

# Stephen C Harrison

## List of Publications by Year in descending order

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182  
papers

35,421  
citations

4388

86  
h-index

3915

177  
g-index

208  
all docs

208  
docs citations

208  
times ranked

26878  
citing authors

#	ARTICLE	IF	CITATIONS
1	Three-dimensional structure of the tyrosine kinase c-Src. <i>Nature</i> , 1997, 385, 595-602.	27.8	1,386
2	The envelope glycoprotein from tick-borne encephalitis virus at 2 Å... resolution. <i>Nature</i> , 1995, 375, 291-298.	27.8	1,344
3	Structure of a Covalently Trapped Catalytic Complex of HIV-1 Reverse Transcriptase: Implications for Drug Resistance. <i>Science</i> , 1998, 282, 1669-1675.	12.6	1,317
4	X-ray structure of a protein-conducting channel. <i>Nature</i> , 2004, 427, 36-44.	27.8	1,134
5	Viral membrane fusion. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 690-698.	8.2	1,060
6	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, 1223-1237.	28.9	1,035
7	Structure of the dengue virus envelope protein after membrane fusion. <i>Nature</i> , 2004, 427, 313-319.	27.8	995
8	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, 6986-6991.	7.1	927
9	Structure and mechanism of DNA topoisomerase II. <i>Nature</i> , 1996, 379, 225-232.	27.8	813
10	Crystal Structures of c-Src Reveal Features of Its Autoinhibitory Mechanism. <i>Molecular Cell</i> , 1999, 3, 629-638.	9.7	786
11	Crystal structure of the heterodimeric bZIP transcription factor c-Fos/c-Jun bound to DNA. <i>Nature</i> , 1995, 373, 257-261.	27.8	736
12	DNA recognition by GAL4: structure of a protein-DNA complex. <i>Nature</i> , 1992, 356, 408-414.	27.8	685
13	A structural taxonomy of DNA-binding domains. <i>Nature</i> , 1991, 353, 715-719.	27.8	672
14	Atomic structure of a fragment of human CD4 containing two immunoglobulin-like domains. <i>Nature</i> , 1990, 348, 411-418.	27.8	610
15	Viral membrane fusion. <i>Virology</i> , 2015, 479-480, 498-507.	2.4	594
16	An Atomic Model of the Interferon- $\beta$ Enhanceosome. <i>Cell</i> , 2007, 129, 1111-1123.	28.9	547
17	Recognition of a high-affinity phosphotyrosyl peptide by the Src homology-2 domain of p56lck. <i>Nature</i> , 1993, 362, 87-91.	27.8	545
18	Structure of the NF- $\kappa$ B p50 homodimer bound to DNA. <i>Nature</i> , 1995, 373, 311-317.	27.8	531

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19	Crystal Structure of Glycoprotein B from Herpes Simplex Virus 1. <i>Science</i> , 2006, 313, 217-220.	12.6	493
20	Structure of an unliganded simian immunodeficiency virus gp120 core. <i>Nature</i> , 2005, 433, 834-841.	27.8	483
21	Structure of PAK1 in an Autoinhibited Conformation Reveals a Multistage Activation Switch. <i>Cell</i> , 2000, 102, 387-397.	28.9	481
22	Structure of the Human Transferrin Receptor-Transferrin Complex. <i>Cell</i> , 2004, 116, 565-576.	28.9	475
23	Molecular model for a complete clathrin lattice from electron cryomicroscopy. <i>Nature</i> , 2004, 432, 573-579.	27.8	464
24	B-cell lineage immunogen design in vaccine development with HIV-1 as a case study. <i>Nature Biotechnology</i> , 2012, 30, 423-433.	17.5	432
25	Structure of the reovirus core at 3.6 Å resolution. <i>Nature</i> , 2000, 404, 960-967.	27.8	428
26	Folding transition in the DMA-binding domain of GCN4 on specific binding to DNA. <i>Nature</i> , 1990, 347, 575-578.	27.8	418
27	Structure of Small Virus-like Particles Assembled from the L1 Protein of Human Papillomavirus 16. <i>Molecular Cell</i> , 2000, 5, 557-567.	9.7	417
28	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.	7.1	402
29	Beam-induced motion of vitrified specimen on holey carbon film. <i>Journal of Structural Biology</i> , 2012, 177, 630-637.	2.8	366
30	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, 1867-1872.	7.1	347
31	Retrovirus envelope domain at 1.7 Å resolution. <i>Nature Structural Biology</i> , 1996, 3, 465-469.	9.7	328
32	Structure and Function of an Essential Component of the Outer Membrane Protein Assembly Machine. <i>Science</i> , 2007, 317, 961-964.	12.6	327
33	RNA Synthesis in a Cage Structural Studies of Reovirus Polymerase 3. <i>Cell</i> , 2002, 111, 733-745.	28.9	309
34	Structure of murine polyomavirus complexed with an oligosaccharide receptor fragment. <i>Nature</i> , 1994, 369, 160-163.	27.8	307
35	The Ndc80/HEC1 complex is a contact point for kinetochore-microtubule attachment. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 54-59.	8.2	307
36	The rhesus rotavirus VP4 sialic acid binding domain has a galectin fold with a novel carbohydrate binding site. <i>EMBO Journal</i> , 2002, 21, 885-897.	7.8	305

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37	Complex Antigens Drive Permissive Clonal Selection in Germinal Centers. <i>Immunity</i> , 2016, 44, 542-552.	14.3	278
38	Movies of Ice-Embedded Particles Enhance Resolution in Electron Cryo-Microscopy. <i>Structure</i> , 2012, 20, 1823-1828.	3.3	277
39	The yeast DASH complex forms closed rings on microtubules. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 138-143.	8.2	258
40	Atomic model of an infectious rotavirus particle. <i>EMBO Journal</i> , 2011, 30, 408-416.	7.8	254
41	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, 15382-15387.	7.1	248
42	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, 5363-5367.	7.1	243
43	Molecular Organization of a Recombinant Subviral Particle from Tick-Borne Encephalitis Virus. <i>Molecular Cell</i> , 2001, 7, 593-602.	9.7	240
44	Effect of non-contacted bases on the affinity of 434 operator for 434 repressor and Cro. <i>Nature</i> , 1987, 326, 886-888.	27.8	235
45	Atomic model of the papillomavirus capsid. <i>EMBO Journal</i> , 2002, 21, 4754-4762.	7.8	232
46	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.	7.1	227
47	Structure of the Reovirus Membrane-Penetration Protein, $\sigma 1$ , in a Complex with Its Protector Protein, $\sigma 3$ . <i>Cell</i> , 2002, 108, 283-295.	28.9	225
48	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.	7.1	225
49	Atomic Structure of Clathrin. <i>Cell</i> , 1998, 95, 563-573.	28.9	217
50	Structure of Rotavirus Outer-Layer Protein VP7 Bound with a Neutralizing Fab. <i>Science</i> , 2009, 324, 1444-1447.	12.6	216
51	Staged induction of HIV-1 glycan-dependent broadly neutralizing antibodies. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	212
52	Structure of a phage 434 Cro/DNA complex. <i>Nature</i> , 1988, 335, 789-795.	27.8	211
53	Structure of the L Protein of Vesicular Stomatitis Virus from Electron Cryomicroscopy. <i>Cell</i> , 2015, 162, 314-327.	28.9	211
54	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.	4.2	209

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55	Structural rearrangements in the membrane penetration protein of a non-enveloped virus. <i>Nature</i> , 2004, 430, 1053-1058.	27.8	200
56	Spatial constraints on the recognition of phosphoproteins by the tandem SH2 domains of the phosphatase SH-PTP2. <i>Nature</i> , 1996, 379, 277-280.	27.8	192
57	Variation on an Src-like Theme. <i>Cell</i> , 2003, 112, 737-740.	28.9	173
58	Crystal structures of murine polyomavirus in complex with straight-chain and branched-chain sialyloligosaccharide receptor fragments. <i>Structure</i> , 1996, 4, 183-194.	3.3	172
59	Peptideâ€“Surface Association: The Case of PDZ and PTB Domains. <i>Cell</i> , 1996, 86, 341-343.	28.9	170
60	Mechanism of Membrane Fusion by Viral Envelope Proteins. <i>Advances in Virus Research</i> , 2005, 64, 231-261.	2.1	162
61	Crystal structure of ATF-2/c-Jun and IRF-3 bound to the interferon-Î² enhancer. <i>EMBO Journal</i> , 2004, 23, 4384-4393.	7.8	156
62	Influenza-virus membrane fusion by cooperative fold-back of stochastically induced hemagglutinin intermediates. <i>ELife</i> , 2013, 2, e00333.	6.0	154
63	Viral Receptor-Binding Site Antibodies with Diverse Germline Origins. <i>Cell</i> , 2015, 161, 1026-1034.	28.9	151
64	Mechanism for Coordinated RNA Packaging and Genome Replication by Rotavirus Polymerase VP1. <i>Structure</i> , 2008, 16, 1678-1688.	3.3	148
65	Near-atomic resolution reconstructions of icosahedral viruses from electron cryo-microscopy. <i>Current Opinion in Structural Biology</i> , 2011, 21, 265-273.	5.7	148
66	A phage repressorâ€“operator complex at 7 Å... resolution. <i>Nature</i> , 1985, 316, 596-601.	27.8	143
67	Antibodies to a Conserved Influenza Head Interface Epitope Protect by an IgG Subtype-Dependent Mechanism. <i>Cell</i> , 2019, 177, 1124-1135.e16.	28.9	141
68	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
69	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.	7.1	135
70	Solution structure of the DNA-binding domain of C <sub>2</sub> -GAL4 from <i>S. cerevisiae</i> . <i>Nature</i> , 1992, 356, 450-453.	27.8	134
71	Subunit interactions in bovine papillomavirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6298-6303.	7.1	134
72	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, 13938-13943.	7.1	133

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73	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.	28.9	126
74	Structural basis for receptor recognition by New World hemorrhagic fever arenaviruses. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 438-444.	8.2	125
75	X-ray Crystal Structure of the Rotavirus Inner Capsid Particle at 3.8Å... Resolution. <i>Journal of Molecular Biology</i> , 2010, 397, 587-599.	4.2	124
76	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.	14.3	124
77	Structure of the MIND Complex Defines a Regulatory Focus for Yeast Kinetochose Assembly. <i>Cell</i> , 2016, 167, 1014-1027.e12.	28.9	121
78	Stu2p binds tubulin and undergoes an open-to-closed conformational change. <i>Journal of Cell Biology</i> , 2006, 172, 1009-1022.	5.2	119
79	The Monopolin Complex Crosslinks Kinetochose Components to Regulate Chromosome-Microtubule Attachments. <i>Cell</i> , 2010, 142, 556-567.	28.9	119
80	Crystal structure of ICAM-2 reveals a distinctive integrin recognition surface. <i>Nature</i> , 1997, 387, 312-315.	27.8	115
81	Structure of a Dengue Virus Envelope Protein Late-Stage Fusion Intermediate. <i>Journal of Virology</i> , 2013, 87, 2287-2293.	3.4	114
82	Peptide Inhibitors of Dengue-Virus Entry Target a Late-Stage Fusion Intermediate. <i>PLoS Pathogens</i> , 2010, 6, e1000851.	4.7	113
83	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.	7.1	113
84	Structures of the ATP-fueled ClpXP proteolytic machine bound to protein substrate. <i>ELife</i> , 2020, 9, .	6.0	105
85	Influenza immunization elicits antibodies specific for an egg-adapted vaccine strain. <i>Nature Medicine</i> , 2016, 22, 1465-1469.	30.7	104
86	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.	8.2	101
87	Structure of a nascent membrane protein as it folds on the BAM complex. <i>Nature</i> , 2020, 583, 473-478.	27.8	101
88	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.	7.1	98
89	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.	3.4	97
90	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.	7.1	95

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91	Memory B cell repertoire for recognition of evolving SARS-CoV-2 spike. <i>Cell</i> , 2021, 184, 4969-4980.e15.	28.9	94
92	Perspective: Discovery of antivirals against smallpox. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11178-11192.	7.1	93
93	The Kinetochores Receptor for the Cohesin Loading Complex. <i>Cell</i> , 2017, 171, 72-84.e13.	28.9	88
94	Structure of a Central Component of the Yeast Kinetochores: The Spc24p/Spc25p Globular Domain. <i>Structure</i> , 2006, 14, 1003-1009.	3.3	86
95	Peptide Inhibitors of Flavivirus Entry Derived from the E Protein Stem. <i>Journal of Virology</i> , 2010, 84, 12549-12554.	3.4	85
96	Autoinhibition of Bruton's tyrosine kinase (Btk) and activation by soluble inositol hexakisphosphate. <i>ELife</i> , 2015, 4, .	6.0	82
97	Features of Reovirus Outer Capsid Protein $\sigma 41$ Revealed by Electron Cryomicroscopy and Image Reconstruction of the Virion at 7.0 Å... Resolution. <i>Structure</i> , 2005, 13, 1545-1557.	3.3	80
98	Small-Molecule Inhibitors of Dengue-Virus Entry. <i>PLoS Pathogens</i> , 2012, 8, e1002627.	4.7	80
99	Initiation of HIV neutralizing B cell lineages with sequential envelope immunizations. <i>Nature Communications</i> , 2017, 8, 1732.	12.8	76
100	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.	7.1	73
101	Sequential conformational rearrangements in flavivirus membrane fusion. <i>ELife</i> , 2014, 3, e04389.	6.0	72
102	Structure of the DASH/Dam1 complex shows its role at the yeast kinetochores-microtubule interface. <i>Science</i> , 2018, 360, 552-558.	12.6	72
103	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.	7.1	72
104	The structure of the Ctf19c/CCAN from budding yeast. <i>ELife</i> , 2019, 8, .	6.0	71
105	Two Distinct Size Classes of Immature and Mature Subviral Particles from Tick-Borne Encephalitis Virus. <i>Journal of Virology</i> , 2003, 77, 11357-11366.	3.4	69
106	Location of the dsRNA-Dependent Polymerase, VP1, in Rotavirus Particles. <i>Journal of Molecular Biology</i> , 2013, 425, 124-132.	4.2	69
107	Structural evidence for Scc4-dependent localization of cohesin loading. <i>ELife</i> , 2015, 4, e06057.	6.0	69
108	Specificity and Affinity of Sialic Acid Binding by the Rhesus Rotavirus VP8* Core. <i>Journal of Virology</i> , 2002, 76, 10512-10517.	3.4	68

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109	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.	7.1	67
110	Immunogenic Stimulus for Germline Precursors of Antibodies that Engage the Influenza Hemagglutinin Receptor-Binding Site. <i>Cell Reports</i> , 2015, 13, 2842-2850.	6.4	67
111	Whither structural biology?. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 12-15.	8.2	64
112	Purified Recombinant Rotavirus VP7 Forms Soluble, Calcium-Dependent Trimers. <i>Virology</i> , 2000, 277, 420-428.	2.4	62
113	RWD domain: a recurring module in kinetochore architecture shown by a Ctf19-Mcm21 complex structure. <i>EMBO Reports</i> , 2012, 13, 216-222.	4.5	62
114	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.	7.1	58
115	Single Particle Reconstructions of the Transferrin-Transferrin Receptor Complex Obtained with Different Specimen Preparation Techniques. <i>Journal of Molecular Biology</i> , 2006, 355, 1048-1065.	4.2	57
116	An Iml3-Chl4 Heterodimer Links the Core Centromere to Factors Required for Accurate Chromosome Segregation. <i>Cell Reports</i> , 2013, 5, 29-36.	6.4	56
117	Protein Arms in the Kinetochore-Microtubule Interface of the Yeast DASH Complex. <i>Molecular Biology of the Cell</i> , 2007, 18, 2503-2510.	2.1	55
118	Requirements for the Formation of Membrane Pores by the Reovirus Myristoylated $\sigma$ 41N Peptide. <i>Journal of Virology</i> , 2009, 83, 7004-7014.	3.4	55
119	Structural Correlates of Rotavirus Cell Entry. <i>PLoS Pathogens</i> , 2014, 10, e1004355.	4.7	55
120	Recognition of Divergent Viral Substrates by the SARS-CoV-2 Main Protease. <i>ACS Infectious Diseases</i> , 2021, 7, 2591-2595.	3.8	55
121	Ndc10 is a platform for inner kinetochore assembly in budding yeast. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 48-55.	8.2	54
122	Distinct functional determinants of influenza hemagglutinin-mediated membrane fusion. <i>ELife</i> , 2015, 4, e11009.	6.0	53
123	Conserved Tetramer Junction in the Kinetochore Ndc80 Complex. <i>Cell Reports</i> , 2016, 17, 1915-1922.	6.4	51
124	Structure of the Vesicular Stomatitis Virus L Protein in Complex with Its Phosphoprotein Cofactor. <i>Cell Reports</i> , 2020, 30, 53-60.e5.	6.4	51
125	A Rotavirus Spike Protein Conformational Intermediate Binds Lipid Bilayers. <i>Journal of Virology</i> , 2010, 84, 1764-1770.	3.4	50
126	Kinetochore Function from the Bottom Up. <i>Trends in Cell Biology</i> , 2018, 28, 22-33.	7.9	50



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127	Autoreactivity profiles of influenza hemagglutinin broadly neutralizing antibodies. <i>Scientific Reports</i> , 2019, 9, 3492.	3.3	49
128	Recapitulation of HIV-1 Env-antibody coevolution in macaques leading to neutralization breadth. <i>Science</i> , 2021, 371, .	12.6	49
129	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.	4.2	47
130	Molecular Architecture of the Yeast Monopilin Complex. <i>Cell Reports</i> , 2012, 1, 583-589.	6.4	46
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.	6.4	45
132	In situ Structure of Rotavirus VP1 RNA-Dependent RNA Polymerase. <i>Journal of Molecular Biology</i> , 2019, 431, 3124-3138.	4.2	45
133	Molecular Basis for Antibody-Mediated Neutralization of New World Hemorrhagic Fever Mammarenaviruses. <i>Cell Host and Microbe</i> , 2015, 18, 705-713.	11.0	44
134	VP5* Rearranges when Rotavirus Uncoats. <i>Journal of Virology</i> , 2009, 83, 11372-11377.	3.4	43
135	Effect of Mutations in VP5* Hydrophobic Loops on Rotavirus Cell Entry. <i>Journal of Virology</i> , 2010, 84, 6200-6207.	3.4	40
136	The pH sensor for flavivirus membrane fusion. <i>Journal of Cell Biology</i> , 2008, 183, 177-179.	5.2	39
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.	4.7	38
138	Looking Inside Adenovirus. <i>Science</i> , 2010, 329, 1026-1027.	12.6	34
139	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.	2.6	34
140	Immunogenic cross-talk between dengue and Zika viruses. <i>Nature Immunology</i> , 2016, 17, 1010-1012.	14.5	34
141	Functional refolding of the penetration protein on a non-enveloped virus. <i>Nature</i> , 2021, 590, 666-670.	27.8	33
142	Self-tolerance curtails the B cell repertoire to microbial epitopes. <i>JCI Insight</i> , 2019, 4, .	5.0	32
143	Kinetics of Proton Transport into Influenza Virions by the Viral M2 Channel. <i>PLoS ONE</i> , 2012, 7, e31566.	2.5	31
144	HIV envelope V3 region mimics key features of a broadly neutralizing antibody lineage epitope. <i>Nature Communications</i> , 2018, 9, 1111.	12.8	30

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145	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.	11.9	28
146	Visualization of Calcium Ion Loss from Rotavirus during Cell Entry. <i>Journal of Virology</i> , 2018, 92, .	3.4	27
147	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
148	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.	7.1	25
149	Cross-Linking of Rotavirus Outer Capsid Protein VP7 by Antibodies or Disulfides Inhibits Viral Entry. <i>Journal of Virology</i> , 2011, 85, 10509-10517.	3.4	24
150	Single-Particle Detection of Transcription following Rotavirus Entry. <i>Journal of Virology</i> , 2017, 91, .	3.4	23
151	CryoEM Structure of an Influenza Virus Receptor-Binding Site Antibody-Antigen Interface. <i>Journal of Molecular Biology</i> , 2017, 429, 1829-1839.	4.2	21
152	Recall of B cell memory depends on relative locations of prime and boost immunization. <i>Science Immunology</i> , 2022, 7, eabn5311.	11.9	20
153	Conformational States of a Soluble, Uncleaved HIV-1 Envelope Trimer. <i>Journal of Virology</i> , 2017, 91, .	3.4	19
154	The Structural Basis for Kinetochores Stabilization by Cnn1/CENP-T. <i>Current Biology</i> , 2020, 30, 3425-3431.e3.	3.9	19
155	Cryoelectron Microscopy Structure of a Yeast Centromeric Nucleosome at 2.7 Å Resolution. <i>Structure</i> , 2020, 28, 363-370.e3.	3.3	19
156	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.	7.1	18
157	Conservation in vesicle coats. <i>Nature</i> , 2010, 466, 1048-1049.	27.8	17
158	A Prevalent Focused Human Antibody Response to the Influenza Virus Hemagglutinin Head Interface. <i>MBio</i> , 2021, 12, e0114421.	4.1	17
159	How small-molecule inhibitors of dengue-virus infection interfere with viral membrane fusion. <i>ELife</i> , 2018, 7, .	6.0	16
160	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, .	7.1	15
161	The structure of the yeast Ctf3 complex. <i>ELife</i> , 2019, 8, .	6.0	15
162	Antibodies That Engage the Hemagglutinin Receptor-Binding Site of Influenza B Viruses. <i>ACS Infectious Diseases</i> , 2021, 7, 1-5.	3.8	11

#	ARTICLE	IF	CITATIONS
163	Structural basis of Stu2 recruitment to yeast kinetochores. <i>ELife</i> , 2021, 10, .	6.0	11
164	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.	1.1	10
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