophagy research. <i>Current Opinion in Structural Biology</i> , 2016 , 41, 211-216	8.1	18
153	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
152	Mechanistic Origin of Microtubule Dynamic Instability and Its Modulation by EB Proteins. <i>Cell</i> , 2015 , 162, 849-59	56.2	277
151	A new protocol to accurately determine microtubule lattice seam location. <i>Journal of Structural Biology</i> , 2015 , 192, 245-54	3.4	42
150	An electron microscopy journey in the study of microtubule structure and dynamics. <i>Protein Science</i> , 2015 , 24, 1912-9	6.3	18
149	Structural biology. Structures of the CRISPR-Cmr complex reveal mode of RNA target positioning. <i>Science</i> , 2015 , 348, 581-5	33.3	94
148	Cryo-EM: A Unique Tool for the Visualization of Macromolecular Complexity. <i>Molecular Cell</i> , 2015 , 58, 677-89	17.6	218
147	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
146	Eva Nogales: See how they run. <i>Journal of Cell Biology</i> , 2015 , 209, 472-3	7.3	
145	Protein domain mapping by internal labeling and single particle electron microscopy. <i>Journal of Structural Biology</i> , 2015 , 192, 159-62	3.4	14
144	Structures of Cas9 endonucleases reveal RNA-mediated conformational activation. <i>Science</i> , 2014 , 343, 1247997	33.3	701
143	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
142	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

141	Remote control of myosin and kinesin motors using light-activated gearshifting. <i>Nature Nanotechnology</i> , 2014 , 9, 693-7	28.7	64
140	Dynamic mechanical responses of Arabidopsis thylakoid membranes during PSII-specific illumination. <i>Biophysical Journal</i> , 2014 , 106, 1864-70	2.9	8
139	High-resolution microtubule structures reveal the structural transitions in β -tubulin upon GTP hydrolysis. <i>Cell</i> , 2014 , 157, 1117-29	56.2	422
138	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
137	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
136	Architecture and dynamics of the autophagic phosphatidylinositol 3-kinase complex. <i>ELife</i> , 2014 , 3,	8.9	106
135	The microtubule binding properties of CENP-E β C-terminus and CENP-F. <i>Journal of Molecular Biology</i> , 2013 , 425, 4427-41	6.5	25
134	Native cysteine residues are dispensable for the structure and function of all five yeast mitotic septins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 1964-79	4.2	5
133	Human TFIID binds to core promoter DNA in a reorganized structural state. <i>Cell</i> , 2013 , 152, 120-31	56.2	89
132	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
131	Ranking TEM cameras by their response to electron shot noise. <i>Ultramicroscopy</i> , 2013 , 133, 1-7	3.1	19
130	Structural visualization of key steps in human transcription initiation. <i>Nature</i> , 2013 , 495, 481-6	50.4	403
129	Tubulin and Its Isoforms 2013 , 450-453		1
128	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
127	Architecture of human translation initiation factor 3. <i>Structure</i> , 2013 , 21, 920-8	5.2	55
126	Substrate-specific structural rearrangements of human Dicer. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 662-70	17.6	72
125	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
124	Two RNA-binding motifs in eIF3 direct HCV IRES-dependent translation. <i>Nucleic Acids Research</i> , 2013 , 41, 7512-21	20.1	52

123	Regulatory interplay between TFIID β conformational transitions and its modular interaction with core promoter DNA. <i>Transcription</i> , 2013 , 4, 120-6	4.8	6
122	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
121	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
120	Complete subunit architecture of the proteasome regulatory particle. <i>Nature</i> , 2012 , 482, 186-91	50.4	465
119	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
118	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
117	4.6 Tubulin and Microtubule Structure: Mechanistic Insights into Dynamic Instability and Its Biological Relevance 2012 , 72-92		3
116	Multimodal microtubule binding by the Ndc80 kinetochore complex. <i>Nature Structural and Molecular Biology</i> , 2012 , 19, 1161-7	17.6	68
115	Molecular architecture of human polycomb repressive complex 2. <i>ELife</i> , 2012 , 1, e00005	8.9	186
114	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
113	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
112	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
111	Septin filament organization in <i>Saccharomyces cerevisiae</i> . <i>Communicative and Integrative Biology</i> , 2012 , 5, 503-5	1.7	12
110	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
109	Molecular architecture of the human Mediator-RNA polymerase II-TFIIF assembly. <i>PLoS Biology</i> , 2011 , 9, e1000603	9.7	77
108	Septin filament formation is essential in budding yeast. <i>Developmental Cell</i> , 2011 , 20, 540-9	10.2	111
107	Structures of the RNA-guided surveillance complex from a bacterial immune system. <i>Nature</i> , 2011 , 477, 486-489	50.4	299
106	Molecular architecture and connectivity of the budding yeast Mtw1 kinetochore complex. <i>Journal of Molecular Biology</i> , 2011 , 405, 548-59	6.5	51

105	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
104	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
103	Visualizing kinetochore architecture. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 661-9	8.1	19
102	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
101	Flexible tethering of primase and DNA Pol β in the eukaryotic primosome. <i>Nucleic Acids Research</i> , 2011 , 39, 8187-99	20.1	51
100	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
99	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
98	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
97	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
96	The Ndc80 kinetochore complex forms oligomeric arrays along microtubules. <i>Nature</i> , 2010 , 467, 805-10	50.4	223
95	My dream of a fantastic voyage to see the inner workings of a cell. <i>Molecular Biology of the Cell</i> , 2010 , 21, 3815	3.5	
94	When cytoskeletal worlds collide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 19609-10	11.5	4
93	Cryo-EM studies of microtubule structural intermediates and kinetochore-microtubule interactions. <i>Methods in Cell Biology</i> , 2010 , 95, 129-56	1.8	2
92	Cryoelectron microscopy applications in the study of tubulin structure, microtubule architecture, dynamics and assemblies, and interaction of microtubules with motors. <i>Methods in Enzymology</i> , 2010 , 483, 121-42	1.7	11
91	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
90	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
89	Simulations of tubulin sheet polymers as possible structural intermediates in microtubule assembly. <i>PLoS ONE</i> , 2009 , 4, e7291	3.7	19
88	Structure-function insights into the yeast Dam1 kinetochore complex. <i>Journal of Cell Science</i> , 2009 , 122, 3831-6	5.3	29

87	Structures of three distinct activator-TFIID complexes. <i>Genes and Development</i> , 2009 , 23, 1510-21	12.6	54
86	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
85	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
84	Computational Modeling of the Benefits Expected For Zernike Phase Contrast in Cryo-EM. <i>Microscopy and Microanalysis</i> , 2009 , 15, 94-95	0.5	
83	Architecture and flexibility of the yeast Ndc80 kinetochore complex. <i>Journal of Molecular Biology</i> , 2008 , 383, 894-903	6.5	86
82	Structural changes in TAF4b-TFIID correlate with promoter selectivity. <i>Molecular Cell</i> , 2008 , 29, 81-91	17.6	52
81	Tubulin and Microtubule Structures 2008 , 211-225		1
80	Saccharomyces cerevisiae 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
79	Single Particle Reconstruction of Yeast RNA Degradation Machine, Exosome, Using Electron Microscopy. <i>Microscopy and Microanalysis</i> , 2008 , 14, 162-163	0.5	
78	Making use of dynamic instability at the microtubule-kinetochore interface. <i>FASEB Journal</i> , 2008 , 22, 537.1	0.9	
77	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
76	Backtracking determines the force sensitivity of RNAP II in a factor-dependent manner. <i>Nature</i> , 2007 , 446, 820-3	50.4	221
75	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
74	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
73	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
72	A revised nomenclature for the human and rodent alpha-tubulin gene family. <i>Genomics</i> , 2007 , 90, 285-9	4.3	50
71	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
70	Structural intermediates in microtubule assembly and disassembly: how and why?. <i>Current Opinion in Cell Biology</i> , 2006 , 18, 179-84	9	151

69	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
68	Cryo-electron microscopy studies of human TFIIID: conformational breathing in the integration of gene regulatory cues. <i>Structure</i> , 2006 , 14, 511-20	5.2	61
67	Molecular architecture and conformational flexibility of human RNA polymerase II. <i>Structure</i> , 2006 , 14, 1691-700	5.2	38
66	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
65	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
64	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
63	The Dam1 kinetochore ring complex moves processively on depolymerizing microtubule ends. <i>Nature</i> , 2006 , 440, 565-9	50.4	236
62	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
61	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
60	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
59	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
58	Structural roles for human translation factor eIF3 in initiation of protein synthesis. <i>Science</i> , 2005 , 310, 1513-5	33.3	236
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9	Discovery and characterization of a novel family of prokaryotic nanocompartments involved in sulfur metabolism		12
8	Structure of the activated Roq1 resistosome directly recognizing the pathogen effector XopQ		4
7	The mechanism of motor inhibition by microtubule-associated proteins		3
6	Visualization of PRC2-Dinucleosome Interactions Leading to Epigenetic Repression		1
5	Atomic model of microtubule-bound tau		3
4	Efficient graphene oxide coating improves cryo-EM sample preparation and data collection from tilted grids		5
3	The encapsulin from <i>Thermatoga maritima</i> is a flavoprotein with a symmetry matched ferritin-like cargo protein		2
2	Structure of the human SAGA coactivator complex: The divergent architecture of human SAGA allows modular coordination of transcription activation and co-transcriptional splicing		3
1	CRISPR-Cas9 bends and twists DNA to read its sequence		6