

# David Ian Stuart

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4036243/publications.pdf>

Version: 2024-02-01

392  
papers

39,276  
citations

1992

101  
h-index

4014

176  
g-index

419  
all docs

419  
docs citations

419  
times ranked

40696  
citing authors

#	ARTICLE	IF	CITATIONS
1	Broad and strong memory CD4+ and CD8+ T cells induced by SARS-CoV-2 in UK convalescent individuals following COVID-19. <i>Nature Immunology</i> , 2020, 21, 1336-1345.	14.5	1,066
2	Evidence of escape of SARS-CoV-2 variant B.1.351 from natural and vaccine-induced sera. <i>Cell</i> , 2021, 184, 2348-2361.e6.	28.9	936
3	The three-dimensional structure of foot-and-mouth disease virus at 2.9 Å... resolution. <i>Nature</i> , 1989, 337, 709-716.	27.8	887
4	Antibody Status and Incidence of SARS-CoV-2 Infection in Health Care Workers. <i>New England Journal of Medicine</i> , 2021, 384, 533-540.	27.0	803
5	SARS-CoV-2 Omicron-B.1.1.529 leads to widespread escape from neutralizing antibody responses. <i>Cell</i> , 2022, 185, 467-484.e15.	28.9	788
6	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	19.0	763
7	Structural basis for the recognition of hydroxyproline in HIF-1 $\alpha$ by pVHL. <i>Nature</i> , 2002, 417, 975-978.	27.8	651
8	Reduced neutralization of SARS-CoV-2 B.1.617 by vaccine and convalescent serum. <i>Cell</i> , 2021, 184, 4220-4236.e13.	28.9	630
9	The Interaction Properties of Costimulatory Molecules Revisited. <i>Immunity</i> , 2002, 17, 201-210.	14.3	587
10	The atomic structure of the bluetongue virus core. <i>Nature</i> , 1998, 395, 470-478.	27.8	543
11	Antibody escape of SARS-CoV-2 Omicron BA.4 and BA.5 from vaccine and BA.1 serum. <i>Cell</i> , 2022, 185, 2422-2433.e13.	28.9	532
12	Antibody evasion by the P.1 strain of SARS-CoV-2. <i>Cell</i> , 2021, 184, 2939-2954.e9.	28.9	519
13	High resolution structures of HIV-1 RT from four RT $\alpha$ inhibitor complexes. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 293-302.	8.2	514
14	A functional and structural basis for TCR cross-reactivity in multiple sclerosis. <i>Nature Immunology</i> , 2002, 3, 940-943.	14.5	500
15	A versatile ligation-independent cloning method suitable for high-throughput expression screening applications. <i>Nucleic Acids Research</i> , 2007, 35, e45-e45.	14.5	499
16	Lysine Methylation as a Routine Rescue Strategy for Protein Crystallization. <i>Structure</i> , 2006, 14, 1617-1622.	3.3	483
17	Crystal structure of cat muscle pyruvate kinase at a resolution of 2.6 Å... <i>Journal of Molecular Biology</i> , 1979, 134, 109-142.	4.2	459
18	A mechanism for initiating RNA-dependent RNA polymerization. <i>Nature</i> , 2001, 410, 235-240.	27.8	458

#	ARTICLE	IF	CITATIONS
19	Reduced neutralization of SARS-CoV-2 B.1.1.7 variant by convalescent and vaccine sera. <i>Cell</i> , 2021, 184, 2201-2211.e7.	28.9	442
20	Neutralizing nanobodies bind SARS-CoV-2 spike RBD and block interaction with ACE2. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 846-854.	8.2	434
21	Crystal structure of the complex between human CD8 $\alpha$ and HLA-A2. <i>Nature</i> , 1997, 387, 630-634.	27.8	428
22	Mechanism of inhibition of HIV-1 reverse transcriptase by non-nucleoside inhibitors. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 303-308.	8.2	415
23	Fitness Cost of Escape Mutations in p24 Gag in Association with Control of Human Immunodeficiency Virus Type 1. <i>Journal of Virology</i> , 2006, 80, 3617-3623.	3.4	408
24	Structure of a major immunogenic site on foot-and-mouth disease virus. <i>Nature</i> , 1993, 362, 566-568.	27.8	360
25	Complexes of HIV-1 Reverse Transcriptase with Inhibitors of the HEPT Series Reveal Conformational Changes Relevant to the Design of Potent Non-Nucleoside Inhibitors. <i>Journal of Medicinal Chemistry</i> , 1996, 39, 1589-1600.	6.4	353
26	What does structure tell us about virus evolution?. <i>Current Opinion in Structural Biology</i> , 2005, 15, 655-663.	5.7	348
27	A sensor-adaptor mechanism for enterovirus uncoating from structures of EV71. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 424-429.	8.2	347
28	Performance characteristics of five immunoassays for SARS-CoV-2: a head-to-head benchmark comparison. <i>Lancet Infectious Diseases</i> , The, 2020, 20, 1390-1400.	9.1	336
29	The antigenic anatomy of SARS-CoV-2 receptor binding domain. <i>Cell</i> , 2021, 184, 2183-2200.e22.	28.9	331
30	Crystal structure at 2.8 Å... resolution of a soluble form of the cell adhesion molecule CD2. <i>Nature</i> , 1992, 360, 232-239.	27.8	330
31	Neutralization of SARS-CoV-2 by Destruction of the Prefusion Spike. <i>Cell Host and Microbe</i> , 2020, 28, 445-454.e6.	11.0	298
32	A structural basis for immunodominant human T cell receptor recognition. <i>Nature Immunology</i> , 2003, 4, 657-663.	14.5	290
33	Structure and functionality in flavivirus NS-proteins: Perspectives for drug design. <i>Antiviral Research</i> , 2010, 87, 125-148.	4.1	289
34	The Crystal Structure of Plasma Gelsolin: Implications for Actin Severing, Capping, and Nucleation. <i>Cell</i> , 1997, 90, 661-670.	28.9	273
35	Glycoprotein Structural Genomics: Solving the Glycosylation Problem. <i>Structure</i> , 2007, 15, 267-273.	3.3	273
36	Structural basis for the neutralization of SARS-CoV-2 by an antibody from a convalescent patient. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 950-958.	8.2	268

#	ARTICLE	IF	CITATIONS
37	A mechanical explanation of RNA pseudoknot function in programmed ribosomal frameshifting. <i>Nature</i> , 2006, 441, 244-247.	27.8	267
38	Antibody responses to SARS-CoV-2 vaccines in 45,965 adults from the general population of the United Kingdom. <i>Nature Microbiology</i> , 2021, 6, 1140-1149.	13.3	254
39	Structural Basis for the Resilience of Efavirenz (DMP-266) to Drug Resistance Mutations in HIV-1 Reverse Transcriptase. <i>Structure</i> , 2000, 8, 1089-1094.	3.3	253
40	Structure Unifies the Viral Universe. <i>Annual Review of Biochemistry</i> , 2012, 81, 795-822.	11.1	252
41	Insights into assembly from structural analysis of bacteriophage PRD1. <i>Nature</i> , 2004, 432, 68-74.	27.8	246
42	Structure of the TRAIL-DR5 complex reveals mechanisms conferring specificity in apoptotic initiation. <i>Nature Structural Biology</i> , 1999, 6, 1048-1053.	9.7	235
43	The Duration, Dynamics, and Determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Antibody Responses in Individual Healthcare Workers. <i>Clinical Infectious Diseases</i> , 2021, 73, e699-e709.	5.8	235
44	A procedure for setting up high-throughput nanolitre crystallization experiments. Crystallization workflow for initial screening, automated storage, imaging and optimization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 651-657.	2.5	234
45	Towards rationalization of crystallization screening for small- to medium-sized academic laboratories: the PACT/JCSG+ strategy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1426-1431.	2.5	228
46	Structure and Dimerization of a Soluble Form of B7-1. <i>Immunity</i> , 2000, 12, 51-60.	14.3	227
47	Crystal structure of human $\alpha$ -lactalbumin at 1.7 Å resolution. <i>Journal of Molecular Biology</i> , 1991, 221, 571-581.	4.2	225
48	The nsp9 Replicase Protein of SARS-Coronavirus, Structure and Functional Insights. <i>Structure</i> , 2004, 12, 341-353.	3.3	225
49	Localized reconstruction of subunits from electron cryomicroscopy images of macromolecular complexes. <i>Nature Communications</i> , 2015, 6, 8843.	12.8	225
50	Structural and serological evidence for a novel mechanism of antigenic variation in foot-and-mouth disease virus. <i>Nature</i> , 1990, 347, 569-572.	27.8	216
51	Toremifene interacts with and destabilizes the Ebola virus glycoprotein. <i>Nature</i> , 2016, 535, 169-172.	27.8	210
52	Crystal structure of SIV matrix antigen and implications for virus assembly. <i>Nature</i> , 1995, 378, 743-747.	27.8	202
53	The structure of HIV-1 reverse transcriptase complexed with 9-chloro-TIBO: lessons for inhibitor design. <i>Structure</i> , 1995, 3, 915-926.	3.3	201
54	Structural basis of Nipah and Hendra virus attachment to their cell-surface receptor ephrin-B2. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 567-572.	8.2	200

#	ARTICLE	IF	CITATIONS
55	A COVID-19 vaccine candidate using SpyCatcher multimerization of the SARS-CoV-2 spike protein receptor-binding domain induces potent neutralising antibody responses. <i>Nature Communications</i> , 2021, 12, 542.	12.8	200
56	The postfusion structure of baculovirus gp64 supports a unified view of viral fusion machines. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1024-1030.	8.2	197
57	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020, 9, .	6.0	196
58	Structural Features Impose Tight Peptide Binding Specificity in the Nonclassical MHC Molecule HLA-E. <i>Molecular Cell</i> , 1998, 1, 531-541.	9.7	190
59	Structural basis of superantigen action inferred from crystal structure of toxic-shock syndrome toxin-1. <i>Nature</i> , 1994, 367, 94-97.	27.8	187
60	The Highly Ordered Double-Stranded RNA Genome of Bluetongue Virus Revealed by Crystallography. <i>Cell</i> , 1999, 97, 481-490.	28.9	181
61	Antibody testing for COVID-19: A report from the National COVID Scientific Advisory Panel. <i>Wellcome Open Research</i> , 2020, 5, 139.	1.8	179
62	Paired Receptor Specificity Explained by Structures of Signal Regulatory Proteins Alone and Complexed with CD47. <i>Molecular Cell</i> , 2008, 31, 266-277.	9.7	171
63	An Altered Position of the $\alpha 2$ Helix of MHC Class I Is Revealed by the Crystal Structure of HLA-B*3501. <i>Immunity</i> , 1996, 4, 203-213.	14.3	169
64	The crystal structure of bluetongue virus VP7. <i>Nature</i> , 1995, 373, 167-170.	27.8	168
65	Hepatitis A virus and the origins of picornaviruses. <i>Nature</i> , 2015, 517, 85-88.	27.8	158
66	The crystal structure of the catalytic domain of human urokinase-type plasminogen activator. <i>Structure</i> , 1995, 3, 681-691.	3.3	155
67	Bound Water Structure and Polymorphic Amino Acids Act Together to Allow the Binding of Different Peptides to MHC Class I HLA-B53. <i>Immunity</i> , 1996, 4, 215-228.	14.3	155
68	Crystal structure of a soluble CD28-Fab complex. <i>Nature Immunology</i> , 2005, 6, 271-279.	14.5	153
69	Functional and structural studies of the vaccinia virus virulence factor N1 reveal a Bcl-2-like anti-apoptotic protein. <i>Journal of General Virology</i> , 2007, 88, 1656-1666.	2.9	153
70	Crystal structure of the extracellular region of the human cell adhesion molecule CD2 at 2.5Å resolution. <i>Structure</i> , 1994, 2, 755-766.	3.3	152
71	Atomic Snapshots of an RNA Packaging Motor Reveal Conformational Changes Linking ATP Hydrolysis to RNA Translocation. <i>Cell</i> , 2004, 118, 743-755.	28.9	151
72	Picornavirus uncoating intermediate captured in atomic detail. <i>Nature Communications</i> , 2013, 4, 1929.	12.8	148

#	ARTICLE	IF	CITATIONS
73	Evolution of Viral Structure. <i>Theoretical Population Biology</i> , 2002, 61, 461-470.	1.1	147
74	Antibody responses and correlates of protection in the general population after two doses of the ChAdOx1 or BNT162b2 vaccines. <i>Nature Medicine</i> , 2022, 28, 1072-1082.	30.7	147
75	Crystal structure of the RNA-dependent RNA polymerase from influenza C virus. <i>Nature</i> , 2015, 527, 114-117.	27.8	145
76	The ligand-binding face of the semaphorins revealed by the high-resolution crystal structure of SEMA4D. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 843-848.	8.2	143
77	Antagonist HIV-1 Gag Peptides Induce Structural Changes in HLA B8. <i>Journal of Experimental Medicine</i> , 1996, 184, 2279-2286.	8.5	136
78	Vaccinia Virus Proteins A52 and B14 Share a Bcl-2-like Fold but Have Evolved to Inhibit NF- $\kappa$ B rather than Apoptosis. <i>PLoS Pathogens</i> , 2008, 4, e1000128.	4.7	136
79	Membrane structure and interactions with protein and DNA in bacteriophage PRD1. <i>Nature</i> , 2004, 432, 122-125.	27.8	133
80	Lentiviral transduction of mammalian cells for fast, scalable and high-level production of soluble and membrane proteins. <i>Nature Protocols</i> , 2018, 13, 2991-3017.	12.0	131
81	Design of MKC-442 (Emivirine) Analogues with Improved Activity Against Drug-Resistant HIV Mutants. <i>Journal of Medicinal Chemistry</i> , 1999, 42, 4500-4505.	6.4	130
82	The structure of a cypovirus and the functional organization of dsRNA viruses. <i>Nature Structural Biology</i> , 1999, 6, 565-568.	9.7	129
83	The Human Low Affinity Fc $\gamma$ 3 Receptors IIa, IIb, and III Bind IgG with Fast Kinetics and Distinct Thermodynamic Properties. <i>Journal of Biological Chemistry</i> , 2001, 276, 44898-44904.	3.4	127
84	Classical and Nonclassical Class I Major Histocompatibility Complex Molecules Exhibit Subtle Conformational Differences That Affect Binding to CD8 $\alpha$ 1 $\beta$ . <i>Journal of Biological Chemistry</i> , 2000, 275, 15232-15238.	3.4	126
85	Rational Engineering of Recombinant Picornavirus Capsids to Produce Safe, Protective Vaccine Antigen. <i>PLoS Pathogens</i> , 2013, 9, e1003255.	4.7	126
86	Signaling Lymphocytic Activation Molecule (CDw150) Is Homophilic but Self-associates with Very Low Affinity. <i>Journal of Biological Chemistry</i> , 2000, 275, 28100-28109.	3.4	125
87	Implications of the HIV-1 Rev dimer structure at 3.2 $\text{Å}$ resolution for multimeric binding to the Rev response element. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5810-5814.	7.1	124
88	Structure of a Pestivirus Envelope Glycoprotein E2 Clarifies Its Role in Cell Entry. <i>Cell Reports</i> , 2013, 3, 30-35.	6.4	124
89	Near-atomic structure of Japanese encephalitis virus reveals critical determinants of virulence and stability. <i>Nature Communications</i> , 2017, 8, 14.	12.8	117
90	Insights into Virus Evolution and Membrane Biogenesis from the Structure of the Marine Lipid-Containing Bacteriophage PM2. <i>Molecular Cell</i> , 2008, 31, 749-761.	9.7	116

#	ARTICLE	IF	CITATIONS
91	Crystal Structure of a Novel Conformational State of the Flavivirus NS3 Protein: Implications for Polyprotein Processing and Viral Replication. <i>Journal of Virology</i> , 2009, 83, 12895-12906.	3.4	115
92	Lessons from Structural Genomics. <i>Annual Review of Biophysics</i> , 2009, 38, 371-383.	10.0	115
93	An atomic model of the outer layer of the bluetongue virus core derived from X-ray crystallography and electron cryomicroscopy. <i>Structure</i> , 1997, 5, 885-893.	3.3	114
94	Structure of the Integrin Binding Fragment from Fibrillin-1 Gives New Insights into Microfibril Organization. <i>Structure</i> , 2004, 12, 717-729.	3.3	114
95	Structure of the Brain-Derived Neurotrophic Factor/Neurotrophin 3 Heterodimer. <i>Biochemistry</i> , 1995, 34, 4139-4146.	2.5	113
96	<i>In situ</i> macromolecular crystallography using microbeams. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 592-600.	2.5	113
97	Binding of the Second Generation Non-nucleoside Inhibitor S-1153 to HIV-1 Reverse Transcriptase Involves Extensive Main Chain Hydrogen Bonding. <i>Journal of Biological Chemistry</i> , 2000, 275, 14316-14320.	3.4	111
98	Killer Cell Immunoglobulin Receptors and T Cell Receptors Bind Peptide-Major Histocompatibility Complex Class I with Distinct Thermodynamic and Kinetic Properties. <i>Journal of Biological Chemistry</i> , 1999, 274, 28329-28334.	3.4	110
99	Crystal Structure and Carbohydrate Analysis of Nipah Virus Attachment Glycoprotein: a Template for Antiviral and Vaccine Design. <i>Journal of Virology</i> , 2008, 82, 11628-11636.	3.4	109
100	Evolution of Complex RNA Polymerases: The Complete Archaeal RNA Polymerase Structure. <i>PLoS Biology</i> , 2009, 7, e1000102.	5.6	109
101	Phenylethylthiazolylthiourea (PETT) Non-nucleoside Inhibitors of HIV-1 and HIV-2 Reverse Transcriptases. <i>Journal of Biological Chemistry</i> , 2000, 275, 5633-5639.	3.4	107
102	High-speed fixed-target serial virus crystallography. <i>Nature Methods</i> , 2017, 14, 805-810.	19.0	106
103	Evidence for the role of His-142 of protein 1C in the acid-induced disassembly of foot-and-mouth disease virus capsids. <i>Journal of General Virology</i> , 1999, 80, 1911-1918.	2.9	106
104	Tandem Fusion of Hepatitis B Core Antigen Allows Assembly of Virus-Like Particles in Bacteria and Plants with Enhanced Capacity to Accommodate Foreign Proteins. <i>PLoS ONE</i> , 2015, 10, e0120751.	2.5	105
105	Potent cross-reactive antibodies following Omicron breakthrough in vaccinees. <i>Cell</i> , 2022, 185, 2116-2131.e18.	28.9	105
106	Three-Dimensional Structures of Translating Ribosomes by Cryo-EM. <i>Molecular Cell</i> , 2004, 14, 57-66.	9.7	104
107	Specificity of the VP1 GH Loop of Foot-and-Mouth Disease Virus for $\beta$ Integrins. <i>Journal of Virology</i> , 2006, 80, 9798-9810.	3.4	104
108	Structural and Functional Insights of RANKL-RANK Interaction and Signaling. <i>Journal of Immunology</i> , 2010, 184, 6910-6919.	0.8	103

#	ARTICLE	IF	CITATIONS
109	Perturbations in the surface structure of A22 Iraq foot-and-mouth disease virus accompanying coupled changes in host cell specificity and antigenicity. <i>Structure</i> , 1996, 4, 135-145.	3.3	100
110	Quantitative SARS-CoV-2 anti-spike responses to Pfizerâ€™BioNTech and Oxfordâ€™AstraZeneca vaccines by previous infection status. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1516.e7-1516.e14.	6.0	100
111	Crystal Structures of HIV-1 Reverse Transcriptase in Complex with Carboxanilide Derivativesâ€™. <i>Biochemistry</i> , 1998, 37, 14394-14403.	2.5	97
112	Structure of Foot-and-mouth disease virus serotype A1061 alone and complexed with oligosaccharide receptor: receptor conservation in the face of antigenic variation. <i>Journal of General Virology</i> , 2005, 86, 1909-1920.	2.9	95
113	A plate-based high-throughput assay for virus stability and vaccine formulation. <i>Journal of Virological Methods</i> , 2012, 185, 166-170.	2.1	94
114	The Crystal Structure of ORF-9b, a Lipid Binding Protein from the SARS Coronavirus. <i>Structure</i> , 2006, 14, 1157-1165.	3.3	91
115	Plant-made polio type 3 stabilized VLPsâ€™a candidate synthetic polio vaccine. <i>Nature Communications</i> , 2017, 8, 245.	12.8	91
116	Hepatitis B small surface antigen particles are octahedral. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14783-14788.	7.1	90
117	How baculovirus polyhedra fit square pegs into round holes to robustly package viruses. <i>EMBO Journal</i> , 2010, 29, 505-514.	7.8	90
118	Dimeric Architecture of the Hendra Virus Attachment Glycoprotein: Evidence for a Conserved Mode of Assembly. <i>Journal of Virology</i> , 2010, 84, 6208-6217.	3.4	90
119	The crystal structure of coxsackievirus A9: new insights into the uncoating mechanisms of enteroviruses. <i>Structure</i> , 1999, 7, 1527-1538.	3.3	89
120	Structure-based energetics of protein interfaces guides foot-and-mouth disease virus vaccine design. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 788-794.	8.2	89
121	More-powerful virus inhibitors from structure-based analysis of HEV71 capsid-binding molecules. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 282-288.	8.2	88
122	Anti-spike antibody response to natural SARS-CoV-2 infection in the general population. <i>Nature Communications</i> , 2021, 12, 6250.	12.8	88
123	Design of Non-Nucleoside Inhibitors of HIV-1 Reverse Transcriptase with Improved Drug Resistance Properties. 1.. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 5912-5922.	6.4	87
124	Structural Plasticity of Eph Receptor A4 Facilitates Cross-Class Ephrin Signaling. <i>Structure</i> , 2009, 17, 1386-1397.	3.3	86
125	Structure and binding kinetics of three different human CD1dâ€™Î±-galactosylceramideâ€™specific T cell receptors. <i>Journal of Experimental Medicine</i> , 2006, 203, 699-710.	8.5	85
126	The N-glycosidase mechanism of ribosome-inactivating proteins implied by crystal structures of Î±-momorcharin. <i>Structure</i> , 1994, 2, 7-16.	3.3	84



#	ARTICLE	IF	CITATIONS
127	Crystal structure of the human p58 killer cell inhibitory receptor (KIR2DL3) specific for HLA-Cw3-related MHC class I. <i>Structure</i> , 1999, 7, 391-398.	3.3	84
128	Î±VÎ²6 Is a Novel Receptor for Human Fibrillin-1. <i>Journal of Biological Chemistry</i> , 2007, 282, 6743-6751.	3.4	83
129	Outrunning free radicals in room-temperature macromolecular crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 810-818.	2.5	83
130	Bluetongue virus VP4 is an RNA-capping assembly line. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 449-451.	8.2	82
131	Structure of pyruvate kinase and similarities with other enzymes: possible implications for protein taxonomy and evolution. <i>Nature</i> , 1978, 271, 626-630.	27.8	81
132	The Structure of an RNAi Polymerase Links RNA Silencing and Transcription. <i>PLoS Biology</i> , 2006, 4, e434.	5.6	80
133	The structures of the neurotrophin 4 homodimer and the brain-derived neurotrophic factor/neurotrophin 4 heterodimer reveal a common Trk binding site. <i>Protein Science</i> , 1999, 8, 2589-2597.	7.6	78
134	Insights into the Evolution of a Complex Virus from the Crystal Structure of Vaccinia Virus D13. <i>Structure</i> , 2011, 19, 1011-1020.	3.3	78
135	Lysosome sorting of Î²-glucocerebrosidase by LIMP-2 is targeted by the mannose 6-phosphate receptor. <i>Nature Communications</i> , 2014, 5, 4321.	12.8	78
136	Incorporation of tetanus-epitope into virus-like particles achieves vaccine responses even in older recipients in models of psoriasis, Alzheimer's and cat allergy. <i>Npj Vaccines</i> , 2017, 2, 30.	6.0	78
137	Structural comparison of two strains of foot-and-mouth disease virus subtype O1 and a laboratory antigenic variant, G67. <i>Structure</i> , 1995, 3, 571-580.	3.3	77
138	Implications for viral uncoating from the structure of bovine enterovirus. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 224-231.	8.2	77
139	Crystal Structures of Penicillin-Binding Protein 3 from <i>Pseudomonas aeruginosa</i> : Comparison of Native and Antibiotic-Bound Forms. <i>Journal of Molecular Biology</i> , 2011, 405, 173-184.	4.2	77
140	2-Amino-6-arylsulfonylbenzimidazoles as Non-nucleoside Reverse Transcriptase Inhibitors of HIV-1. <i>Journal of Medicinal Chemistry</i> , 2001, 44, 1866-1882.	6.4	75
141	High-resolution structure of the catalytic region of MICAL (molecule interacting with CasL), a multidomain flavoenzyme-signaling molecule. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16836-16841.	7.1	75
142	Rules of engagement between Î±VÎ²6 integrin and foot-and-mouth disease virus. <i>Nature Communications</i> , 2017, 8, 15408.	12.8	75
143	Inhibition of Apoptosis and NF-Î±B Activation by Vaccinia Protein N1 Occur via Distinct Binding Surfaces and Make Different Contributions to Virulence. <i>PLoS Pathogens</i> , 2011, 7, e1002430.	4.7	73
144	Unexpected mode of engagement between enterovirus 71 and its receptor SCARB2. <i>Nature Microbiology</i> , 2019, 4, 414-419.	13.3	73

#	ARTICLE	IF	CITATIONS
145	3D Correlative Cryo-Structured Illumination Fluorescence and Soft X-ray Microscopy Elucidates Reovirus Intracellular Release Pathway. <i>Cell</i> , 2020, 182, 515-530.e17.	28.9	73
146	Unexpected structure for the N-terminal domain of hepatitis C virus envelope glycoprotein E1. <i>Nature Communications</i> , 2014, 5, 4874.	12.8	72
147	Exploiting fast detectors to enter a new dimension in room-temperature crystallography. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1248-1256.	2.5	72
148	Low-dose phase retrieval of biological specimens using cryo-electron ptychography. <i>Nature Communications</i> , 2020, 11, 2773.	12.8	72
149	3-azido-2-deoxythymidine drug resistance mutations in HIV-1 reverse transcriptase can induce long range conformational changes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 9518-9523.	7.1	71
150	Rhabdovirus Matrix Protein Structures Reveal a Novel Mode of Self-Association. <i>PLoS Pathogens</i> , 2008, 4, e1000251.	4.7	71
151	Unusual Molecular Architecture of the Machupo Virus Attachment Glycoprotein. <i>Journal of Virology</i> , 2009, 83, 8259-8265.	3.4	71
152	Fixed target combined with spectral mapping: approaching 100% hit rates for serial crystallography. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 944-955.	2.3	71
153	Machining protein microcrystals for structure determination by electron diffraction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9569-9573.	7.1	69
154	A Similar Pattern of Interaction for Different Antibodies with a Major Antigenic Site of Foot-and-Mouth Disease Virus: Implications for Intratypic Antigenic Variation. <i>Journal of Virology</i> , 1998, 72, 739-748.	3.4	69
155	Determination of the Affinity and Kinetic Constants for the Interaction between the Human Virus Echovirus 11 and Its Cellular Receptor, CD55. <i>Journal of Biological Chemistry</i> , 1998, 273, 30443-30447.	3.4	68
156	Nonstandard Peptide Binding Revealed by Crystal Structures of HLA-B*5101 Complexed with HIV Immunodominant Epitopes. <i>Journal of Immunology</i> , 2000, 165, 3260-3267.	0.8	68
157	Carbohydrate and Domain Architecture of an Immature Antibody Glycoform Exhibiting Enhanced Effector Functions. <i>Journal of Molecular Biology</i> , 2009, 387, 1061-1066.	4.2	67
158	The Structure of the Macrophage Signal Regulatory Protein $\beta$ (SIRP $\beta$ ) Inhibitory Receptor Reveals a Binding Face Reminiscent of That Used by T Cell Receptors. <i>Journal of Biological Chemistry</i> , 2007, 282, 14567-14575.	3.4	66
159	Structure and Function of A41, a Vaccinia Virus Chemokine Binding Protein. <i>PLoS Pathogens</i> , 2008, 4, e5.	4.7	66
160	How vaccinia virus has evolved to subvert the host immune response. <i>Journal of Structural Biology</i> , 2011, 175, 127-134.	2.8	66
161	Target Identification and Mode of Action of Four Chemically Divergent Drugs against Ebolavirus Infection. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 724-733.	6.4	66
162	Chemical and Structural Analysis of an Antibody Folding Intermediate Trapped during Glycan Biosynthesis. <i>Journal of the American Chemical Society</i> , 2012, 134, 17554-17563.	13.7	65

#	ARTICLE	IF	CITATIONS
163	The structure of CrgA from <i>Neisseria meningitidis</i> reveals a new octameric assembly state for LysR transcriptional regulators. <i>Nucleic Acids Research</i> , 2009, 37, 4545-4558.	14.5	64
164	Equine Rhinitis A Virus and Its Low pH Empty Particle: Clues Towards an Aphthovirus Entry Mechanism?. <i>PLoS Pathogens</i> , 2009, 5, e1000620.	4.7	64
165	An Observational Cohort Study on the Incidence of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection and B.1.1.7 Variant Infection in Healthcare Workers by Antibody and Vaccination Status. <i>Clinical Infectious Diseases</i> , 2022, 74, 1208-1219.	5.8	64
166	Design of Non-nucleoside Inhibitors of HIV-1 Reverse Transcriptase with Improved Drug Resistance Properties. 2.. <i>Journal of Medicinal Chemistry</i> , 2004, 47, 5923-5936.	6.4	61
167	Antigenic Switching of Hepatitis B Virus by Alternative Dimerization of the Capsid Protein. <i>Structure</i> , 2013, 21, 133-142.	3.3	61
168	A revised partiality model and post-refinement algorithm for X-ray free-electron laser data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 1400-1410.	2.5	60
169	Ligand Binding by the Immunoglobulin Superfamily Recognition Molecule CD2 Is Glycosylation-independent. <i>Journal of Biological Chemistry</i> , 1995, 270, 369-375.	3.4	59
170	Multiple liquid crystalline geometries of highly compacted nucleic acid in a dsRNA virus. <i>Nature</i> , 2019, 570, 252-256.	27.8	59
171	Structures of Coxsackievirus A16 Capsids with Native Antigenicity: Implications for Particle Expansion, Receptor Binding, and Immunogenicity. <i>Journal of Virology</i> , 2015, 89, 10500-10511.	3.4	58
172	A Tick Protein with a Modified Kunitz Fold Inhibits Human Trypsin. <i>Journal of Molecular Biology</i> , 2007, 368, 1172-1186.	4.2	57
173	CryoSIM: super-resolution 3D structured illumination cryogenic fluorescence microscopy for correlated ultrastructural imaging. <i>Optica</i> , 2020, 7, 802.	9.3	57
174	New methods for indexing multi-lattice diffraction data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2652-2666.	2.5	56
175	Structure of CPV17 polyhedrin determined by the improved analysis of serial femtosecond crystallographic data. <i>Nature Communications</i> , 2015, 6, 6435.	12.8	56
176	Using Structural Information to Change the Phosphotransfer Specificity of a Two-Component Chemotaxis Signalling Complex. <i>PLoS Biology</i> , 2010, 8, e1000306.	5.6	55
177	Automation of large scale transient protein expression in mammalian cells. <i>Journal of Structural Biology</i> , 2011, 175, 209-215.	2.8	55
178	Expression of soluble recombinant glycoproteins with predefined glycosylation: application to the crystallization of the T-cell glycoprotein CD2. <i>Protein Engineering, Design and Selection</i> , 1993, 6, 229-232.	2.1	54
179	Site-Specific Steric Control of SARS-CoV-2 Spike Glycosylation. <i>Biochemistry</i> , 2021, 60, 2153-2169.	2.5	54
180	Where is crystallography going?. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 152-166.	2.3	54

#	ARTICLE	IF	CITATIONS
181	Flexibility of the Major Antigenic Loop of Foot-and-Mouth Disease Virus Bound to a Fab Fragment of a Neutralising Antibody: Structure and Neutralisation. <i>Virology</i> , 1999, 255, 260-268.	2.4	53
182	Atomic Resolution Structure of Moloney Murine Leukemia Virus Matrix Protein and Its Relationship to Other Retroviral Matrix Proteins. <i>Structure</i> , 2002, 10, 1627-1636.	3.3	53
183	Crystal structure of the Murray Valley encephalitis virus NS5 methyltransferase domain in complex with cap analogues. <i>Journal of General Virology</i> , 2007, 88, 2228-2236.	2.9	52
184	The antibody response to SARS-CoV-2 Beta underscores the antigenic distance to other variants. <i>Cell Host and Microbe</i> , 2022, 30, 53-68.e12.	11.0	52
185	Efficient production of foot-and-mouth disease virus empty capsids in insect cells following down regulation of 3C protease activity. <i>Journal of Virological Methods</i> , 2013, 187, 406-412.	2.1	51
186	Building meaningful models of glycoproteins. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 354-354.	8.2	48
187	Structural explanation for the role of Mn <sup>2+</sup> in the activity of $\phi$ 6 RNA-dependent RNA polymerase. <i>Nucleic Acids Research</i> , 2008, 36, 6633-6644.	14.5	48
188	Mapping the I $\kappa$ B Kinase $\hat{\gamma}$ 2 (IKK $\hat{\gamma}$ 2)-binding Interface of the B14 Protein, a Vaccinia Virus Inhibitor of IKK $\hat{\gamma}$ 2-mediated Activation of Nuclear Factor $\hat{\gamma}$ B. <i>Journal of Biological Chemistry</i> , 2011, 286, 20727-20735.	3.4	48
189	Determination of the Structure of a Decay Accelerating Factor-Binding Clinical Isolate of Echovirus 11 Allows Mapping of Mutants with Altered Receptor Requirements for Infection. <i>Journal of Virology</i> , 2002, 76, 7694-7704.	3.4	46
190	Potential long-term effects of SARS-CoV-2 infection on the pulmonary vasculature: a global perspective. <i>Nature Reviews Cardiology</i> , 2022, 19, 314-331.	13.7	46
191	Plate Tectonics of Virus Shell Assembly and Reorganization in Phage $\hat{\gamma}$ 8, a Distant Relative of Mammalian Reoviruses. <i>Structure</i> , 2013, 21, 1384-1395.	3.3	45
192	Virus found in a boreal lake links ssDNA and dsDNA viruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8378-8383.	7.1	44
193	A critical evaluation of the predicted and X-ray structures of $\gamma$ -Lactalbumin. <i>The Protein Journal</i> , 1990, 9, 549-563.	1.1	43
194	Structure of CrmE, a Virus-encoded Tumour Necrosis Factor Receptor. <i>Journal of Molecular Biology</i> , 2007, 372, 660-671.	4.2	43
195	Structure of Ljungan virus provides insight into genome packaging of this picornavirus. <i>Nature Communications</i> , 2015, 6, 8316.	12.8	43
196	Crystallographic Analysis of the Binding Modes of Thiazoloisoindolinone Non-Nucleoside Inhibitors to HIV-1 Reverse Transcriptase and Comparison with Modeling Studies. <i>Journal of Medicinal Chemistry</i> , 1999, 42, 3845-3851.	6.4	42
197	The Structural Basis for RNA Specificity and Ca <sup>2+</sup> Inhibition of an RNA-Dependent RNA Polymerase. <i>Structure</i> , 2004, 12, 307-316.	3.3	42
198	Benefits of Automated Crystallization Plate Tracking, Imaging, and Analysis. <i>Structure</i> , 2005, 13, 175-182.	3.3	42

#	ARTICLE	IF	CITATIONS
199	An Ion-channel Modulator from the Saliva of the Brown Ear Tick has a Highly Modified Kunitz/BPTI Structure. <i>Journal of Molecular Biology</i> , 2009, 389, 734-747.	4.2	42
200	Automatic comparison and classification of protein structures. <i>Journal of Structural Biology</i> , 2013, 183, 47-56.	2.8	42
201	Potent neutralization of hepatitis A virus reveals a receptor mimic mechanism and the receptor recognition site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 770-775.	7.1	42
202	Automated Structural Comparisons Clarify the Phylogeny of the Right-Hand-Shaped Polymerases. <i>Molecular Biology and Evolution</i> , 2014, 31, 2741-2752.	8.9	41
203	Rigid-body Ligand Recognition Drives Cytotoxic T-lymphocyte Antigen 4 (CTLA-4) Receptor Triggering. <i>Journal of Biological Chemistry</i> , 2011, 286, 6685-6696.	3.4	39
204	<i>In cellulo</i> structure determination of a novel cypovirus polyhedrin. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1435-1441.	2.5	39
205	Structure of glycosylated NPC1 luminal domain C reveals insights into NPC2 and Ebola virus interactions. <i>FEBS Letters</i> , 2016, 590, 605-612.	2.8	39
206	Structure of Equine Infectious Anemia Virus Matrix Protein. <i>Journal of Virology</i> , 2002, 76, 1876-1883.	3.4	38
207	Bacteriophage P23-77 Capsid Protein Structures Reveal the Archetype of an Ancient Branch from a Major Virus Lineage. <i>Structure</i> , 2013, 21, 718-726.	3.3	38
208	Structures of Ebola Virus Glycoprotein Complexes with Tricyclic Antidepressant and Antipsychotic Drugs. <i>Journal of Medicinal Chemistry</i> , 2018, 61, 4938-4945.	6.4	38
209	Effects of N-butyldeoxynojirimycin and the Lec3.2.8.1 mutant phenotype on N-glycan processing in Chinese hamster ovary cells: Application to glycoprotein crystallization. <i>Protein Science</i> , 1999, 8, 1696-1701.	7.6	37
210	Evaluation and Use of In-Silico Structure-Based Epitope Prediction with Foot-and-Mouth Disease Virus. <i>PLoS ONE</i> , 2013, 8, e61122.	2.5	37
211	The structure of a prokaryotic viral envelope protein expands the landscape of membrane fusion proteins. <i>Nature Communications</i> , 2019, 10, 846.	12.8	37
212	Diffraction quality crystals of PRD1, a 66-MDa dsDNA virus with an internal membrane. <i>Journal of Structural Biology</i> , 2002, 139, 103-112.	2.8	36
213	Structure of human Aichi virus and implications for receptor binding. <i>Nature Microbiology</i> , 2016, 1, 16150.	13.3	36
214	Assembly intermediates of orthoreovirus captured in the cell. <i>Nature Communications</i> , 2020, 11, 4445.	12.8	36
215	Models Which Explain the Inhibition of Reverse Transcriptase by HIV-1-Specific (Thio)carboxanilide Derivatives1. <i>Biochemical and Biophysical Research Communications</i> , 1997, 234, 458-464.	2.1	35
216	The Structure and Function of the Outer Coat Protein VP9 of Banna Virus. <i>Structure</i> , 2005, 13, 17-28.	3.3	35

#	ARTICLE	IF	CITATIONS
217	A Human Embryonic Kidney 293T Cell Line Mutated at the Golgi Î±-Mannosidase II Locus. <i>Journal of Biological Chemistry</i> , 2009, 284, 21684-21695.	3.4	35
218	Structure of Signal-regulatory Protein Î±. <i>Journal of Biological Chemistry</i> , 2009, 284, 26613-26619.	3.4	35
219	<i>TakeTwo</i> : an indexing algorithm suited to still images with known crystal parameters. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 956-965.	2.3	35
220	The democratization of cryo-EM. <i>Nature Methods</i> , 2016, 13, 607-608.	19.0	35
221	Double-stranded RNA virus outer shell assembly by bona fide domain-swapping. <i>Nature Communications</i> , 2017, 8, 14814.	12.8	35
222	Structures of orbivirus VP7: implications for the role of this protein in the viral life cycle. <i>Structure</i> , 1997, 5, 871-883.	3.3	34
223	Lipofectin increases the specific activity of cypovirus particles for cultured insect cells. <i>Journal of Virological Methods</i> , 1999, 78, 177-189.	2.1	34
224	Shared paramyxoviral glycoprotein architecture is adapted for diverse attachment strategies. <i>Biochemical Society Transactions</i> , 2010, 38, 1349-1355.	3.4	34
225	The N-Terminus of the RNA Polymerase from Infectious Pancreatic Necrosis Virus Is the Determinant of Genome Attachment. <i>PLoS Pathogens</i> , 2011, 7, e1002085.	4.7	34
226	Structure-Based in Silico Screening Identifies a Potent Ebolavirus Inhibitor from a Traditional Chinese Medicine Library. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 2928-2937.	6.4	34
227	Production and crystallization of MHC class I B allele single peptide complexes. <i>FEBS Letters</i> , 1996, 383, 119-123.	2.8	33
228	Crystal Structure and Binding Properties of the CD2 and CD244 (2B4)-binding Protein, CD48. <i>Journal of Biological Chemistry</i> , 2006, 281, 29309-29320.	3.4	33
229	Pushing the limits of sulfur SAD phasing: <i>de novo</i> structure solution of the N-terminal domain of the ectodomain of HCV E1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2197-2203.	2.5	33
230	Production, crystallization, and preliminary X-ray analysis of the human MHC class Ib molecule HLA*E. <i>Protein Science</i> , 1998, 7, 1264-1266.	7.6	32
231	Semi-automated microseeding of nanolitre crystallization experiments. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 14-18.	0.7	31
232	Noncatalytic Ions Direct the RNA-Dependent RNA Polymerase of Bacterial Double-Stranded RNA Virus Î±6 from <i>De Novo</i> Initiation to Elongation. <i>Journal of Virology</i> , 2012, 86, 2837-2849.	3.4	31
233	The Human Otubain2-Ubiquitin Structure Provides Insights into the Cleavage Specificity of Poly-Ubiquitin-Linkages. <i>PLoS ONE</i> , 2015, 10, e0115344.	2.5	31
234	Redundant Late Domain Functions of Tandem VP2 YPX <sub>3</sub> L Motifs in Nonlytic Cellular Egress of Quasi-enveloped Hepatitis A Virus. <i>Journal of Virology</i> , 2018, 92, .	3.4	31

#	ARTICLE	IF	CITATIONS
235	Crystallization and preliminary X-ray diffraction analysis of foot-and-mouth disease virus. <i>Journal of Molecular Biology</i> , 1987, 196, 591-597.	4.2	30
236	Structure of the Murray Valley encephalitis virus RNA helicase at 1.9 Å... resolution. <i>Protein Science</i> , 2007, 16, 2294-2300.	7.6	30
237	Structural Basis of Mechanochemical Coupling in a Hexameric Molecular Motor. <i>Journal of Biological Chemistry</i> , 2008, 283, 3607-3617.	3.4	30
238	Characterization of epitope-tagged foot-and-mouth disease virus. <i>Journal of General Virology</i> , 2012, 93, 2371-2381.	2.9	30
239	Seneca Valley virus attachment and uncoating mediated by its receptor anthrax toxin receptor 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13087-13092.	7.1	30
240	Cells under siege: Viral glycoprotein interactions at the cell surface. <i>Journal of Structural Biology</i> , 2011, 175, 120-126.	2.8	29
241	Models of the three-dimensional structures of echidna, horse, and pigeon lysozymes: Calcium-binding lysozymes and their relationship with $\beta$ -lactalbumins. <i>The Protein Journal</i> , 1994, 13, 569-584.	1.1	28
242	Utility of recombinant integrin $\alpha$ 6 as a capture reagent in immunoassays for the diagnosis of foot-and-mouth disease. <i>Journal of Virological Methods</i> , 2005, 127, 69-79.	2.1	28
243	Back-priming mode of $\beta$ 6 RNA-dependent RNA polymerase. <i>Journal of General Virology</i> , 2005, 86, 521-526.	2.9	28
244	Generation and Characterization of a Chimeric Rabbit/Human Fab for Co-Crystallization of HIV-1 Rev. <i>Journal of Molecular Biology</i> , 2010, 397, 697-708.	4.2	28
245	SAT2 Foot-and-Mouth Disease Virus Structurally Modified for Increased Thermostability. <i>Journal of Virology</i> , 2017, 91, .	3.4	28
246	Atomic structure of the Epstein-Barr virus portal. <i>Nature Communications</i> , 2019, 10, 3891.	12.8	28
247	Hand-foot-and-mouth disease virus receptor KREMEN1 binds the canyon of Coxsackie Virus A10. <i>Nature Communications</i> , 2020, 11, 38.	12.8	28
248	On the release of <i>cppxfel</i> for processing X-ray free-electron laser images. <i>Journal of Applied Crystallography</i> , 2016, 49, 1065-1072.	4.5	28
249	Expression cloning of an equine T-lymphocyte glycoprotein CD2 cDNA. Structure-based analysis of conserved sequence elements. <i>FEBS Journal</i> , 1994, 219, 969-976.	0.2	27
250	Design of a data model for developing laboratory information management and analysis systems for protein production. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 278-284.	2.6	27
251	Crystal lattice as biological phenotype for insect viruses. <i>Protein Science</i> , 2005, 14, 2741-2743.	7.6	26
252	Neutralization Mechanisms of Two Highly Potent Antibodies against Human Enterovirus 71. <i>MBio</i> , 2018, 9, .	4.1	26

#	ARTICLE	IF	CITATIONS
253	Crystal Structure of Swine Vesicular Disease Virus and Implications for Host Adaptation. <i>Journal of Virology</i> , 2003, 77, 5475-5486.	3.4	25
254	Polyhedra structures and the evolution of the insect viruses. <i>Journal of Structural Biology</i> , 2015, 192, 88-99.	2.8	25
255	Cutting complexity down to size. <i>Nature</i> , 1997, 386, 437-438.	27.8	24
256	Bispecific repurposed medicines targeting the viral and immunological arms of COVID-19. <i>Scientific Reports</i> , 2021, 11, 13208.	3.3	24
257	Electron Bio-Imaging Centre (eBIC): the UK national research facility for biological electron microscopy. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 488-495.	2.3	24
258	Crystallization and preliminary X-ray analysis of three serotypes of foot-and-mouth disease virus. <i>Journal of Molecular Biology</i> , 1992, 228, 1263-1268.	4.2	23
259	Gene silencing pathway RNA-dependent RNA polymerase of <i>Neurospora crassa</i> : yeast expression and crystallization of selenomethionated QDE-1 protein. <i>Journal of Structural Biology</i> , 2005, 149, 111-115.	2.8	23
260	Binding of (5 <i>S</i> )-Penicilloic Acid to Penicillin Binding Protein 3. <i>ACS Chemical Biology</i> , 2013, 8, 2112-2116.	3.4	23
261	Tracking in atomic detail the functional specializations in viral RecA helicases that occur during evolution. <i>Nucleic Acids Research</i> , 2013, 41, 9396-9410.	14.5	23
262	Stringent thresholds in SARS-CoV-2 IgG assays lead to under-detection of mild infections. <i>BMC Infectious Diseases</i> , 2021, 21, 187.	2.9	23
263	Mammalian expression of virus-like particles as a proof of principle for next generation polio vaccines. <i>Npj Vaccines</i> , 2021, 6, 5.	6.0	23
264	Time-resolved structural studies on catalysis in the crystal with glycogen phosphorylase b. <i>Biochemical Society Transactions</i> , 1986, 14, 538-541.	3.4	22
265	Characterizing sequence variation in the VP1 capsid proteins of foot and mouth disease virus (serotype 0) with respect to virion structure. <i>Journal of Molecular Evolution</i> , 1998, 46, 465-475.	1.8	22
266	Virus Crystallography. <i>Molecular Biotechnology</i> , 1999, 12, 13-24.	2.4	22
267	Crystal structure of a 3-oxoacyl-(acylcarrier protein) reductase (BA3989) from <i>Bacillus anthracis</i> at 2.4-Å resolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 70, 562-567.	2.6	22
268	Insights into the pre-initiation events of bacteriophage $\phi$ 6 RNA-dependent RNA polymerase: towards the assembly of a productive binary complex. <i>Nucleic Acids Research</i> , 2009, 37, 1182-1192.	14.5	22
269	The structure of a reduced form of OxyR from <i>Neisseria meningitidis</i> . <i>BMC Structural Biology</i> , 2010, 10, 10.	2.3	22
270	Potent antiviral agents fail to elicit genetically-stable resistance mutations in either enterovirus 71 or Coxsackievirus A16. <i>Antiviral Research</i> , 2015, 124, 77-82.	4.1	22



#	ARTICLE	IF	CITATIONS
271	A national facility for biological cryo-electron microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 127-135.	2.5	22
272	The Structure of HIV-1 Rev Filaments Suggests a Bilateral Model for Rev-RRE Assembly. <i>Structure</i> , 2016, 24, 1068-1080.	3.3	22
273	Docking mission accomplished. <i>Nature</i> , 1994, 371, 19-20.	27.8	21
274	Recognition surfaces of MHC class I. <i>Immunological Reviews</i> , 1998, 163, 121-128.	6.0	21
275	Reconfiguration of yeast 40S ribosomal subunit domains by the translation initiation multifactor complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5788-5793.	7.1	21
276	Structures of foot and mouth disease virus pentamers: Insight into capsid dissociation and unexpected pentamer reassociation. <i>PLoS Pathogens</i> , 2017, 13, e1006607.	4.7	21
277	Crystallization and preliminary X-ray crystallographic studies on the bacteriophage $\phi$ 6 RNA-dependent RNA polymerase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1473-1475.	2.5	20
278	Macromolecular assemblies: greater than their parts. <i>Current Opinion in Structural Biology</i> , 2001, 11, 107-113.	5.7	20
279	The Mechanics of Translocation: A Molecular "Spring-and-Ratchet" System. <i>Structure</i> , 2008, 16, 664-672.	3.3	20
280	Structure Elucidation of Coxsackievirus A16 in Complex with GPP3 Informs a Systematic Review of Highly Potent Capsid Binders to Enteroviruses. <i>PLoS Pathogens</i> , 2015, 11, e1005165.	4.7	20
281	Uridine(5')diphospho(1)-alpha-d-glucose. A binding study to glycogen phosphorylase b in the crystal. <i>FEBS Journal</i> , 1988, 173, 569-578.	0.2	19
282	The structure of foot-and-mouth disease virus: implications for its physical and biological properties. <i>Veterinary Microbiology</i> , 1990, 23, 21-34.	1.9	19
283	Specific Interactions between Human Integrin $\alpha$ 5 $\beta$ 1 and Chimeric Hepatitis B Virus Core Particles Bearing the Receptor-Binding Epitope of Foot-and-Mouth Disease Virus. <i>Virology</i> , 1997, 239, 150-157.	2.4	19
284	Functional characteristics of HIV-1 subtype C compatible with increased heterosexual transmissibility. <i>Aids</i> , 2009, 23, 1047-1057.	2.2	19
285	Disruption of $\alpha$ -mannosidase processing induces non-canonical hybrid-type glycosylation. <i>FEBS Letters</i> , 2007, 581, 1963-1968.	2.8	18
286	Domain Metastability: A Molecular Basis for Immunoglobulin Deposition?. <i>Journal of Molecular Biology</i> , 2010, 399, 207-213.	4.2	18
287	The Protein Information Management System (PiMS): a generic tool for any structural biology research laboratory. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 249-260.	2.5	18
288	Hepatitis A Virus Capsid Structure. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2019, 9, a031807.	6.2	18

#	ARTICLE	IF	CITATIONS
289	Application of In Situ Diffraction in High-Throughput Structure Determination Platforms. <i>Methods in Molecular Biology</i> , 2015, 1261, 233-253.	0.9	18
290	Crystallization and functional analysis of a soluble deglycosylated form of the human costimulatory molecule B7-1. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 605-608.	2.5	17
291	Expression, purification and crystallization of a lyssavirus matrix (M) protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 258-262.	0.7	17
292	Use of the $\alpha$ -mannosidase I inhibitor kifunensine allows the crystallization of apo CTLA-4 homodimer produced in long-term cultures of Chinese hamster ovary cells. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 785-789.	0.7	17
293	Crystal structures of penicillin-binding protein 3 in complexes with azlocillin and cefoperazone in both acylated and deacylated forms. <i>FEBS Letters</i> , 2016, 590, 288-297.	2.8	17
294	Assembly of complex viruses exemplified by a halophilic euryarchaeal virus. <i>Nature Communications</i> , 2019, 10, 1456.	12.8	17
295	What Does it Take to Make a Virus: The Concept of the Viral 'Self'. , 2010, , 35-58.		17
296	SARS-CoV-2 antibody prevalence, titres and neutralising activity in an antenatal cohort, United Kingdom, 14 April to 15 June 2020. <i>Eurosurveillance</i> , 2020, 25, .	7.0	17
297	Structures of an alanine racemase from <i>Bacillus anthracis</i> (BA0252) in the presence and absence of (R)-1-aminoethylphosphonic acid (Ala-P). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 327-333.	0.7	16
298	Crystallization and preliminary X-ray analysis of CrgA, a LysR-type transcriptional regulator from pathogenic <i>Neisseria meningitidis</i> MC58. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 797-801.	0.7	16
299	Glutathione facilitates enterovirus assembly by binding at a druggable pocket. <i>Communications Biology</i> , 2020, 3, 9.	4.4	16
300	Structure of a VP1-VP3 Complex Suggests How Birnaviruses Package the VP1 Polymerase. <i>Journal of Virology</i> , 2013, 87, 3229-3236.	3.4	15
301	Weissenberg data collection for macromolecular crystallography. <i>Current Opinion in Structural Biology</i> , 1993, 3, 737-740.	5.7	14
302	Recognition at the cell surface: recent structural insights. <i>Current Opinion in Structural Biology</i> , 1995, 5, 735-743.	5.7	14
303	Complementing crystallography: the role of cryo-electron microscopy in structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1742-1749.	2.5	14
304	In Vitro Activities of the Multifunctional RNA Silencing Polymerase QDE-1 of <i>Neurospora crassa</i> *. <i>Journal of Biological Chemistry</i> , 2010, 285, 29367-29374.	3.4	14
305	A RANKL mutant used as an inter-species vaccine for efficient immunotherapy of osteoporosis. <i>Scientific Reports</i> , 2015, 5, 14150.	3.3	14
306	Production, crystallization and preliminary X-ray crystallographic studies of the bacteriophage $\phi$ 12 packaging motor. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 588-590.	2.5	13

#	ARTICLE	IF	CITATIONS
307	The Crystal Structure of UMP Kinase from <i>Bacillus anthracis</i> (BA1797) Reveals an Allosteric Nucleotide-Binding Site. <i>Journal of Molecular Biology</i> , 2008, 381, 1098-1105.	4.2	13
308	Some lessons from the systematic production and structural analysis of soluble $\hat{\pm}^2$ T-cell receptors. <i>Journal of Immunological Methods</i> , 2009, 350, 14-21.	1.4	13
309	Crystal structure of equine rhinitis A virus in complex with its sialic acid receptor. <i>Journal of General Virology</i> , 2010, 91, 1971-1977.	2.9	13
310	The Tandem Zinc-Finger Region of Human ZHX Adopts a Novel C2H2 Zinc Finger Structure with a C-Terminal Extension. <i>Biochemistry</i> , 2009, 48, 4431-4439.	2.5	12
311	Diamond Light Source: status and perspectives. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2015, 373, 20130161.	3.4	12
312	Viral envelope glycoproteins swing into action. <i>Structure</i> , 1995, 3, 645-648.	3.3	11
313	Model of the equine rhinitis A virus capsid: identification of a major neutralizing immunogenic site. <i>Journal of General Virology</i> , 2003, 84, 2365-2373.	2.9	11
314	Structure of 5-formyltetrahydrofolate cyclo-ligase from <i>Bacillus anthracis</i> (BA4489). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 168-172.	0.7	11
315	From lows to highs: using low-resolution models to phase X-ray data. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2257-2265.	2.5	11
316	Towards in cellulo virus crystallography. <i>Scientific Reports</i> , 2018, 8, 3771.	3.3	11
317	Chimeric O1K foot-and-mouth disease virus with SAT2 outer capsid as an FMD vaccine candidate. <i>Scientific Reports</i> , 2018, 8, 13654.	3.3	11
318	The role of the light chain in the structure and binding activity of two cattle antibodies that neutralize bovine respiratory syncytial virus. <i>Molecular Immunology</i> , 2019, 112, 123-130.	2.2	11
319	Structural and functional analysis of protective antibodies targeting the threefold plateau of enterovirus 71. <i>Nature Communications</i> , 2020, 11, 5253.	12.8	11
320	Preliminary Crystallographic Analysis of Bovine Enterovirus. <i>Journal of Molecular Biology</i> , 1993, 231, 930-932.	4.2	10
321	SPINE: Structural Proteomics IN Europe – the best of both worlds. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, ii-i.	2.5	10
322	Crystal structure of signal regulatory protein gamma (SIRP $\hat{1}^3$ ) in complex with an antibody Fab fragment. <i>BMC Structural Biology</i> , 2013, 13, 13.	2.3	10
323	Cloning, expression, purification, and crystallisation of HIV-2 reverse transcriptase. <i>Protein Expression and Purification</i> , 2003, 27, 12-18.	1.3	9
324	Preliminary crystallographic analysis of the major capsid protein P2 of the lipid-containing bacteriophage PM2. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 762-765.	0.7	9

#	ARTICLE	IF	CITATIONS
325	Selenomethionine labeling of large biological macromolecular complexes: Probing the structure of marine bacterial virus PM2. <i>Journal of Structural Biology</i> , 2008, 161, 204-210.	2.8	9
326	The C-terminal priming domain is strongly associated with the main body of bacteriophage $\phi$ 6 RNA-dependent RNA polymerase. <i>Virology</i> , 2012, 432, 184-193.	2.4	9
327	Crystallization and X-ray Diffraction Study of Recombinant Platelet-derived Endothelial Cell Growth Factor. <i>Journal of Molecular Biology</i> , 1993, 234, 879-880.	4.2	8
328	xtalPiMS: A PiMS-based web application for the management and monitoring of crystallization trials. <i>Journal of Structural Biology</i> , 2011, 175, 230-235.	2.8	8
329	Crystallization and preliminary crystallographic analysis of the major capsid proteins VP16 and VP17 of bacteriophage P23-77. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 580-583.	0.7	8
330	Expression, purification and crystallization of the ectodomain of the envelope glycoprotein E2 from Bovine viral diarrhoea virus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 35-38.	0.7	8
331	Structure determination from a single high-pressure-frozen virus crystal. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 308-312.	2.5	8
332	Journey to the core of HIV. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 818-820.	8.2	7
333	Recovery of data from perfectly twinned virus crystals revisited. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 817-822.	2.3	7
334	Structure of Cat Muscle Pyruvate Kinase at 0.26 nm Resolution. <i>Biochemical Society Transactions</i> , 1977, 5, 654-657.	3.4	6
335	Preliminary Crystallographic Analysis of Coxsackievirus A9. <i>Journal of Molecular Biology</i> , 1993, 230, 667-669.	4.2	6
336	Crystallization and Preliminary X-ray Investigation of Recombinant Simian Immunodeficiency Virus Matrix Protein. <i>Journal of Molecular Biology</i> , 1994, 241, 744-746.	4.2	6
337	Hybrid Vigor: Hybrid Methods In Viral Structure Determination. <i>Advances in Protein Chemistry</i> , 2003, 64, 37-91.	4.4	6
338	Overcoming the false-minima problem in direct methods: structure determination of the packaging enzyme P4 from bacteriophage $\phi$ 13. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 1238-1244.	2.5	6
339	An idea whose time has come. <i>Genome Biology</i> , 2007, 8, 408.	9.6	6
340	Humidity control as a strategy for lattice optimization applied to crystals of HLA-A*1101 complexed with variant peptides from dengue virus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 386-392.	0.7	6
341	The use of low-resolution phasing followed by phase extension from 7.6 to 2.5 Å resolution with noncrystallographic symmetry to solve the structure of a bacteriophage capsid protein. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011, 67, 228-232.	2.5	6
342	Diamond Light Source: contributions to SARS-CoV-2 biology and therapeutics. <i>Biochemical and Biophysical Research Communications</i> , 2021, 538, 40-46.	2.1	6

#	ARTICLE	IF	CITATIONS
343	Structures and therapeutic potential of anti-RBD human monoclonal antibodies against SARS-CoV-2. <i>Theranostics</i> , 2022, 12, 1-17.	10.0	6
344	Crystallization of human tumour necrosis factor. <i>Journal of Crystal Growth</i> , 1990, 100, 168-170.	1.5	5
345	HEPT: From an investigation of lithiation of nucleosides towards a rational design of non-nucleoside reverse transcriptase inhibitors of HIV-1. <i>Advances in Antiviral Drug Design</i> , 1999, , 93-144.	0.6	5
346	Going soft and SAD with manganese. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 108-111.	2.5	5
347	Structure determination of human semaphorin 4D as an example of the use of MAD in non-optimal cases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 108-115.	2.5	5
348	The B Cell Response to Foot-and-Mouth Disease Virus in Cattle following Sequential Vaccination with Multiple Serotypes. <i>Journal of Virology</i> , 2017, 91, .	3.4	5
349	<i>SynchLink</i> : an iOS app for ISPyB. <i>Journal of Applied Crystallography</i> , 2014, 47, 1781-1783.	4.5	5
350	Imperfection and radiation damage in protein crystals studied with coherent radiation. <i>Journal of Synchrotron Radiation</i> , 2016, 23, 228-237.	2.4	5
351	The slip-and-slide algorithm: a refinement protocol for detector geometry. <i>Journal of Synchrotron Radiation</i> , 2017, 24, 1152-1162.	2.4	5
352	Scanning electron microscopy as a method for sample visualization in protein X-ray crystallography. <i>IUCr</i> , 2020, 7, 500-508.	2.2	5
353	Some problems in relation to the structures of insulin derivatives. <i>Biochemical Society Transactions</i> , 1983, 11, 419-425.	3.4	4
354	Large unit cells and cellular mechanics. <i>Nature Structural Biology</i> , 1998, 5, 630-634.	9.7	4
355	Crystallization and preliminary X-ray analysis of human rhinovirus serotype 2 (HRV2). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1999, 55, 1459-1461.	2.5	4
356	Order and disorder in crystals of hexameric NTPases from dsRNA bacteriophages. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2337-2341.	2.5	4
357	Phosphate-recognition sites in catalysis and control of glycogen phosphorylase <i>b</i> . <i>Biochemical Society Transactions</i> , 1987, 15, 1001-1005.	3.4	3
358	Structure of Foot-and-Mouth Disease Virus. , 1990, , 161-171.		3
359	Crystallization and preliminary X-ray analysis of mouse RANK and its complex with RANKL. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 597-600.	0.7	3
360	Recording information on protein complexes in an information management system. <i>Journal of Structural Biology</i> , 2011, 175, 224-229.	2.8	3

#	ARTICLE	IF	CITATIONS
361	Building the atomic model of a boreal lake virus of unknown fold in a 3.9Å... cryo-EM map. <i>Journal of Structural Biology</i> , 2018, 202, 94-99.	2.8	3
362	Generation and characterisation of recombinant FMDV antibodies: Applications for advancing diagnostic and laboratory assays. <i>PLoS ONE</i> , 2018, 13, e0201853.	2.5	3
363	Symmetrical arrangement of positively charged residues around the 5-fold axes of SAT type foot-and-mouth disease virus enhances cell culture of field viruses. <i>PLoS Pathogens</i> , 2020, 16, e1008828.	4.7	3
364	Combined Approaches to Study Virus Structures. <i>Sub-Cellular Biochemistry</i> , 2013, 68, 203-246.	2.4	3
365	European Structural Proteomics – A Perspective. , 2008, , 463-504.		3
366	Bacteriophage PRD1 as a nanoscaffold for drug loading. <i>Nanoscale</i> , 2021, 13, 19875-19883.	5.6	3
367	Virus Crystallography. , 1996, 56, 319-364.		2
368	–4D Biology for health and disease–workshop report. <i>New Biotechnology</i> , 2011, 28, 291-293.	4.4	2
369	Universal detection of foot and mouth disease virus based on the conserved VP0 protein. <i>Wellcome Open Research</i> , 0, 3, 88.	1.8	2
370	Looking-glass land. <i>Nature</i> , 1989, 338, 196-196.	27.8	1
371	Crystals of the neurotrophins. <i>Protein Science</i> , 1996, 5, 973-977.	7.6	1
372	Crystallization and preliminary diffraction studies of the extracellular region of human p58 killer cell inhibitory receptor (KIR2). <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 433-435.	2.5	1
373	From SPINE to SPINE-2 complexes and beyond. <i>Journal of Structural Biology</i> , 2011, 175, 105.	2.8	1
374	Louise N. Johnson 1940–2012. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1216-1217.	8.2	1
375	Structure of the regulatory domain of the LysR family regulator NMB2055 (MetR-like protein) from <i>Neisseria meningitidis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 730-737.	0.7	1
376	Ptychographic Single Particle Analysis for Biological Science. <i>Microscopy and Microanalysis</i> , 2021, 27, 190-192.	0.4	1
377	Sample Preparation and Data Collection for High-Speed Fixed-Target Serial Femtosecond Crystallography. <i>Protocol Exchange</i> , 0, , .	0.3	1
378	Virus crystallography. , 2007, , 245-264.		1

#	ARTICLE	IF	CITATIONS
379	Bluetongue virus: the role of synchrotron radiation. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 865-874.	2.4	0
380	The crystal structure and dimerization of a co-stimulator B7-1. <i>Seibutsu Butsuri</i> , 2000, 40, S30.	0.1	0
381	Structural studies on the leukocyte co-stimulatory molecule, B7-1. , 2001, , 63-72.		0
382	Molecular recognition by Ig-like receptors, KIRs and Fc $\gamma$ Rs. , 2001, , 45-54.		0
383	High-throughput cloning, expression, and purification. , 2007, , 23-44.		0
384	Virion Structure. , 0, , 57-71.		0
385	iNEXT-Discovery and Instruct-ERIC: Integrating High-End Services for Translational Research in Structural Biology. <i>Journal of Visualized Experiments</i> , 2021, , .	0.3	0
386	Title is missing!. , 2020, 16, e1008828.		0
387	Title is missing!. , 2020, 16, e1008828.		0
388	Title is missing!. , 2020, 16, e1008828.		0
389	Title is missing!. , 2020, 16, e1008828.		0
390	Title is missing!. , 2020, 16, e1008828.		0
391	Title is missing!. , 2020, 16, e1008828.		0
392	Purification of African Swine Fever Virus. <i>Methods in Molecular Biology</i> , 2022, 2503, 179-186.	0.9	0