

Stephen C Harrison

List of Publications by Year in descending order

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182
papers

35,421
citations

5430

85
h-index

4622

176
g-index

208
all docs

208
docs citations

208
times ranked

29987
citing authors

#	ARTICLE	IF	CITATIONS
1	Recall of B cell memory depends on relative locations of prime and boost immunization. <i>Science Immunology</i> , 2022, 7, eabn5311.	5.6	20
2	Antibodies induced by an ancestral SARS-CoV-2 strain that cross-neutralize variants from Alpha to Omicron BA.1. <i>Science Immunology</i> , 2022, 7, eabo3425.	5.6	28
3	Antibodies That Engage the Hemagglutinin Receptor-Binding Site of Influenza B Viruses. <i>ACS Infectious Diseases</i> , 2021, 7, 1-5.	1.8	11
4	Recapitulation of HIV-1 Env-antibody coevolution in macaques leading to neutralization breadth. <i>Science</i> , 2021, 371, .	6.0	49
5	Functional refolding of the penetration protein on a non-enveloped virus. <i>Nature</i> , 2021, 590, 666-670.	13.7	33
6	Structural basis of Stu2 recruitment to yeast kinetochores. <i>ELife</i> , 2021, 10, .	2.8	11
7	Differential immune imprinting by influenza virus vaccination and infection in nonhuman primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	15
8	A Prevalent Focused Human Antibody Response to the Influenza Virus Hemagglutinin Head Interface. <i>MBio</i> , 2021, 12, e0114421.	1.8	17
9	Ctf3/CENP-I provides a docking site for the desumoylase Ulp2 at the kinetochore. <i>Journal of Cell Biology</i> , 2021, 220, .	2.3	4
10	Recognition of Divergent Viral Substrates by the SARS-CoV-2 Main Protease. <i>ACS Infectious Diseases</i> , 2021, 7, 2591-2595.	1.8	55
11	Memory B cell repertoire for recognition of evolving SARS-CoV-2 spike. <i>Cell</i> , 2021, 184, 4969-4980.e15.	13.5	94
12	Structure of the Vesicular Stomatitis Virus L Protein in Complex with Its Phosphoprotein Cofactor. <i>Cell Reports</i> , 2020, 30, 53-60.e5.	2.9	51
13	The Structural Basis for Kinetochore Stabilization by Cnn1/CENP-T. <i>Current Biology</i> , 2020, 30, 3425-3431.e3.	1.8	19
14	Structure of a nascent membrane protein as it folds on the BAM complex. <i>Nature</i> , 2020, 583, 473-478.	13.7	101
15	Structure of a rabies virus polymerase complex from electron cryo-microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2099-2107.	3.3	58
16	Cryoelectron Microscopy Structure of a Yeast Centromeric Nucleosome at 2.7Å... Resolution. <i>Structure</i> , 2020, 28, 363-370.e3.	1.6	19
17	Cryo-EM Structure of Full-length HIV-1 Env Bound With the Fab of Antibody PG16. <i>Journal of Molecular Biology</i> , 2020, 432, 1158-1168.	2.0	47
18	The human dimension in contemporary biological research. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 107-108.	3.6	0

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19	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate. <i>ELife</i> , 2020, 9, .	2.8	105
20	Horace's hymn to Bacchus (Odes 2.19): poetics and politics. , 2020, , 231-252.		2
21	Structure of the Centromere Binding Factor 3 Complex from <i>Kluyveromyces lactis</i> . <i>Journal of Molecular Biology</i> , 2019, 431, 4444-4454.	2.0	3
22	In situ Structure of Rotavirus VP1 RNA-Dependent RNA Polymerase. <i>Journal of Molecular Biology</i> , 2019, 431, 3124-3138.	2.0	45
23	Antibodies to a Conserved Influenza Head Interface Epitope Protect by an IgG Subtype-Dependent Mechanism. <i>Cell</i> , 2019, 177, 1124-1135.e16.	13.5	141
24	Autoreactivity profiles of influenza hemagglutinin broadly neutralizing antibodies. <i>Scientific Reports</i> , 2019, 9, 3492.	1.6	49
25	Affinity maturation in a human humoral response to influenza hemagglutinin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 26745-26751.	3.3	25
26	Self-tolerance curtails the B cell repertoire to microbial epitopes. <i>JCI Insight</i> , 2019, 4, .	2.3	32
27	The structure of the Ctf19c/CCAN from budding yeast. <i>ELife</i> , 2019, 8, .	2.8	71
28	The structure of the yeast Ctf3 complex. <i>ELife</i> , 2019, 8, .	2.8	15
29	Memory B Cells that Cross-React with Group 1 and Group 2 Influenza A Viruses Are Abundant in Adult Human Repertoires. <i>Immunity</i> , 2018, 48, 174-184.e9.	6.6	124
30	Conserved epitope on influenza-virus hemagglutinin head defined by a vaccine-induced antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 168-173.	3.3	113
31	Structure of the DASH/Dam1 complex shows its role at the yeast kinetochore-microtubule interface. <i>Science</i> , 2018, 360, 552-558.	6.0	72
32	HIV envelope V3 region mimic embodies key features of a broadly neutralizing antibody lineage epitope. <i>Nature Communications</i> , 2018, 9, 1111.	5.8	30
33	Kinetochore Function from the Bottom Up. <i>Trends in Cell Biology</i> , 2018, 28, 22-33.	3.6	50
34	Visualization of Calcium Ion Loss from Rotavirus during Cell Entry. <i>Journal of Virology</i> , 2018, 92, .	1.5	27
35	Structure of the membrane proximal external region of HIV-1 envelope glycoprotein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E8892-E8899.	3.3	72
36	Intra-seasonal antibody repertoire analysis of a subject immunized with an MF59®-adjuvanted pandemic 2009 H1N1 vaccine. <i>Vaccine</i> , 2018, 36, 5325-5332.	1.7	4

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37	How small-molecule inhibitors of dengue-virus infection interfere with viral membrane fusion. <i>ELife</i> , 2018, 7, .	2.8	16
38	Conformational States of a Soluble, Uncleaved HIV-1 Envelope Trimer. <i>Journal of Virology</i> , 2017, 91, .	1.5	19
39	Antigenicity-defined conformations of an extremely neutralization-resistant HIV-1 envelope spike. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4477-4482.	3.3	18
40	Protein tentacles. <i>Journal of Structural Biology</i> , 2017, 200, 244-247.	1.3	8
41	CryoEM Structure of an Influenza Virus Receptor-Binding Site Antibodyâ€™s Antigen Interface. <i>Journal of Molecular Biology</i> , 2017, 429, 1829-1839.	2.0	21
42	Staged induction of HIV-1 glycanâ€™-dependent broadly neutralizing antibodies. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	212
43	Mechanism of membrane fusion induced by vesicular stomatitis virus G protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E28-E36.	3.3	98
44	The Kinetochores Receptor for the Cohesin Loading Complex. <i>Cell</i> , 2017, 171, 72-84.e13.	13.5	88
45	Single-Particle Detection of Transcription following Rotavirus Entry. <i>Journal of Virology</i> , 2017, 91, .	1.5	23
46	Pictures of the prologue to neurotransmitter release. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8920-8922.	3.3	3
47	Initiation of HIV neutralizing B cell lineages with sequential envelope immunizations. <i>Nature Communications</i> , 2017, 8, 1732.	5.8	76
48	Molecular Structures of Yeast Kinetochores Subcomplexes and Their Roles in Chromosome Segregation. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2017, 82, 83-89.	2.0	10
49	Boosting of HIV envelope CD4 binding site antibodies with long variable heavy third complementarity determining region in the randomized double blind RV305 HIV-1 vaccine trial. <i>PLoS Pathogens</i> , 2017, 13, e1006182.	2.1	38
50	Conserved Tetramer Junction in the Kinetochores Ndc80 Complex. <i>Cell Reports</i> , 2016, 17, 1915-1922.	2.9	51
51	Complex Antigens Drive Permissive Clonal Selection in Germinal Centers. <i>Immunity</i> , 2016, 44, 542-552.	6.6	278
52	Immunogenic cross-talk between dengue and Zika viruses. <i>Nature Immunology</i> , 2016, 17, 1010-1012.	7.0	34
53	Structure of the MIS12 Complex and Molecular Basis of Its Interaction with CENP-C at Human Kinetochores. <i>Cell</i> , 2016, 167, 1028-1040.e15.	13.5	126
54	Structure of the MIND Complex Defines a Regulatory Focus for Yeast Kinetochores Assembly. <i>Cell</i> , 2016, 167, 1014-1027.e12.	13.5	121

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55	Influenza immunization elicits antibodies specific for an egg-adapted vaccine strain. <i>Nature Medicine</i> , 2016, 22, 1465-1469.	15.2	104
56	Structural Constraints of Vaccine-Induced Tier-2 Autologous HIV Neutralizing Antibodies Targeting the Receptor-Binding Site. <i>Cell Reports</i> , 2016, 14, 43-54.	2.9	45
57	Immunogenic Stimulus for Germline Precursors of Antibodies that Engage the Influenza Hemagglutinin Receptor-Binding Site. <i>Cell Reports</i> , 2015, 13, 2842-2850.	2.9	67
58	Molecular Basis for Antibody-Mediated Neutralization of New World Hemorrhagic Fever Mammarenaviruses. <i>Cell Host and Microbe</i> , 2015, 18, 705-713.	5.1	44
59	Structure of the L Protein of Vesicular Stomatitis Virus from Electron Cryomicroscopy. <i>Cell</i> , 2015, 162, 314-327.	13.5	211
60	Viral Receptor-Binding Site Antibodies with Diverse Germline Origins. <i>Cell</i> , 2015, 161, 1026-1034.	13.5	151
61	Viral membrane fusion. <i>Virology</i> , 2015, 479-480, 498-507.	1.1	594
62	Key mutations stabilize antigen-binding conformation during affinity maturation of a broadly neutralizing influenza antibody lineage. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 771-780.	1.5	34
63	Veritas per structuram. <i>Annual Review of Biochemistry</i> , 2015, 84, 37-60.	5.0	1
64	Structural evidence for Scc4-dependent localization of cohesin loading. <i>ELife</i> , 2015, 4, e06057.	2.8	69
65	Autoinhibition of Bruton's tyrosine kinase (Btk) and activation by soluble inositol hexakisphosphate. <i>ELife</i> , 2015, 4, .	2.8	82
66	Distinct functional determinants of influenza hemagglutinin-mediated membrane fusion. <i>ELife</i> , 2015, 4, e11009.	2.8	53
67	Sequential conformational rearrangements in flavivirus membrane fusion. <i>ELife</i> , 2014, 3, e04389.	2.8	72
68	Structural Correlates of Rotavirus Cell Entry. <i>PLoS Pathogens</i> , 2014, 10, e1004355.	2.1	55
69	Affinity maturation in an HIV broadly neutralizing B-cell lineage through reorientation of variable domains. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 10275-10280.	3.3	73
70	Stable, uncleaved HIV-1 envelope glycoprotein gp140 forms a tightly folded trimer with a native-like structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18542-18547.	3.3	67
71	An Iml3-Chl4 Heterodimer Links the Core Centromere to Factors Required for Accurate Chromosome Segregation. <i>Cell Reports</i> , 2013, 5, 29-36.	2.9	56
72	Structure of a Dengue Virus Envelope Protein Late-Stage Fusion Intermediate. <i>Journal of Virology</i> , 2013, 87, 2287-2293.	1.5	114

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73	Location of the dsRNA-Dependent Polymerase, VP1, in Rotavirus Particles. <i>Journal of Molecular Biology</i> , 2013, 425, 124-132.	2.0	69
74	Antigenicity and Immunogenicity of RV144 Vaccine AIDSVAX Clade E Envelope Immunogen Is Enhanced by a gp120 N-Terminal Deletion. <i>Journal of Virology</i> , 2013, 87, 1554-1568.	1.5	97
75	Preconfiguration of the antigen-binding site during affinity maturation of a broadly neutralizing influenza virus antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 264-269.	3.3	227
76	Influenza-virus membrane fusion by cooperative fold-back of stochastically induced hemagglutinin intermediates. <i>ELife</i> , 2013, 2, e00333.	2.8	154
77	Small-Molecule Inhibitors of Dengue-Virus Entry. <i>PLoS Pathogens</i> , 2012, 8, e1002627.	2.1	80
78	Ndc10 is a platform for inner kinetochore assembly in budding yeast. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 48-55.	3.6	54
79	RWD domain: a recurring module in kinetochore architecture shown by a Ctf19-Mcm21 complex structure. <i>EMBO Reports</i> , 2012, 13, 216-222.	2.0	62
80	Beam-induced motion of vitrified specimen on holey carbon film. <i>Journal of Structural Biology</i> , 2012, 177, 630-637.	1.3	366
81	Molecular Architecture of the Yeast Monopolin Complex. <i>Cell Reports</i> , 2012, 1, 583-589.	2.9	46
82	B-cell lineage immunogen design in vaccine development with HIV-1 as a case study. <i>Nature Biotechnology</i> , 2012, 30, 423-433.	9.4	432
83	Movies of Ice-Embedded Particles Enhance Resolution in Electron Cryo-Microscopy. <i>Structure</i> , 2012, 20, 1823-1828.	1.6	277
84	Kinetics of Proton Transport into Influenza Virions by the Viral M2 Channel. <i>PLoS ONE</i> , 2012, 7, e31566.	1.1	31
85	Single-molecule analysis of a molecular disassemblase reveals the mechanism of Hsc70-driven clathrin uncoating. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 295-301.	3.6	101
86	Atomic model of an infectious rotavirus particle. <i>EMBO Journal</i> , 2011, 30, 408-416.	3.5	254
87	Near-atomic resolution reconstructions of icosahedral viruses from electron cryo-microscopy. <i>Current Opinion in Structural Biology</i> , 2011, 21, 265-273.	2.6	148
88	Broadly neutralizing human antibody that recognizes the receptor-binding pocket of influenza virus hemagglutinin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 14216-14221.	3.3	402
89	Recognition of the centromere-specific histone Cse4 by the chaperone Scm3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9367-9371.	3.3	95
90	Cross-Linking of Rotavirus Outer Capsid Protein VP7 by Antibodies or Disulfides Inhibits Viral Entry. <i>Journal of Virology</i> , 2011, 85, 10509-10517.	1.5	24

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91	Structural basis for receptor recognition by New World hemorrhagic fever arenaviruses. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 438-444.	3.6	125
92	Conservation in vesicle coats. <i>Nature</i> , 2010, 466, 1048-1049.	13.7	17
93	Peptide Inhibitors of Flavivirus Entry Derived from the E Protein Stem. <i>Journal of Virology</i> , 2010, 84, 12549-12554.	1.5	85
94	Effect of Mutations in VP5* Hydrophobic Loops on Rotavirus Cell Entry. <i>Journal of Virology</i> , 2010, 84, 6200-6207.	1.5	40
95	Peptide Inhibitors of Dengue-Virus Entry Target a Late-Stage Fusion Intermediate. <i>PLoS Pathogens</i> , 2010, 6, e1000851.	2.1	113
96	Mechanistic Biology in the Next Quarter Century. <i>Molecular Biology of the Cell</i> , 2010, 21, 3799-3800.	0.9	2
97	Looking Inside Adenovirus. <i>Science</i> , 2010, 329, 1026-1027.	6.0	34
98	X-ray Crystal Structure of the Rotavirus Inner Capsid Particle at 3.8Å... Resolution. <i>Journal of Molecular Biology</i> , 2010, 397, 587-599.	2.0	124
99	The Monopolin Complex Crosslinks Kinetochores Components to Regulate Chromosome-Microtubule Attachments. <i>Cell</i> , 2010, 142, 556-567.	13.5	119
100	A Rotavirus Spike Protein Conformational Intermediate Binds Lipid Bilayers. <i>Journal of Virology</i> , 2010, 84, 1764-1770.	1.5	50
101	Subunit interactions in bovine papillomavirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6298-6303.	3.3	134
102	Structure of Rotavirus Outer-Layer Protein VP7 Bound with a Neutralizing Fab. <i>Science</i> , 2009, 324, 1444-1447.	6.0	216
103	Molecular interactions in rotavirus assembly and uncoating seen by high-resolution cryo-EM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 10644-10648.	3.3	135
104	VP5* Rearranges when Rotavirus Uncoats. <i>Journal of Virology</i> , 2009, 83, 11372-11377.	1.5	43
105	Requirements for the Formation of Membrane Pores by the Reovirus Myristoylated 1/4IN Peptide. <i>Journal of Virology</i> , 2009, 83, 7004-7014.	1.5	55
106	Role of HIV membrane in neutralization by two broadly neutralizing antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20234-20239.	3.3	225
107	Viral membrane fusion. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 690-698.	3.6	1,060
108	Mechanism for Coordinated RNA Packaging and Genome Replication by Rotavirus Polymerase VP1. <i>Structure</i> , 2008, 16, 1678-1688.	1.6	148

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109	Single-particle kinetics of influenza virus membrane fusion. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15382-15387.	3.3	248
110	The pH sensor for flavivirus membrane fusion. Journal of Cell Biology, 2008, 183, 177-179.	2.3	39
111	Near-atomic resolution using electron cryomicroscopy and single-particle reconstruction. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1867-1872.	3.3	347
112	Structure and Function of an Essential Component of the Outer Membrane Protein Assembly Machine. Science, 2007, 317, 961-964.	6.0	327
113	Protein Arms in the Kinetochore-Microtubule Interface of the Yeast DASH Complex. Molecular Biology of the Cell, 2007, 18, 2503-2510.	0.9	55
114	An Atomic Model of the Interferon- β Enhanceosome. Cell, 2007, 129, 1111-1123.	13.5	547
115	The Ndc80/HEC1 complex is a contact point for kinetochore-microtubule attachment. Nature Structural and Molecular Biology, 2007, 14, 54-59.	3.6	307
116	Three-dimensional intricacies in protein-DNA recognition and transcriptional control. Nature Structural and Molecular Biology, 2007, 14, 1118-1119.	3.6	5
117	Comments on the NIGMS PSI. Structure, 2007, 15, 1344-1346.	1.6	8
118	Single Particle Reconstructions of the Transferrin-Transferrin Receptor Complex Obtained with Different Specimen Preparation Techniques. Journal of Molecular Biology, 2006, 355, 1048-1065.	2.0	57
119	PL-6 Structure of the aquaporin-0 mediated membrane junction(Plenary Lecture,Abstract,Meeting) Tj ETQq1 1 0.784314 rgBT ₀ /Overlock	0.0	0.0
120	Structure of a Central Component of the Yeast Kinetochore: The Spc24p/Spc25p Globular Domain. Structure, 2006, 14, 1003-1009.	1.6	86
121	Small molecules that bind the inner core of gp41 and inhibit HIV envelope-mediated fusion. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13938-13943.	3.3	133
122	Stu2p binds tubulin and undergoes an open-to-closed conformational change. Journal of Cell Biology, 2006, 172, 1009-1022.	2.3	119
123	Crystal Structure of Glycoprotein B from Herpes Simplex Virus 1. Science, 2006, 313, 217-220.	6.0	493
124	The yeast DASH complex forms closed rings on microtubules. Nature Structural and Molecular Biology, 2005, 12, 138-143.	3.6	258
125	Structure of an unliganded simian immunodeficiency virus gp120 core. Nature, 2005, 433, 834-841.	13.7	483
126	Features of Reovirus Outer Capsid Protein σ 41 Revealed by Electron Cryomicroscopy and Image Reconstruction of the Virion at 7.0 Å... Resolution. Structure, 2005, 13, 1545-1557.	1.6	80

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127	Molecular organization of the Ndc80 complex, an essential kinetochore component. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 5363-5367.	3.3	243
128	Mechanism of Membrane Fusion by Viral Envelope Proteins. Advances in Virus Research, 2005, 64, 231-261.	0.9	162
129	Perspective: Discovery of antivirals against smallpox. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11178-11192.	3.3	93
130	Crystal structure of ATF-2/c-Jun and IRF-3 bound to the interferon- β enhancer. EMBO Journal, 2004, 23, 4384-4393.	3.5	156
131	Whither structural biology?. Nature Structural and Molecular Biology, 2004, 11, 12-15.	3.6	64
132	Structure of the dengue virus envelope protein after membrane fusion. Nature, 2004, 427, 313-319.	13.7	995
133	X-ray structure of a protein-conducting channel. Nature, 2004, 427, 36-44.	13.7	1,134
134	Structural rearrangements in the membrane penetration protein of a non-enveloped virus. Nature, 2004, 430, 1053-1058.	13.7	200
135	Molecular model for a complete clathrin lattice from electron cryomicroscopy. Nature, 2004, 432, 573-579.	13.7	464
136	Structure of the Human Transferrin Receptor-Transferrin Complex. Cell, 2004, 116, 565-576.	13.5	475
137	Two Distinct Size Classes of Immature and Mature Subviral Particles from Tick-Borne Encephalitis Virus. Journal of Virology, 2003, 77, 11357-11366.	1.5	69
138	Variation on an Src-like Theme. Cell, 2003, 112, 737-740.	13.5	173
139	A ligand-binding pocket in the dengue virus envelope glycoprotein. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 6986-6991.	3.3	927
140	Specificity and Affinity of Sialic Acid Binding by the Rhesus Rotavirus VP8* Core. Journal of Virology, 2002, 76, 10512-10517.	1.5	68
141	The rhesus rotavirus VP4 sialic acid binding domain has a galectin fold with a novel carbohydrate binding site. EMBO Journal, 2002, 21, 885-897.	3.5	305
142	Structure of the Reovirus Membrane-Penetration Protein, $\sigma 4$, in a Complex with Its Protector Protein, $\sigma 3$. Cell, 2002, 108, 283-295.	13.5	225
143	Don C. Wiley (1944-2001). Cell, 2002, 108, 313-315.	13.5	2
144	RNA Synthesis in a Cage-Structural Studies of Reovirus Polymerase $\sigma 3$. Cell, 2002, 111, 733-745.	13.5	309

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145	Don C. Wiley (1944–2001). <i>Molecular Cell</i> , 2002, 9, 225-227.	4.5	0
146	Atomic model of the papillomavirus capsid. <i>EMBO Journal</i> , 2002, 21, 4754-4762.	3.5	232
147	Molecular Organization of a Recombinant Subviral Particle from Tick-Borne Encephalitis Virus. <i>Molecular Cell</i> , 2001, 7, 593-602.	4.5	240
148	Structure of the reovirus core at 3.6 Å resolution. <i>Nature</i> , 2000, 404, 960-967.	13.7	428
149	Purified Recombinant Rotavirus VP7 Forms Soluble, Calcium-Dependent Trimers. <i>Virology</i> , 2000, 277, 420-428.	1.1	62
150	Structure of Small Virus-like Particles Assembled from the L1 Protein of Human Papillomavirus 16. <i>Molecular Cell</i> , 2000, 5, 557-567.	4.5	417
151	Structure of PAK1 in an Autoinhibited Conformation Reveals a Multistage Activation Switch. <i>Cell</i> , 2000, 102, 387-397.	13.5	481
152	Selection of gp41-mediated HIV-1 cell entry inhibitors from biased combinatorial libraries of non-natural binding elements. <i>Nature Structural Biology</i> , 1999, 6, 953-960.	9.7	140
153	Crystal Structures of c-Src Reveal Features of Its Autoinhibitory Mechanism. <i>Molecular Cell</i> , 1999, 3, 629-638.	4.5	786
154	Atomic Structure of Clathrin. <i>Cell</i> , 1998, 95, 563-573.	13.5	217
155	Structure of a Covalently Trapped Catalytic Complex of HIV-1 Reverse Transcriptase: Implications for Drug Resistance. , 1998, 282, 1669-1675.		1,317
156	Three-dimensional structure of the tyrosine kinase c-Src. <i>Nature</i> , 1997, 385, 595-602.	13.7	1,386
157	Crystal structure of ICAM-2 reveals a distinctive integrin recognition surface. <i>Nature</i> , 1997, 387, 312-315.	13.7	115
158	Peptide–Surface Association: The Case of PDZ and PTB Domains. <i>Cell</i> , 1996, 86, 341-343.	13.5	170
159	Phosphorylated T Cell Receptor zeta-chain and ZAP70 Tandem SH2 Domains form a 1:3 Complex in vitro. <i>FEBS Journal</i> , 1996, 238, 440-445.	0.2	26
160	Crystal structures of murine polyomavirus in complex with straight-chain and branched-chain sialyloligosaccharide receptor fragments. <i>Structure</i> , 1996, 4, 183-194.	1.6	172
161	Retrovirus envelope domain at 1.7 Å resolution. <i>Nature Structural Biology</i> , 1996, 3, 465-469.	9.7	328
162	Structure and mechanism of DNA topoisomerase II. <i>Nature</i> , 1996, 379, 225-232.	13.7	813

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163	Spatial constraints on the recognition of phosphoproteins by the tandem SH2 domains of the phosphatase SH-PTP2. <i>Nature</i> , 1996, 379, 277-280.	13.7	192
164	Varmus at Harvard. <i>Science</i> , 1996, 273, 413-413.	6.0	0
165	Crystal structure of the heterodimeric bZIP transcription factor c-Fos/c-Jun bound to DNA. <i>Nature</i> , 1995, 373, 257-261.	13.7	736
166	Structure of the NF- κ B p50 homodimer bound to DNA. <i>Nature</i> , 1995, 373, 311-317.	13.7	531
167	The envelope glycoprotein from tick-borne encephalitis virus at 2 Å... resolution. <i>Nature</i> , 1995, 375, 291-298.	13.7	1,344
168	Structure of murine polyomavirus complexed with an oligosaccharide receptor fragment. <i>Nature</i> , 1994, 369, 160-163.	13.7	307
169	Recognition of a high-affinity phosphotyrosyl peptide by the Src homology-2 domain of p56lck. <i>Nature</i> , 1993, 362, 87-91.	13.7	545
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