

Jonathan Mark Grimes

List of Publications by Year in descending order

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144
papers

11,904
citations

30070

54
h-index

30087

103
g-index

155
all docs

155
docs citations

155
times ranked

15354
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping inhibitory sites on the RNA polymerase of the 1918 pandemic influenza virus using nanobodies. <i>Nature Communications</i> , 2022, 13, 251.	12.8	14
2	The C-Terminal Domains of the PB2 Subunit of the Influenza A Virus RNA Polymerase Directly Interact with Cellular GTPase Rab11a. <i>Journal of Virology</i> , 2022, 96, jvi0197921.	3.4	7
3	Characterization of the SARS-CoV-2 ExoN (nsp14ExoNâ€™nsp10) complex: implications for its role in viral genome stability and inhibitor identification. <i>Nucleic Acids Research</i> , 2022, 50, 1484-1500.	14.5	36
4	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
5	Structural insights into RNA polymerases of negative-sense RNA viruses. <i>Nature Reviews Microbiology</i> , 2021, 19, 303-318.	28.6	71
6	Flavivirus maturation leads to the formation of an occupied lipid pocket in the surface glycoproteins. <i>Nature Communications</i> , 2021, 12, 1238.	12.8	37
7	Structure of an H3N2 influenza virus nucleoprotein. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2021, 77, 208-214.	0.8	8
8	Virus Crystallography. , 2021, , 199-207.		0
9	The SARS-CoV-2 RNA polymerase is a viral RNA capping enzyme. <i>Nucleic Acids Research</i> , 2021, 49, 13019-13030.	14.5	29
10	Host ANP32A mediates the assembly of the influenza virus replicase. <i>Nature</i> , 2020, 587, 638-643.	27.8	89
11	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
12	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
13	Design, Synthesis, and Biological Evaluation of Novel Indoles Targeting the Influenza PB2 Cap Binding Region. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9680-9690.	6.4	21
14	Structures of influenza A virus RNA polymerase offer insight into viral genome replication. <i>Nature</i> , 2019, 573, 287-290.	27.8	151
15	High-resolution crystal structure of arthropod Eiger TNF suggests a mode of receptor engagement and altered surface charge within endosomes. <i>Communications Biology</i> , 2019, 2, 293.	4.4	4
16	Insights from the crystal structure of the chicken CREB3 bZIP suggest that members of the CREB3 subfamily transcription factors may be activated in response to oxidative stress. <i>Protein Science</i> , 2019, 28, 779-787.	7.6	5
17	The role of gelsolin domain 3 in familial amyloidosis (Finnish type). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13958-13963.	7.1	14
18	Multiple liquid crystalline geometries of highly compacted nucleic acid in a dsRNA virus. <i>Nature</i> , 2019, 570, 252-256.	27.8	59

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19	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
20	Towards in cellulo virus crystallography. <i>Scientific Reports</i> , 2018, 8, 3771.	3.3	11
21	Characterization of a potent and highly unusual minimally enhancing antibody directed against dengue virus. <i>Nature Immunology</i> , 2018, 19, 1248-1256.	14.5	31
22	The methyltransferase domain of the Sudan ebolavirus L protein specifically targets internal adenosines of RNA substrates, in addition to the cap structure. <i>Nucleic Acids Research</i> , 2018, 46, 7902-7912.	14.5	39
23	<i>Mycobacterium tuberculosis</i> CarD, an essential global transcriptional regulator forms amyloid-like fibrils. <i>Scientific Reports</i> , 2018, 8, 10124.	3.3	22
24	A Mechanism for the Activation of the Influenza Virus Transcriptase. <i>Molecular Cell</i> , 2018, 70, 1101-1110.e4.	9.7	42
25	Where is crystallography going?. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 152-166.	2.3	54
26	Mechanisms of <i>Yersinia</i> YopO kinase substrate specificity. <i>Scientific Reports</i> , 2017, 7, 39998.	3.3	10
27	The conserved protein Seb1 drives transcription termination by binding RNA polymerase II and nascent RNA. <i>Nature Communications</i> , 2017, 8, 14861.	12.8	48
28	<i>Yersinia</i> effector protein (YopO)-mediated phosphorylation of host gelsolin causes calcium-independent activation leading to disruption of actin dynamics. <i>Journal of Biological Chemistry</i> , 2017, 292, 8092-8100.	3.4	13
29	Structural dissection of human metapneumovirus phosphoprotein using small angle x-ray scattering. <i>Scientific Reports</i> , 2017, 7, 14865.	3.3	20
30	The matrix protein of rabies virus binds to RelAp43 to modulate NF- κ B-dependent gene expression related to innate immunity. <i>Scientific Reports</i> , 2016, 6, 39420.	3.3	35
31	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
32	Nucleocapsid assembly in pneumoviruses is regulated by conformational switching of the N protein. <i>ELife</i> , 2016, 5, e12627.	6.0	72
33	Structure of CPV17 polyhedrin determined by the improved analysis of serial femtosecond crystallographic data. <i>Nature Communications</i> , 2015, 6, 6435.	12.8	56
34	An in cellulo-derived structure of PAK4 in complex with its inhibitor Inka1. <i>Nature Communications</i> , 2015, 6, 8681.	12.8	60
35	X-ray structure and activities of an essential Mononegavirales L-protein domain. <i>Nature Communications</i> , 2015, 6, 8749.	12.8	49
36	Calcium-controlled conformational choreography in the N-terminal half of adseverin. <i>Nature Communications</i> , 2015, 6, 8254.	12.8	13

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37	<i>Yersinia</i> effector YopO uses actin as bait to phosphorylate proteins that regulate actin polymerization. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 248-255.	8.2	47
38	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
39	Crystal structure of the RNA-dependent RNA polymerase from influenza C virus. <i>Nature</i> , 2015, 527, 114-117.	27.8	145
40	A new class of highly potent, broadly neutralizing antibodies isolated from viremic patients infected with dengue virus. <i>Nature Immunology</i> , 2015, 16, 170-177.	14.5	415
41	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
42	Structural Insights into the Human Metapneumovirus Glycoprotein Ectodomain. <i>Journal of Virology</i> , 2014, 88, 11611-11616.	3.4	21
43	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
44	Structure and Self-Assembly of the Calcium Binding Matrix Protein of Human Metapneumovirus. <i>Structure</i> , 2014, 22, 136-148.	3.3	44
45	Structural basis of thymosin- β 4/profilin exchange leading to actin filament polymerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4596-605.	7.1	68
46	Unexpected structure for the N-terminal domain of hepatitis C virus envelope glycoprotein E1. <i>Nature Communications</i> , 2014, 5, 4874.	12.8	72
47	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
48	<i>SynchLink</i> : an iOS app for ISPyB. <i>Journal of Applied Crystallography</i> , 2014, 47, 1781-1783.	4.5	5
49	Drastic changes in conformational dynamics of the antiterminator M2-1 regulate transcription efficiency in Pneumovirinae. <i>ELife</i> , 2014, 3, e02674.	6.0	39
50	Structure of a Pestivirus Envelope Glycoprotein E2 Clarifies Its Role in Cell Entry. <i>Cell Reports</i> , 2013, 3, 30-35.	6.4	124
51	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
52	Plate Tectonics of Virus Shell Assembly and Reorganization in Phage ϕ 8, a Distant Relative of Mammalian Reoviruses. <i>Structure</i> , 2013, 21, 1384-1395.	3.3	45
53	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
54	Antigenic Switching of Hepatitis B Virus by Alternative Dimerization of the Capsid Protein. <i>Structure</i> , 2013, 21, 133-142.	3.3	61

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55	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
56	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
57	Solution and Crystallographic Structures of the Central Region of the Phosphoprotein from Human Metapneumovirus. <i>PLoS ONE</i> , 2013, 8, e80371.	2.5	34
58	Noncatalytic Ions Direct the RNA-Dependent RNA Polymerase of Bacterial Double-Stranded RNA Virus ϕ 6 from <i>De Novo</i> Initiation to Elongation. <i>Journal of Virology</i> , 2012, 86, 2837-2849.	3.4	31
59	Structural Analysis of a Dengue Cross-Reactive Antibody Complexed with Envelope Domain III Reveals the Molecular Basis of Cross-Reactivity. <i>Journal of Immunology</i> , 2012, 188, 4971-4979.	0.8	82
60	The C-terminal priming domain is strongly associated with the main body of bacteriophage ϕ 6 RNA-dependent RNA polymerase. <i>Virology</i> , 2012, 432, 184-193.	2.4	9
61	Structure Unifies the Viral Universe. <i>Annual Review of Biochemistry</i> , 2012, 81, 795-822.	11.1	252
62	<i>In situ</i> macromolecular crystallography using microbeams. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 592-600.	2.5	113
63	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
64	How vaccinia virus has evolved to subvert the host immune response. <i>Journal of Structural Biology</i> , 2011, 175, 127-134.	2.8	66
65	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
66	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
67	An In-Depth Analysis of Original Antigenic Sin in Dengue Virus Infection. <i>Journal of Virology</i> , 2011, 85, 410-421.	3.4	165
68	Mapping the $\text{I}\kappa\text{B}$ Kinase $\text{I}\kappa\text{B}\alpha$ -binding Interface of the B14 Protein, a Vaccinia Virus Inhibitor of $\text{I}\kappa\text{B}\alpha$ -mediated Activation of Nuclear Factor $\text{I}\kappa\text{B}$. <i>Journal of Biological Chemistry</i> , 2011, 286, 20727-20735.	3.4	48
69	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
70	Inhibition of Apoptosis and NF- $\text{I}\kappa\text{B}$ 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
71	Detection of a Fourth Orbivirus Non-Structural Protein. <i>PLoS ONE</i> , 2011, 6, e25697.	2.5	174
72	Structure and functionality in flavivirus NS-proteins: Perspectives for drug design. <i>Antiviral Research</i> , 2010, 87, 125-148.	4.1	289

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73	Genomics and structure/function studies of Rhabdoviridae proteins involved in replication and transcription. <i>Antiviral Research</i> , 2010, 87, 149-161.	4.1	57
74	Implications of the HIV-1 Rev dimer structure at 3.2Å 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
75	Complete sequence of Great Island virus and comparison with the T2 and outer-capsid proteins of Kemerovo, Lipovnik and Tribec viruses (genus Orbivirus, family Reoviridae). <i>Journal of General Virology</i> , 2010, 91, 2985-2993.	2.9	54
76	Structure of the Nucleoprotein Binding Domain of Mokola Virus Phosphoprotein. <i>Journal of Virology</i> , 2010, 84, 1089-1096.	3.4	27
77	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
78	The structure of the nucleoprotein binding domain of lyssavirus phosphoprotein reveals a structural relationship between the N-RNA binding domains of Rhabdoviridae and Paramyxoviridae. <i>RNA Biology</i> , 2010, 7, 322-327.	3.1	18
79	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
80	What Does it Take to Make a Virus: The Concept of the Viral 'Self'. , 2010, , 35-58.		17
81	Unusual Molecular Architecture of the Machupo Virus Attachment Glycoprotein. <i>Journal of Virology</i> , 2009, 83, 8259-8265.	3.4	71
82	Insights into the pre-initiation events of bacteriophage ϕ 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
83	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
84	Semi-automated microseeding of nanolitre crystallization experiments. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 14-18.	0.7	31
85	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
86	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
87	The VIZIER project: Preparedness against pathogenic RNA viruses. <i>Antiviral Research</i> , 2008, 78, 37-46.	4.1	26
88	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
89	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
90	Structural Basis of Mechanochemical Coupling in a Hexameric Molecular Motor. <i>Journal of Biological Chemistry</i> , 2008, 283, 3607-3617.	3.4	30

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91	Structural explanation for the role of Mn ²⁺ in the activity of ϕ 6 RNA-dependent RNA polymerase. <i>Nucleic Acids Research</i> , 2008, 36, 6633-6644.	14.5	48
92	Rhabdovirus Matrix Protein Structures Reveal a Novel Mode of Self-Association. <i>PLoS Pathogens</i> , 2008, 4, e1000251.	4.7	71
93	Vaccinia Virus Proteins A52 and B14 Share a Bcl-2-like Fold but Have Evolved to Inhibit NF- κ B rather than Apoptosis. <i>PLoS Pathogens</i> , 2008, 4, e1000128.	4.7	136
94	Structure and Function of A41, a Vaccinia Virus Chemokine Binding Protein. <i>PLoS Pathogens</i> , 2008, 4, e5.	4.7	66
95	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
96	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
97	Structure of CrmE, a Virus-encoded Tumour Necrosis Factor Receptor. <i>Journal of Molecular Biology</i> , 2007, 372, 660-671.	4.2	43
98	Bluetongue virus VP4 is an RNA-capping assembly line. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 449-451.	8.2	82
99	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
100	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
101	Application of the use of high-throughput technologies to the determination of protein structures of bacterial and viral pathogens. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1196-1207.	2.5	23
102	The Crystal Structure of ORF-9b, a Lipid Binding Protein from the SARS Coronavirus. <i>Structure</i> , 2006, 14, 1157-1165.	3.3	91
103	Lysine Methylation as a Routine Rescue Strategy for Protein Crystallization. <i>Structure</i> , 2006, 14, 1617-1622.	3.3	483
104	The Structure of an RNAi Polymerase Links RNA Silencing and Transcription. <i>PLoS Biology</i> , 2006, 4, e434.	5.6	80
105	Crystal lattice as biological phenotype for insect viruses. <i>Protein Science</i> , 2005, 14, 2741-2743.	7.6	26
106	The Structure and Function of the Outer Coat Protein VP9 of Banna Virus. <i>Structure</i> , 2005, 13, 17-28.	3.3	35
107	What does structure tell us about virus evolution?. <i>Current Opinion in Structural Biology</i> , 2005, 15, 655-663.	5.7	348
108	Going soft and SAD with manganese. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 108-111.	2.5	5

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109	A procedure for setting up high-throughput nanolitre crystallization experiments. Crystallization workflow for initial screening, automated storage, imaging and optimization. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 651-657.	2.5	234
110	Overcoming the false-minima problem in direct methods: structure determination of the packaging enzyme P4 from bacteriophage ϕ 13. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 1238-1244.	2.5	6
111	Preliminary crystallographic analysis of the major capsid protein P2 of the lipid-containing bacteriophage PM2. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 762-765.	0.7	9
112	Back-priming mode of ϕ 6 RNA-dependent RNA polymerase. Journal of General Virology, 2005, 86, 521-526.	2.9	28
113	Gene silencing pathway RNA-dependent RNA polymerase of Neurospora crassa: yeast expression and crystallization of selenomethionated QDE-1 protein. Journal of Structural Biology, 2005, 149, 111-115.	2.8	23
114	Membrane structure and interactions with protein and DNA in bacteriophage PRD1. Nature, 2004, 432, 122-125.	27.8	133
115	Insights into assembly from structural analysis of bacteriophage PRD1. Nature, 2004, 432, 68-74.	27.8	246
116	The Structural Basis for RNA Specificity and Ca ²⁺ Inhibition of an RNA-Dependent RNA Polymerase. Structure, 2004, 12, 307-316.	3.3	42
117	The nsp9 Replicase Protein of SARS-Coronavirus, Structure and Functional Insights. Structure, 2004, 12, 341-353.	3.3	225
118	Structure of the Integrin Binding Fragment from Fibrillin-1 Gives New Insights into Microfibril Organization. Structure, 2004, 12, 717-729.	3.3	114
119	Production, crystallization and preliminary X-ray crystallographic studies of the bacteriophage ϕ 12 packaging motor. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 588-590.	2.5	13
120	The Structural Basis for RNA Specificity and Ca Inhibition of an RNA-Dependent RNA Polymerase. Structure, 2004, 12, 307-316.	3.3	54
121	Atomic Snapshots of an RNA Packaging Motor Reveal Conformational Changes Linking ATP Hydrolysis to RNA Translocation. Cell, 2004, 118, 743-755.	28.9	151
122	RNA-dependent RNA polymerases of dsRNA bacteriophages. Virus Research, 2004, 101, 45-55.	2.2	33
123	Order and disorder in crystals of hexameric NTPases from dsRNA bacteriophages. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 2337-2341.	2.5	4
124	Hybrid Vigor: Hybrid Methods In Viral Structure Determination. Advances in Protein Chemistry, 2003, 64, 37-91.	4.4	6
125	The Core of Bluetongue Virus Binds Double-Stranded RNA. Journal of Virology, 2002, 76, 9533-9536.	3.4	25
126	Diffraction quality crystals of PRD1, a 66-MDa dsDNA virus with an internal membrane. Journal of Structural Biology, 2002, 139, 103-112.	2.8	36

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127	Translocation portals for the substrates and products of a viral transcription complex: the bluetongue virus core. <i>EMBO Journal</i> , 2001, 20, 7229-7239.	7.8	75
128	A mechanism for initiating RNA-dependent RNA polymerization. <i>Nature</i> , 2001, 410, 235-240.	27.8	458
129	Macromolecular assemblies: greater than their parts. <i>Current Opinion in Structural Biology</i> , 2001, 11, 107-113.	5.7	20
130	Crystallization and preliminary X-ray crystallographic studies on the bacteriophage ϕ 6 RNA-dependent RNA polymerase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1473-1475.	2.5	20
131	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
132	Bluetongue virus: the role of synchrotron radiation. <i>Journal of Synchrotron Radiation</i> , 1999, 6, 865-874.	2.4	0
133	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
134	The structure of a cyovirus and the functional organization of dsRNA viruses. <i>Nature Structural Biology</i> , 1999, 6, 565-568.	9.7	129
135	Virus Crystallography. <i>Molecular Biotechnology</i> , 1999, 12, 13-24.	2.4	22
136	The Highly Ordered Double-Stranded RNA Genome of Bluetongue Virus Revealed by Crystallography. <i>Cell</i> , 1999, 97, 481-490.	28.9	181
137	Large unit cells and cellular mechanics. <i>Nature Structural Biology</i> , 1998, 5, 630-634.	9.7	4
138	The atomic structure of the bluetongue virus core. <i>Nature</i> , 1998, 395, 470-478.	27.8	543
139	The Crystal Structure of Plasma Gelsolin: Implications for Actin Severing, Capping, and Nucleation. <i>Cell</i> , 1997, 90, 661-670.	28.9	273
140	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
141	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
142	Crystal structure of the top domain of African horse sickness virus VP7: comparisons with bluetongue virus VP7. <i>Journal of Virology</i> , 1996, 70, 3797-3806.	3.4	55
143	The crystal structure of bluetongue virus VP7. <i>Nature</i> , 1995, 373, 167-170.	27.8	168
144	Activity and specificity of human aldolases. <i>Journal of Molecular Biology</i> , 1991, 219, 573-576.	4.2	111