Edward H Egelman

List of Publications by Year in Descending Order

194 papers	12,655 citations	66 h-index	105 g-index
211 ext. papers	14,407 ext. citations	11.7 avg, IF	6.54 L-index

#	Paper	IF	Citations
194	Cryo-EM of Helical Polymers.. *Chemical Reviews*, **2022**,	68.1	3
193	Phenol-soluble modulins PSMβ3 and PSMβ2 form nanotubes that are cross-β amyloids.. *Proceedings of the National Academy of Sciences of the United States of America*, **2022**, 119, e2121586119	11.5	0
192	Distinct axial and lateral interactions within homologous filaments dictate the signaling specificity and order of the AIM2-ASC inflammasome. *Nature Communications*, **2021**, 12, 2735	17.4	6
191	: a New Realm for Archaeal Filamentous Viruses with Linear A-Form Double-Stranded DNA Genomes. *Journal of Virology*, **2021**, 95, e0067321	6.6	9
190	Deterministic chaos in the self-assembly of β sheet nanotubes from an amphipathic oligopeptide. *Matter*, **2021**, 4, 3217-3231	12.7	14
189	Cryo-EM is a powerful tool, but helical applications can have pitfalls. *Soft Matter*, **2021**, 17, 3291-3293	3.6	4
188	Structural analysis of cross β helical nanotubes provides insight into the designability of filamentous peptide nanomaterials. *Nature Communications*, **2021**, 12, 407	17.4	18
187	Artificial Intracellular Filaments. *Cell Reports Physical Science*, **2020**, 1,	6.1	37
186	Atomic structure of the flagellar filament reveals how β Proteobacteria escaped Toll-like receptor 5 surveillance. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 16985-16991	11.5	16
185	Cryo-EM: Ice Is Nice, but Good Ice Can Be Hard to Find. *Biophysical Journal*, **2020**, 118, 1238-1239	2.9	7
184	Structural Determination of a Filamentous Chaperone to Fabricate Electronically Conductive Metalloprotein Nanowires. *ACS Nano*, **2020**, 14, 6559-6569	16.7	13
183	The structure of helical lipoprotein lipase reveals an unexpected twist in lipase storage. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 10254-10264	11.5	13
182	Osteogenesis imperfecta mutations in plastin 3 lead to impaired calcium regulation of actin bundling. *Bone Research*, **2020**, 8, 21	13.3	7
181	Cryoelectron-Microscopic Structure of the pKpQIL Conjugative Pili from Carbapenem-Resistant Klebsiella pneumoniae. *Structure*, **2020**, 28, 1321-1328.e2	5.2	6
180	Structure of a filamentous virus uncovers familial ties within the archaeal virosphere. *Virus Evolution*, **2020**, 6, veaa023	3.7	11
179	The structures of two archaeal type IV pili illuminate evolutionary relationships. *Nature Communications*, **2020**, 11, 3424	17.4	7
178	Structures of filamentous viruses infecting hyperthermophilic archaea explain DNA stabilization in extreme environments. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 19643-19652	11.5	14

177	Structure and assembly of archaeal viruses. *Advances in Virus Research*, **2020**, 108, 127-164	10.7	8
176	Molecular mechanism for NLRP6 inflammasome assembly and activation. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 2052-2057	11.5	54
175	An extensively glycosylated archaeal pilus survives extreme conditions. *Nature Microbiology*, **2019**, 4, 1401-1410	26.6	21
174	Structure and Assembly of the Enterohemorrhagic Escherichia coli Type 4 Pilus. *Structure*, **2019**, 27, 1082-1093.e5	5.2	29
173	Structure of Microbial Nanowires Reveals Stacked Hemes that Transport Electrons over Micrometers. *Cell*, **2019**, 177, 361-369.e10	56.2	223
172	The AAA + ATPase TorsinA polymerizes into hollow helical tubes with 8.5 subunits per turn. *Nature Communications*, **2019**, 10, 3262	17.4	16
171	Ambidextrous helical nanotubes from self-assembly of designed helical hairpin motifs. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 14456-14464	11.5	22
170	A packing for A-form DNA in an icosahedral virus. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 22591-22597	11.5	17
169	Functional role of the type 1 pilus rod structure in mediating host-pathogen interactions. *ELife*, **2018**, 7,	8.9	37
168	Structural conservation in a membrane-enveloped filamentous virus infecting a hyperthermophilic acidophile. *Nature Communications*, **2018**, 9, 3360	17.4	18
167	Direct imaging and computational cryo-electron microscopy of ribbons and nanotubes. *Current Opinion in Colloid and Interface Science*, **2018**, 34, 100-113	7.6	5
166	Cryo-EM structure of the NLRC4 filament provides insights into how symmetric and asymmetric supramolecular structures drive inflammasome assembly. *Journal of Biological Chemistry*, **2018**, 293, 20240-20248	5.4	22
165	RosettaES: a sampling strategy enabling automated interpretation of difficult cryo-EM maps. *Nature Methods*, **2017**, 14, 797-800	21.6	84
164	Cryo-EM of bacterial pili and archaeal flagellar filaments. *Current Opinion in Structural Biology*, **2017**, 46, 31-37	8.1	16
163	Structure of the calcium-dependent type 2 secretion pseudopilus. *Nature Microbiology*, **2017**, 2, 1686-1695	26.6	38
162	A structural model of flagellar filament switching across multiple bacterial species. *Nature Communications*, **2017**, 8, 960	17.4	63
161	Cryoelectron Microscopy Reconstructions of the Pseudomonas aeruginosa and Neisseria gonorrhoeae Type IV Pili at Sub-nanometer Resolution. *Structure*, **2017**, 25, 1423-1435.e4	5.2	58
160	Refined Cryo-EM Structure of the T4 Tail Tube: Exploring the Lowest Dose Limit. *Structure*, **2017**, 25, 1436-1441.e2	5.2	24

159	Structural basis of TIR-domain-assembly formation in MAL- and MyD88-dependent TLR4 signaling. *Nature Structural and Molecular Biology*, **2017**, 24, 743-751	17.6	82
158	Structural basis for high-affinity actin binding revealed by a βIII-spectrin SCA5 missense mutation. *Nature Communications*, **2017**, 8, 1350	17.4	27
157	Model for a novel membrane envelope in a filamentous hyperthermophilic virus. *ELife*, **2017**, 6,	8.9	32
156	Resolution advances in cryo-EM enable application to drug discovery. *Current Opinion in Structural Biology*, **2016**, 41, 194-202	8.1	73
155	Archaeal flagellin combines a bacterial type IV pilin domain with an Ig-like domain. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 10352-7	11.5	31
154	Cryo-EM Structure of Caspase-8 Tandem DED Filament Reveals Assembly and Regulation Mechanisms of the Death-Inducing Signaling Complex. *Molecular Cell*, **2016**, 64, 236-250	17.6	89
153	Structure of the Neisseria meningitidis Type IV pilus. *Nature Communications*, **2016**, 7, 13015	17.4	87
152	Structure of a Chaperone-Usher Pilus Reveals the Molecular Basis of Rod Uncoiling. *Cell*, **2016**, 164, 269-278	56.2	41
151	The Current Revolution in Cryo-EM. *Biophysical Journal*, **2016**, 110, 1008-12	2.9	76
150	Actin polymerization is stimulated by actin cross-linking protein palladin. *Biochemical Journal*, **2016**, 473, 383-96	3.8	17
149	Structure of the Bacterial Sex F Pilus Reveals an Assembly of a Stoichiometric Protein-Phospholipid Complex. *Cell*, **2016**, 166, 1436-1444.e10	56.2	67
148	Near-atomic resolution for one state of F-actin. *Structure*, **2015**, 23, 173-182	5.2	98
147	Structure of the type VI secretion system contractile sheath. *Cell*, **2015**, 160, 952-962	56.2	172
146	De novo protein structure determination from near-atomic-resolution cryo-EM maps. *Nature Methods*, **2015**, 12, 335-8	21.6	131
145	Archaeal actin from a hyperthermophile forms a single-stranded filament. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 9340-5	11.5	18
144	Assembly-driven activation of the AIM2 foreign-dsDNA sensor provides a polymerization template for downstream ASC. *Nature Communications*, **2015**, 6, 7827	17.4	95
143	Rad51 Paralogs Remodel Pre-synaptic Rad51 Filaments to Stimulate Homologous Recombination. *Cell*, **2015**, 162, 271-286	56.2	95
142	The molecular basis for flexibility in the flexible filamentous plant viruses. *Nature Structural and Molecular Biology*, **2015**, 22, 642-4	17.6	45

141	Structure and assembly of the mouse ASC inflammasome by combined NMR spectroscopy and cryo-electron microscopy. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 13237-42	11.5	100
140	Three-dimensional reconstruction of helical polymers. *Archives of Biochemistry and Biophysics*, **2015**, 581, 54-8	4.1	22
139	Virology. A virus that infects a hyperthermophile encapsidates A-form DNA. *Science*, **2015**, 348, 914-7	33.3	79
138	Unified polymerization mechanism for the assembly of ASC-dependent inflammasomes. *Cell*, **2014**, 156, 1193-1206	56.2	741
137	Direct interaction of actin filaments with F-BAR protein pacsin2. *EMBO Reports*, **2014**, 15, 1154-62	6.5	47
136	Molecular imprinting as a signal-activation mechanism of the viral RNA sensor RIG-I. *Molecular Cell*, **2014**, 55, 511-23	17.6	176
135	A PH domain in ACAP1 possesses key features of the BAR domain in promoting membrane curvature. *Developmental Cell*, **2014**, 31, 73-86	10.2	25
134	Identification of an actin binding surface on vinculin that mediates mechanical cell and focal adhesion properties. *Structure*, **2014**, 22, 697-706	5.2	38
133	Distinct docking and stabilization steps of the Pseudopilus conformational transition path suggest rotational assembly of type IV pilus-like fibers. *Structure*, **2014**, 22, 685-96	5.2	40
132	Ambiguities in helical reconstruction. *ELife*, **2014**, 3,	8.9	36
131	Organization of F-actin by Fesselin (avian smooth muscle synaptopodin 2). *Biochemistry*, **2013**, 52, 4955-61	3.2	9
130	Structural architecture of the CARMA1/Bcl10/MALT1 signalosome: nucleation-induced filamentous assembly. *Molecular Cell*, **2013**, 51, 766-79	17.6	123
129	The structure of the CS1 pilus of enterotoxigenic Escherichia coli reveals structural polymorphism. *Journal of Bacteriology*, **2013**, 195, 1360-70	3.5	15
128	Actin filaments as tension sensors. *Current Biology*, **2012**, 22, R96-101	6.3	123
127	Stepwise molecular display utilizing icosahedral and helical complexes of phage coat and decoration proteins in the development of robust nanoscale display vehicles. *Biomaterials*, **2012**, 33, 5628-37	15.6	29
126	MDA5 assembles into a polar helical filament on dsRNA. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 18437-41	11.5	91
125	Structure of the Vibrio cholerae Type IVb Pilus and stability comparison with the Neisseria gonorrhoeae type IVa pilus. *Journal of Molecular Biology*, **2012**, 418, 47-64	6.5	52
124	Filaments from Ignicoccus hospitalis show diversity of packing in proteins containing N-terminal type IV pilin helices. *Journal of Molecular Biology*, **2012**, 422, 274-81	6.5	30

123	Real-space processing of helical filaments in SPARX. *Journal of Structural Biology*, **2012**, 177, 302-13	3.4	29
122	Are ParM filaments polar or bipolar?. *Journal of Molecular Biology*, **2012**, 423, 482-5	6.5	5
121	Crystal structure of the phage T4 recombinase UvsX and its functional interaction with the T4 SF2 helicase UvsW. *Journal of Molecular Biology*, **2011**, 405, 65-76	6.5	19
120	Two modes of binding of DinI to RecA filament provide a new insight into the regulation of SOS response by DinI protein. *Journal of Molecular Biology*, **2011**, 408, 815-24	6.5	11
119	The N-terminal domains of myosin binding protein C can bind polymorphically to F-actin. *Journal of Molecular Biology*, **2011**, 412, 379-86	6.5	45
118	Remodeling of actin filaments by ADF/cofilin proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 20568-72	11.5	158
117	Opening of tandem calponin homology domains regulates their affinity for F-actin. *Nature Structural and Molecular Biology*, **2010**, 17, 614-6	17.6	71
116	Structural polymorphism in F-actin. *Nature Structural and Molecular Biology*, **2010**, 17, 1318-23	17.6	148
115	Cryo-reconstructions of P22 polyheads suggest that phage assembly is nucleated by trimeric interactions among coat proteins. *Physical Biology*, **2010**, 7, 045004	3	24
114	Reconstruction of helical filaments and tubes. *Methods in Enzymology*, **2010**, 482, 167-83	1.7	90
113	ParA2, a Vibrio cholerae chromosome partitioning protein, forms left-handed helical filaments on DNA. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 4590-5	11.5	45
112	The structure of the Salmonella typhimurium type III secretion system needle shows divergence from the flagellar system. *Journal of Molecular Biology*, **2010**, 396, 1392-7	6.5	34
111	Mapping of drebrin binding site on F-actin. *Journal of Molecular Biology*, **2010**, 398, 542-54	6.5	41
110	Helical filaments of human Dmc1 protein on single-stranded DNA: a cautionary tale. *Journal of Molecular Biology*, **2010**, 401, 544-51	6.5	18
109	Reducing irreducible complexity: divergence of quaternary structure and function in macromolecular assemblies. *Current Opinion in Cell Biology*, **2010**, 22, 68-74	9	12
108	Loop 2 in Saccharomyces cerevisiae Rad51 protein regulates filament formation and ATPase activity. *Nucleic Acids Research*, **2009**, 37, 158-71	20.1	7
107	Structural polymorphism of the ParM filament and dynamic instability. *Structure*, **2009**, 17, 1253-64	5.2	34
106	Electron microscopy of helical filaments: rediscovering buried treasures in negative stain. *BioEssays*, **2009**, 31, 909-11	4.1	7

105	The structure of F-pili. *Journal of Molecular Biology*, **2009**, 385, 22-9	6.5	39
104	Cleavage of bacteriophage lambda cI repressor involves the RecA C-terminal domain. *Journal of Molecular Biology*, **2009**, 385, 779-87	6.5	27
103	The bipolar filaments formed by herpes simplex virus type 1 SSB/recombination protein (ICP8) suggest a mechanism for DNA annealing. *Journal of Molecular Biology*, **2009**, 386, 273-9	6.5	17
102	The RecB nuclease domain binds to RecA-DNA filaments: implications for filament loading. *Journal of Molecular Biology*, **2009**, 391, 269-74	6.5	9
101	Implications of the RecA structure. *F1000 Biology Reports*, **2009**, 1, 7		
100	Functional and structural basis for a bacteriophage homolog of human RAD52. *Current Biology*, **2008**, 18, 1142-6	6.3	51
99	Structure and disassembly of filaments formed by the ESCRT-III subunit Vps24. *Structure*, **2008**, 16, 1345-56	5.6	115
98	Divergence of quaternary structures among bacterial flagellar filaments. *Science*, **2008**, 320, 382-5	33.3	87
97	Actin hydrophobic loop 262-274 and filament nucleation and elongation. *Journal of Molecular Biology*, **2008**, 375, 793-801	6.5	11
96	Coronin-1A stabilizes F-actin by bridging adjacent actin protomers and stapling opposite strands of the actin filament. *Journal of Molecular Biology*, **2008**, 376, 607-13	6.5	42
95	The structure of an archaeal pilus. *Journal of Molecular Biology*, **2008**, 381, 456-66	6.5	41
94	Structural basis of membrane invagination by F-BAR domains. *Cell*, **2008**, 132, 807-17	56.2	427
93	High-resolution cryo-EM structure of the F-actin-fimbrin/plastin ABD2 complex. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 1494-8	11.5	94
92	Assembly of Weibel-Palade body-like tubules from N-terminal domains of von Willebrand factor. *Proceedings of the National Academy of Sciences of the United States of America*, **2008**, 105, 482-7	11.5	122
91	A comparative analysis of Dmc1 and Rad51 nucleoprotein filaments. *Nucleic Acids Research*, **2008**, 36, 4057-66	20.1	84
90	Problems in fitting high resolution structures into electron microscopic reconstructions. *HFSP Journal*, **2008**, 2, 324-31		8
89	Mapping the interaction of cofilin with subdomain 2 on actin. *Biochemistry*, **2007**, 46, 225-33	3.2	11
88	Stabilization of RAD51 nucleoprotein filaments by the C-terminal region of BRCA2. *Nature Structural and Molecular Biology*, **2007**, 14, 468-74	17.6	193

87	The structure of bacterial ParM filaments. *Nature Structural and Molecular Biology*, **2007**, 14, 921-6	17.6	66
86	Single-particle reconstruction from EM images of helical filaments. *Current Opinion in Structural Biology*, **2007**, 17, 556-61	8.1	28
85	Stabilization of RAD-51-DNA filaments via an interaction domain in Caenorhabditis elegans BRCA2. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 8299-304	11.5	52
84	The iterative helical real space reconstruction method: surmounting the problems posed by real polymers. *Journal of Structural Biology*, **2007**, 157, 83-94	3.4	187
83	Actin structure and function: what we still do not understand. *Journal of Biological Chemistry*, **2007**, 282, 36133-7	5.4	76
82	The Rad51/RadA N-terminal domain activates nucleoprotein filament ATPase activity. *Structure*, **2006**, 14, 983-92	5.2	51
81	Structural polymorphism in bacterial EspA filaments revealed by cryo-EM and an improved approach to helical reconstruction. *Structure*, **2006**, 14, 1189-96	5.2	32
80	RecA assembly, one molecule at a time. *Structure*, **2006**, 14, 1600-2	5.2	2
79	Xin-repeats and nebulin-like repeats bind to F-actin in a similar manner. *Journal of Molecular Biology* , **2006**, 356, 714-23	6.5	22
78	The CH-domain of calponin does not determine the modes of calponin binding to F-actin. *Journal of Molecular Biology*, **2006**, 359, 478-85	6.5	35
77	The structure of a filamentous bacteriophage. *Journal of Molecular Biology*, **2006**, 361, 209-15	6.5	82
76	Type IV pilus structure by cryo-electron microscopy and crystallography: implications for pilus assembly and functions. *Molecular Cell*, **2006**, 23, 651-62	17.6	317
75	Structural polymorphism of Methanothermobacter thermautotrophicus MCM. *Journal of Molecular Biology*, **2005**, 346, 389-94	6.5	64
74	The Arg non-receptor tyrosine kinase modifies F-actin structure. *Journal of Molecular Biology*, **2005**, 346, 565-75	6.5	25
73	Refining the structure of the Halobacterium salinarum flagellar filament using the iterative helical real space reconstruction method: insights into polymorphism. *Journal of Molecular Biology*, **2005**, 346, 665-76	6.5	43
72	Atomic model of a myosin filament in the relaxed state. *Nature*, **2005**, 436, 1195-9	50.4	236
71	BRCA2 BRC motifs bind RAD51-DNA filaments. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 8537-42	11.5	111
70	Actin-destabilizing factors disrupt filaments by means of a time reversal of polymerization. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 17664-8	11.5	68

69	The stalk region of dynamin drives the constriction of dynamin tubes. *Nature Structural and Molecular Biology*, **2004**, 11, 574-5	17.6	128
68	More insights into structural plasticity of actin binding proteins. *Structure*, **2004**, 12, 909-10	5.2	4
67	Acrosomal actin: twists and turns of a versatile filament. *Current Biology*, **2004**, 14, R959-61	6.3	5
66	Helical structure of the needle of the type III secretion system of Shigella flexneri. *Journal of Biological Chemistry*, **2003**, 278, 17103-7	5.4	152
65	Actin's prokaryotic homologs. *Current Opinion in Structural Biology*, **2003**, 13, 244-8	8.1	27
64	ATP-mediated conformational changes in the RecA filament. *Structure*, **2003**, 11, 187-96	5.2	133
63	A tale of two polymers: new insights into helical filaments. *Nature Reviews Molecular Cell Biology*, **2003**, 4, 621-30	48.7	38
62	Issues of resolution and polymorphism in single-particle reconstruction. *Journal of Structural Biology*, **2003**, 144, 162-71	3.4	35
61	Complexes of RecA with LexA and RecX differentiate between active and inactive RecA nucleoprotein filaments. *Journal of Molecular Biology*, **2003**, 333, 345-54	6.5	57
60	The location of ubiquitin in Lethocerus arthrin. *Journal of Molecular Biology*, **2003**, 325, 623-8	6.5	18
59	Do the utrophin tandem calponin homology domains bind F-actin in a compact or extended conformation?. *Journal of Molecular Biology*, **2003**, 331, 967-72	6.5	41
58	Salmonella SipA polymerizes actin by stapling filaments with nonglobular protein arms. *Science*, **2003**, 301, 1918-21	33.3	97
57	A DNA pairing-enhanced conformation of bacterial RecA proteins. *Journal of Biological Chemistry*, **2003**, 278, 52710-23	5.4	40
56	ADF/cofilin use an intrinsic mode of F-actin instability to disrupt actin filaments. *Journal of Cell Biology*, **2003**, 163, 1057-66	7.3	93
55	Each actin subunit has three nebulin binding sites: implications for steric blocking. *Current Biology*, **2002**, 12, 383-8	6.3	59
54	SV40 large T antigen hexamer structure: domain organization and DNA-induced conformational changes. *Current Biology*, **2002**, 12, 472-6	6.3	46
53	A new internal mode in F-actin helps explain the remarkable evolutionary conservation of actin's sequence and structure. *Current Biology*, **2002**, 12, 570-5	6.3	101
52	The Methanobacterium thermoautotrophicum MCM protein can form heptameric rings. *EMBO Reports*, **2002**, 3, 792-7	6.5	83

51	The utrophin actin-binding domain binds F-actin in two different modes: implications for the spectrin superfamily of proteins. *Journal of Cell Biology*, **2002**, 157, 243-51	7.3	75
50	Structure and function of Hib pili from Haemophilus influenzae type b. *Journal of Bacteriology*, **2002**, 184, 4868-74	3.5	28
49	Homologous-pairing activity of the Bacillus subtilis bacteriophage SPP1 replication protein G35P. *Journal of Biological Chemistry*, **2002**, 277, 35969-79	5.4	50
48	How does ATP hydrolysis control actin's associations?. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 10945-7	11.5	55
47	The hexameric ring structure of the Escherichia coli RuvB branch migration protein. *Journal of Molecular Biology*, **2002**, 319, 587-91	6.5	21
46	Flexibility of the rings: structural asymmetry in the DnaB hexameric helicase. *Journal of Molecular Biology*, **2002**, 321, 839-49	6.5	69
45	The bacterial protein SipA polymerizes G-actin and mimics muscle nebulin. *Nature Structural Biology* , **2002**, 9, 518-21		33
44	Bacterial conjugation: running rings around DNA. *Current Biology*, **2001**, 11, R103-5	6.3	5
43	Molecular evolution: actin's long lost relative found. *Current Biology*, **2001**, 11, R1022-4	6.3	15
42	Actin depolymerizing factor stabilizes an existing state of F-actin and can change the tilt of F-actin subunits. *Journal of Cell Biology*, **2001**, 153, 75-86	7.3	218
41	Archaeal RadA protein binds DNA as both helical filaments and octameric rings. *Journal of Molecular Biology*, **2001**, 314, 1077-85	6.5	82
40	Does a stretched DNA structure dictate the helical geometry of RecA-like filaments?. *Journal of Molecular Biology*, **2001**, 309, 539-42	6.5	46
39	The primase active site is on the outside of the hexameric bacteriophage T7 gene 4 helicase-primase ring. *Journal of Molecular Biology*, **2001**, 311, 951-6	6.5	28
38	Probing the structure of F-actin: cross-links constrain atomic models and modify actin dynamics. *Journal of Molecular Biology*, **2001**, 312, 95-106	6.5	51
37	Comparison of bacteriophage T4 UvsX and human Rad51 filaments suggests that RecA-like polymers may have evolved independently. *Journal of Molecular Biology*, **2001**, 312, 999-1009	6.5	35
36	Electron microscopic studies of the translin octameric ring. *Journal of Structural Biology*, **2001**, 135, 58-66	3.4	32
35	Binding of dystrophin's tandem calponin homology domain to F-actin is modulated by actin's structure. *Biophysical Journal*, **2001**, 80, 1926-31	2.9	18
34	Two conformations of G-actin related to two conformations of F-actin. *Results and Problems in Cell Differentiation*, **2001**, 32, 95-101	1.4	5

33	A robust algorithm for the reconstruction of helical filaments using single-particle methods. *Ultramicroscopy*, **2000**, 85, 225-34	3.1	394
32	The human Rad52 protein exists as a heptameric ring. *Current Biology*, **2000**, 10, 337-40	6.3	156
31	Visualization of two binding sites for the Escherichia coli UmuD(2)C complex (DNA pol V) on RecA-ssDNA filaments. *Journal of Molecular Biology*, **2000**, 297, 585-97	6.5	33
30	Three-dimensional reconstruction of transcription termination factor rho: orientation of the N-terminal domain and visualization of an RNA-binding site. *Journal of Molecular Biology*, **2000**, 299, 1279-87	6.5	44
29	F-actin retains a memory of angular order. *Biophysical Journal*, **2000**, 78, 2180-5	2.9	20
28	Biochemical and electron microscopic image analysis of the hexameric E1 helicase. *Journal of Biological Chemistry*, **1999**, 274, 4447-58	5.4	101
27	Identification of a defined epitope on the surface of the active RecA-DNA filament using a monoclonal antibody and three-dimensional reconstruction. *Journal of Molecular Biology*, **1998**, 283, 985-92	6.5	16
26	Bacterial helicases. *Journal of Structural Biology*, **1998**, 124, 123-8	3.4	31
25	Intrastrand cross-linked actin between Gln-41 and Cys-374. III. Inhibition of motion and force generation with myosin. *Biochemistry*, **1998**, 37, 17801-9	3.2	49
24	Cooperative rigor binding of myosin to actin is a function of F-actin structure. *Journal of Molecular Biology*, **1997**, 265, 469-74	6.5	90
23	Structure and subunit composition of the RuvAB-Holliday junction complex. *Journal of Molecular Biology*, **1997**, 266, 217-22	6.5	76
22	Modulation of yeast F-actin structure by a mutation in the nucleotide-binding cleft. *Journal of Molecular Biology*, **1997**, 271, 235-43	6.5	44
21	The RecA hexamer is a structural homologue of ring helicases. *Nature Structural Biology*, **1997**, 4, 101-4		106
20	Only one F-actin model. *Nature Structural Biology*, **1997**, 4, 683-4		7
19	New angles on actin dynamics. *Structure*, **1997**, 5, 1135-7	5.2	16
18	Sickle cell anemia research and a recombinant DNA technique. *Science*, **1997**, 277, 460-2	33.3	8
17	The hexameric E. coli DnaB helicase can exist in different Quaternary states. *Journal of Molecular Biology*, **1996**, 259, 7-14	6.5	137
16	Homomorphous hexameric helicases: tales from the ring cycle. *Structure*, **1996**, 4, 759-62	5.2	37

15	DNA is bound within the central hole to one or two of the six subunits of the T7 DNA helicase. *Nature Structural and Molecular Biology*, **1996**, 3, 740-3	17.6	111
14	New insights into actin filament dynamics. *Current Opinion in Structural Biology*, **1995**, 5, 172-80	8.1	80
13	Structural dynamics of F-actin: I. Changes in the C terminus. *Journal of Molecular Biology*, **1995**, 245, 582-97	6.5	114
12	Structural dynamics of F-actin: II. Cooperativity in structural transitions. *Journal of Molecular Biology* , **1995**, 245, 598-607	6.5	152
11	The LexA repressor binds within the deep helical groove of the activated RecA filament. *Journal of Molecular Biology*, **1993**, 231, 29-40	6.5	88
10	DNA conformation induced by the bacteriophage T4 UvsX protein appears identical to the conformation induced by the Escherichia coli RecA protein. *Journal of Molecular Biology*, **1993**, 232, 1-4	6.5	45
9	Two key questions raised by an atomic model for F-actin: Current Opinion in Structural Biology 1992, 2:286292. *Current Opinion in Structural Biology*, **1992**, 2, 286-292	8.1	12
8	Structural basis for the destabilization of F-actin by phosphate release following ATP hydrolysis. *Journal of Molecular Biology*, **1992**, 227, 1043-53	6.5	128
7	Direct visualization of dynamics and co-operative conformational changes within RecA filaments that appear to be associated with the hydrolysis of adenosine 5SO-(3-thiotriphosphate). *Journal of Molecular Biology*, **1992**, 225, 193-216	6.5	43
6	Angular disorder in actin: is it consistent with general principles of protein structure?. *Journal of Molecular Biology*, **1991**, 217, 405-8	6.5	14
5	Structure of helical RecA-DNA complexes. II. Local conformational changes visualized in bundles of RecA-ATP gamma S filaments. *Journal of Molecular Biology*, **1988**, 200, 329-49	6.5	67
4	Structure of helical RecA-DNA complexes. III. The structural polarity of RecA filaments and functional polarity in the RecA-mediated strand exchange reaction. *Journal of Molecular Biology*, **1988**, 202, 659-62	6.5	48
3	RecA-DNA helical complexes in genetic recombination. *Biochemical Society Transactions*, **1986**, 14, 218-20	3.1	8
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