

Stephen C Harrison

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.

182
papers

29,947
citations

82
h-index

173
g-index

208
ext. papers

33,058
ext. citations

22.3
avg, IF

7.32
L-index

#	Paper	IF	Citations
182	Recall of B cell memory depends on relative locations of prime and boost immunization.. <i>Science Immunology</i> , 2022 , 7, eabn5311	28	2
181	Antibodies induced by ancestral SARS-CoV-2 strain that cross-neutralize variants from Alpha to Omicron BA.1.. <i>Science Immunology</i> , 2022 , eabo3425	28	2
180	Memory B cell repertoire for recognition of evolving SARS-CoV-2 spike 2021 ,		4
179	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,	11.5	2
178	A Prevalent Focused Human Antibody Response to the Influenza Virus Hemagglutinin Head Interface. <i>MBio</i> , 2021 , 12, e0114421	7.8	2
177	Ctf3/CENP-I provides a docking site for the desumoylase Ulp2 at the kinetochore. <i>Journal of Cell Biology</i> , 2021 , 220,	7.3	2
176	Antibodies That Engage the Hemagglutinin Receptor-Binding Site of Influenza B Viruses. <i>ACS Infectious Diseases</i> , 2021 , 7, 1-5	5.5	1
175	Recapitulation of HIV-1 Env-antibody coevolution in macaques leading to neutralization breadth. <i>Science</i> , 2021 , 371,	33.3	22
174	Functional refolding of the penetration protein on a non-enveloped virus. <i>Nature</i> , 2021 , 590, 666-670	50.4	12
173	Recognition of Divergent Viral Substrates by the SARS-CoV-2 Main Protease. <i>ACS Infectious Diseases</i> , 2021 , 7, 2591-2595	5.5	15
172	Memory B cell repertoire for recognition of evolving SARS-CoV-2 spike. <i>Cell</i> , 2021 , 184, 4969-4980.e15	56.2	42
171	Structure of a nascent membrane protein as it folds on the BAM complex. <i>Nature</i> , 2020 , 583, 473-478	50.4	49
170	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	11.5	30
169	Cryoelectron Microscopy Structure of a Yeast Centromeric Nucleosome at 2.7Å Resolution. <i>Structure</i> , 2020 , 28, 363-370.e3	5.2	7
168	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	6.5	27
167	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate. <i>ELife</i> , 2020 , 9,	8.9	50
166	Structure of the Vesicular Stomatitis Virus L Protein in Complex with Its Phosphoprotein Cofactor. <i>Cell Reports</i> , 2020 , 30, 53-60.e5	10.6	26

165	The Structural Basis for Kinetochore Stabilization by Cnn1/CENP-T. <i>Current Biology</i> , 2020 , 30, 3425-3431.e3	6.3	9
164	Structure of the Centromere Binding Factor 3 Complex from <i>Kluyveromyces lactis</i> . <i>Journal of Molecular Biology</i> , 2019 , 431, 4444-4454	6.5	1
163	In situ Structure of Rotavirus VP1 RNA-Dependent RNA Polymerase. <i>Journal of Molecular Biology</i> , 2019 , 431, 3124-3138	6.5	28
162	Antibodies to a Conserved Influenza Head Interface Epitope Protect by an IgG Subtype-Dependent Mechanism. <i>Cell</i> , 2019 , 177, 1124-1135.e16	56.2	86
161	Autoreactivity profiles of influenza hemagglutinin broadly neutralizing antibodies. <i>Scientific Reports</i> , 2019 , 9, 3492	4.9	32
160	Self-tolerance curtails the B cell repertoire to microbial epitopes. <i>JCI Insight</i> , 2019 , 4,	9.9	14
159	The structure of the Ctf19c/CCAN from budding yeast. <i>ELife</i> , 2019 , 8,	8.9	41
158	The structure of the yeast Ctf3 complex. <i>ELife</i> , 2019 , 8,	8.9	12
157	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 ,	11.5	12
156	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	32.3	76
155	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	11.5	80
154	Structure of the DASH/Dam1 complex shows its role at the yeast kinetochore-microtubule interface. <i>Science</i> , 2018 , 360, 552-558	33.3	31
153	HIV envelope V3 region mimic embodies key features of a broadly neutralizing antibody lineage epitope. <i>Nature Communications</i> , 2018 , 9, 1111	17.4	17
152	Kinetochore Function from the Bottom Up. <i>Trends in Cell Biology</i> , 2018 , 28, 22-33	18.3	34
151	Intra-seasonal antibody repertoire analysis of a subject immunized with an MF59 -adjuvanted pandemic 2009 H1N1 vaccine. <i>Vaccine</i> , 2018 , 36, 5325-5332	4.1	2
150	How small-molecule inhibitors of dengue-virus infection interfere with viral membrane fusion. <i>ELife</i> , 2018 , 7,	8.9	13
149	Visualization of Calcium Ion Loss from Rotavirus during Cell Entry. <i>Journal of Virology</i> , 2018 , 92,	6.6	14
148	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	11.5	49

147	Conformational States of a Soluble, Uncleaved HIV-1 Envelope Trimer. <i>Journal of Virology</i> , 2017 , 91,	6.6	11
146	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	11.5	13
145	Protein tentacles. <i>Journal of Structural Biology</i> , 2017 , 200, 244-247	3.4	6
144	CryoEM Structure of an Influenza Virus Receptor-Binding Site Antibody-Antigen Interface. <i>Journal of Molecular Biology</i> , 2017 , 429, 1829-1839	6.5	19
143	Staged induction of HIV-1 glycan-dependent broadly neutralizing antibodies. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	127
142	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	11.5	64
141	The Kinetochore Receptor for the Cohesin Loading Complex. <i>Cell</i> , 2017 , 171, 72-84.e13	56.2	58
140	Initiation of HIV neutralizing B cell lineages with sequential envelope immunizations. <i>Nature Communications</i> , 2017 , 8, 1732	17.4	52
139	Single-Particle Detection of Transcription following Rotavirus Entry. <i>Journal of Virology</i> , 2017 , 91,	6.6	15
138	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	11.5	2
137	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	7.6	30
136	Molecular Structures of Yeast Kinetochore Subcomplexes and Their Roles in Chromosome Segregation. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2017 , 82, 83-89	3.9	5
135	Immunogenic cross-talk between dengue and Zika viruses. <i>Nature Immunology</i> , 2016 , 17, 1010-2	19.1	27
134	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	56.2	85
133	Structure of the MIND Complex Defines a Regulatory Focus for Yeast Kinetochore Assembly. <i>Cell</i> , 2016 , 167, 1014-1027.e12	56.2	74
132	Influenza immunization elicits antibodies specific for an egg-adapted vaccine strain. <i>Nature Medicine</i> , 2016 , 22, 1465-1469	50.5	73
131	Structural Constraints of Vaccine-Induced Tier-2 Autologous HIV Neutralizing Antibodies Targeting the Receptor-Binding Site. <i>Cell Reports</i> , 2016 , 14, 43-54	10.6	45
130	Conserved Tetramer Junction in the Kinetochore Ndc80 Complex. <i>Cell Reports</i> , 2016 , 17, 1915-1922	10.6	27

129	Complex Antigens Drive Permissive Clonal Selection in Germinal Centers. <i>Immunity</i> , 2016 , 44, 542-552	32.3	170
128	Structure of the L Protein of Vesicular Stomatitis Virus from Electron Cryomicroscopy. <i>Cell</i> , 2015 , 162, 314-327	56.2	167
127	Viral receptor-binding site antibodies with diverse germline origins. <i>Cell</i> , 2015 , 161, 1026-1034	56.2	114
126	Viral membrane fusion. <i>Virology</i> , 2015 , 479-480, 498-507	3.6	409
125	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, 771-801	4.2	24
124	Veritas per structuram. <i>Annual Review of Biochemistry</i> , 2015 , 84, 37-60	29.1	1
123	Immunogenic Stimulus for Germline Precursors of Antibodies that Engage the Influenza Hemagglutinin Receptor-Binding Site. <i>Cell Reports</i> , 2015 , 13, 2842-50	10.6	43
122	Molecular Basis for Antibody-Mediated Neutralization of New World Hemorrhagic Fever Mammarenaviruses. <i>Cell Host and Microbe</i> , 2015 , 18, 705-13	23.4	38
121	Structural evidence for Scc4-dependent localization of cohesin loading. <i>ELife</i> , 2015 , 4, e06057	8.9	49
120	Autoinhibition of Bruton's tyrosine kinase (Btk) and activation by soluble inositol hexakisphosphate. <i>ELife</i> , 2015 , 4,	8.9	53
119	Distinct functional determinants of influenza hemagglutinin-mediated membrane fusion. <i>ELife</i> , 2015 , 4, e11009	8.9	32
118	Sequential conformational rearrangements in flavivirus membrane fusion. <i>ELife</i> , 2014 , 3, e04389	8.9	48
117	Structural correlates of rotavirus cell entry. <i>PLoS Pathogens</i> , 2014 , 10, e1004355	7.6	34
116	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, 10275-80	11.5	63
115	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, 18542-7	11.5	54
114	An Iml3-Chl4 heterodimer links the core centromere to factors required for accurate chromosome segregation. <i>Cell Reports</i> , 2013 , 5, 29-36	10.6	47
113	Structure of a dengue virus envelope protein late-stage fusion intermediate. <i>Journal of Virology</i> , 2013 , 87, 2287-93	6.6	85
112	Location of the dsRNA-dependent polymerase, VP1, in rotavirus particles. <i>Journal of Molecular Biology</i> , 2013 , 425, 124-32	6.5	61

111	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, 1554-68	6.6	85
110	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, 264-9	11.5	170
109	Influenza-virus membrane fusion by cooperative fold-back of stochastically induced hemagglutinin intermediates. <i>ELife</i> , 2013 , 2, e00333	8.9	112
108	Beam-induced motion of vitrified specimen on holey carbon film. <i>Journal of Structural Biology</i> , 2012 , 177, 630-7	3.4	299
107	Molecular architecture of the yeast monopolin complex. <i>Cell Reports</i> , 2012 , 1, 583-9	10.6	36
106	B-cell-lineage immunogen design in vaccine development with HIV-1 as a case study. <i>Nature Biotechnology</i> , 2012 , 30, 423-33	44.5	351
105	Movies of ice-embedded particles enhance resolution in electron cryo-microscopy. <i>Structure</i> , 2012 , 20, 1823-8	5.2	230
104	Kinetics of proton transport into influenza virions by the viral M2 channel. <i>PLoS ONE</i> , 2012 , 7, e31566	3.7	24
103	Small-molecule inhibitors of dengue-virus entry. <i>PLoS Pathogens</i> , 2012 , 8, e1002627	7.6	68
102	RWD domain: a recurring module in kinetochore architecture shown by a Ctf19-Mcm21 complex structure. <i>EMBO Reports</i> , 2012 , 13, 216-22	6.5	51
101	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	17.6	90
100	Atomic model of an infectious rotavirus particle. <i>EMBO Journal</i> , 2011 , 30, 408-16	13	195
99	Near-atomic resolution reconstructions of icosahedral viruses from electron cryo-microscopy. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 265-73	8.1	130
98	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, 14216-21	11.5	331
97	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, 9367-71	11.5	81
96	Cross-linking of rotavirus outer capsid protein VP7 by antibodies or disulfides inhibits viral entry. <i>Journal of Virology</i> , 2011 , 85, 10509-17	6.6	17
95	Ndc10 is a platform for inner kinetochore assembly in budding yeast. <i>Nature Structural and Molecular Biology</i> , 2011 , 19, 48-55	17.6	40
94	Structural basis for receptor recognition by New World hemorrhagic fever arenaviruses. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 438-44	17.6	105

93	Peptide inhibitors of flavivirus entry derived from the E protein stem. <i>Journal of Virology</i> , 2010 , 84, 12549-54	49.64	72
92	Effect of mutations in VP5 hydrophobic loops on rotavirus cell entry. <i>Journal of Virology</i> , 2010 , 84, 6200-6	7.6	33
91	Peptide inhibitors of dengue-virus entry target a late-stage fusion intermediate. <i>PLoS Pathogens</i> , 2010 , 6, e1000851	7.6	105
90	Mechanistic biology in the next quarter century. <i>Molecular Biology of the Cell</i> , 2010 , 21, 3799-800	3.5	1
89	Virology. Looking inside adenovirus. <i>Science</i> , 2010 , 329, 1026-7	33.3	29
88	X-ray crystal structure of the rotavirus inner capsid particle at 3.8 Å resolution. <i>Journal of Molecular Biology</i> , 2010 , 397, 587-99	6.5	113
87	The monopolin complex crosslinks kinetochore components to regulate chromosome-microtubule attachments. <i>Cell</i> , 2010 , 142, 556-67	56.2	99
86	A rotavirus spike protein conformational intermediate binds lipid bilayers. <i>Journal of Virology</i> , 2010 , 84, 1764-70	6.6	39
85	Subunit interactions in bovine papillomavirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 6298-303	11.5	121
84	Structure of rotavirus outer-layer protein VP7 bound with a neutralizing Fab. <i>Science</i> , 2009 , 324, 1444-7	33.3	182
83	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, 10644-8	11.5	120
82	VP5* rearranges when rotavirus uncoats. <i>Journal of Virology</i> , 2009 , 83, 11372-7	6.6	35
81	Requirements for the formation of membrane pores by the reovirus myristoylated micro1N peptide. <i>Journal of Virology</i> , 2009 , 83, 7004-14	6.6	48
80	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, 20234-9	11.5	205
79	Viral membrane fusion. <i>Nature Structural and Molecular Biology</i> , 2008 , 15, 690-8	17.6	918
78	Mechanism for coordinated RNA packaging and genome replication by rotavirus polymerase VP1. <i>Structure</i> , 2008 , 16, 1678-88	5.2	130
77	Single-particle kinetics of influenza virus membrane fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 15382-7	11.5	196
76	The pH sensor for flavivirus membrane fusion. <i>Journal of Cell Biology</i> , 2008 , 183, 177-9	7.3	33

75	Near-atomic resolution using electron cryomicroscopy and single-particle reconstruction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 1867-72	11.5	312
74	The Ndc80/HEC1 complex is a contact point for kinetochore-microtubule attachment. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 54-9	17.6	263
73	Comments on the NIGMS PSI. <i>Structure</i> , 2007 , 15, 1344-6	5.2	7
72	Structure and function of an essential component of the outer membrane protein assembly machine. <i>Science</i> , 2007 , 317, 961-4	33.3	302
71	Protein arms in the kinetochore-microtubule interface of the yeast DASH complex. <i>Molecular Biology of the Cell</i> , 2007 , 18, 2503-10	3.5	46
70	An atomic model of the interferon-beta enhanceosome. <i>Cell</i> , 2007 , 129, 1111-23	56.2	452
69	Structure of a central component of the yeast kinetochore: the Spc24p/Spc25p globular domain. <i>Structure</i> , 2006 , 14, 1003-9	5.2	82
68	Small molecules that bind the inner core of gp41 and inhibit HIV envelope-mediated fusion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 13938-43	11.5	110
67	Stu2p binds tubulin and undergoes an open-to-closed conformational change. <i>Journal of Cell Biology</i> , 2006 , 172, 1009-22	7.3	96
66	Crystal structure of glycoprotein B from herpes simplex virus 1. <i>Science</i> , 2006 , 313, 217-20	33.3	440
65	Single particle reconstructions of the transferrin-transferrin receptor complex obtained with different specimen preparation techniques. <i>Journal of Molecular Biology</i> , 2006 , 355, 1048-65	6.5	55
64	PL-6 Structure of the aquaporin-0 mediated membrane junction (Plenary Lecture, Abstract, Meeting Program of EABS & BSJ 2006). <i>Seibutsu Butsuri</i> , 2006 , 46, S104	0	
63	The yeast DASH complex forms closed rings on microtubules. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 138-43	17.6	227
62	Structure of an unliganded simian immunodeficiency virus gp120 core. <i>Nature</i> , 2005 , 433, 834-41	50.4	451
61	Features of reovirus outer capsid protein mu1 revealed by electron cryomicroscopy and image reconstruction of the virion at 7.0 Angstrom resolution. <i>Structure</i> , 2005 , 13, 1545-57	5.2	62
60	Molecular organization of the Ndc80 complex, an essential kinetochore component. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 5363-7	11.5	216
59	Mechanism of membrane fusion by viral envelope proteins. <i>Advances in Virus Research</i> , 2005 , 64, 231-61	10.7	139
58	Discovery of antivirals against smallpox. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 11178-92	11.5	74

57	Crystal structure of ATF-2/c-Jun and IRF-3 bound to the interferon-beta enhancer. <i>EMBO Journal</i> , 2004 , 23, 4384-93	13	133
56	Whither structural biology?. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 12-5	17.6	55
55	Structure of the dengue virus envelope protein after membrane fusion. <i>Nature</i> , 2004 , 427, 313-9	50.4	866
54	X-ray structure of a protein-conducting channel. <i>Nature</i> , 2004 , 427, 36-44	50.4	994
53	Structural rearrangements in the membrane penetration protein of a non-enveloped virus. <i>Nature</i> , 2004 , 430, 1053-8	50.4	173
52	Molecular model for a complete clathrin lattice from electron cryomicroscopy. <i>Nature</i> , 2004 , 432, 573-9	50.4	411
51	Structure of the human transferrin receptor-transferrin complex. <i>Cell</i> , 2004 , 116, 565-76	56.2	388
50	Two distinct size classes of immature and mature subviral particles from tick-borne encephalitis virus. <i>Journal of Virology</i> , 2003 , 77, 11357-66	6.6	49
49	Variation on an Src-like theme. <i>Cell</i> , 2003 , 112, 737-40	56.2	157
48	A ligand-binding pocket in the dengue virus envelope glycoprotein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 6986-91	11.5	806
47	Atomic model of the papillomavirus capsid. <i>EMBO Journal</i> , 2002 , 21, 4754-62	13	197
46	Specificity and affinity of sialic acid binding by the rhesus rotavirus VP8* core. <i>Journal of Virology</i> , 2002 , 76, 10512-7	6.6	62
45	The rhesus rotavirus VP4 sialic acid binding domain has a galectin fold with a novel carbohydrate binding site. <i>EMBO Journal</i> , 2002 , 21, 885-97	13	266
44	Structure of the reovirus membrane-penetration protein, Mu1, in a complex with its protector protein, Sigma3. <i>Cell</i> , 2002 , 108, 283-95	56.2	201
43	Don C. Wiley (1944-2001). <i>Cell</i> , 2002 , 108, 313-5	56.2	0
42	RNA synthesis in a cage--structural studies of reovirus polymerase lambda3. <i>Cell</i> , 2002 , 111, 733-45	56.2	285
41	Don C. Wiley (1944--2001). <i>Molecular Cell</i> , 2002 , 9, 225-7	17.6	
40	Molecular organization of a recombinant subviral particle from tick-borne encephalitis virus. <i>Molecular Cell</i> , 2001 , 7, 593-602	17.6	208

39	Structure of the reovirus core at 3.6 Å resolution. <i>Nature</i> , 2000 , 404, 960-7	50.4	392
38	Purified recombinant rotavirus VP7 forms soluble, calcium-dependent trimers. <i>Virology</i> , 2000 , 277, 420-8.	5.6	52
37	Structure of small virus-like particles assembled from the L1 protein of human papillomavirus 16. <i>Molecular Cell</i> , 2000 , 5, 557-67	17.6	363
36	Structure of PAK1 in an autoinhibited conformation reveals a multistage activation switch. <i>Cell</i> , 2000 , 102, 387-97	56.2	440
35	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, 953-60		127
34	Crystal structures of c-Src reveal features of its autoinhibitory mechanism. <i>Molecular Cell</i> , 1999 , 3, 629-38.	7.6	712
33	Atomic structure of clathrin: a beta propeller terminal domain joins an alpha zigzag linker. <i>Cell</i> , 1998 , 95, 563-73	56.2	194
32	Structure of a covalently trapped catalytic complex of HIV-1 reverse transcriptase: implications for drug resistance. <i>Science</i> , 1998 , 282, 1669-75	33.3	1205
31	Three-dimensional structure of the tyrosine kinase c-Src. <i>Nature</i> , 1997 , 385, 595-602	50.4	1272
30	Crystal structure of ICAM-2 reveals a distinctive integrin recognition surface. <i>Nature</i> , 1997 , 387, 312-5	50.4	105
29	Peptide-surface association: the case of PDZ and PTB domains. <i>Cell</i> , 1996 , 86, 341-3	56.2	155
28	Phosphorylated T cell receptor zeta-chain and ZAP70 tandem SH2 domains form a 1:3 complex in vitro. <i>FEBS Journal</i> , 1996 , 238, 440-5		21
27	Crystal structures of murine polyomavirus in complex with straight-chain and branched-chain sialyloligosaccharide receptor fragments. <i>Structure</i> , 1996 , 4, 183-94	5.2	156
26	Retrovirus envelope domain at 1.7 Å resolution. <i>Nature Structural Biology</i> , 1996 , 3, 465-9		280
25	Structure and mechanism of DNA topoisomerase II. <i>Nature</i> , 1996 , 379, 225-32	50.4	723
24	Spatial constraints on the recognition of phosphoproteins by the tandem SH2 domains of the phosphatase SH-PTP2. <i>Nature</i> , 1996 , 379, 277-80	50.4	174
23	Varmus at Harvard. <i>Science</i> , 1996 , 273, 413-413	33.3	
22	Crystal structure of the heterodimeric bZIP transcription factor c-Fos-c-Jun bound to DNA. <i>Nature</i> , 1995 , 373, 257-61	50.4	663

21	Structure of the NF-kappa B p50 homodimer bound to DNA. <i>Nature</i> , 1995 , 373, 311-7	50.4	480
20	The envelope glycoprotein from tick-borne encephalitis virus at 2 A resolution. <i>Nature</i> , 1995 , 375, 291-8	50.4	1162
19	Structure of murine polyomavirus complexed with an oligosaccharide receptor fragment. <i>Nature</i> , 1994 , 369, 160-3	50.4	279
18	Recognition of a high-affinity phosphotyrosyl peptide by the Src homology-2 domain of p56lck. <i>Nature</i> , 1993 , 362, 87-91	50.4	501
17	The GCN4 basic region leucine zipper binds DNA as a dimer of uninterrupted alpha helices: crystal structure of the protein-DNA complex. <i>Cell</i> , 1992 , 71, 1223-37	56.2	917
16	DNA recognition by GAL4: structure of a protein-DNA complex. <i>Nature</i> , 1992 , 356, 408-14	50.4	617
15	Solution structure of the DNA-binding domain of Cd2-GAL4 from <i>S. cerevisiae</i> . <i>Nature</i> , 1992 , 356, 450-3	50.4	122
14	A structural taxonomy of DNA-binding domains. <i>Nature</i> , 1991 , 353, 715-9	50.4	608
13	Folding transition in the DNA-binding domain of GCN4 on specific binding to DNA. <i>Nature</i> , 1990 , 347, 575-8	50.4	382
12	Atomic structure of a fragment of human CD4 containing two immunoglobulin-like domains. <i>Nature</i> , 1990 , 348, 411-8	50.4	539
11	Structure of a phage 434 Cro/DNA complex. <i>Nature</i> , 1988 , 335, 789-95	50.4	187
10	Effect of non-contacted bases on the affinity of 434 operator for 434 repressor and Cro. <i>Nature</i> , 1987 , 326, 886-8	50.4	214
9	A phage repressor-operator complex at 7 A resolution. <i>Nature</i> , 1985 , 316, 596-601	50.4	126
8	Assembly of the head of bacteriophage P22: x-ray diffraction from heads, proheads and related structures. <i>Journal of Molecular Biology</i> , 1976 , 104, 387-410	6.5	187
7	Structural Basis of Stu2 Recruitment to Yeast Kinetochores		1
6	The structural basis for kinetochore stabilization by Cnn1/CENP-T		1
5	Recapitulation of HIV-1 Env-Antibody Coevolution in Macaques Leading to Neutralization Breadth		1
4	In situ structure of rotavirus VP1 RNA-dependent RNA polymerase		1

3	Cryo-EM structure of full-length HIV-1 Env bound with the Fab of antibody PG16	2
2	Structure of the Vesicular Stomatitis Virus L Protein in Complex with Its Phosphoprotein Cofactor	1
1	Structure of a rabies virus polymerase complex from electron cryo-microscopy	2