

BV Venkataram Prasad

List of Publications by Year in descending order

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174
papers

11,185
citations

25034

57
h-index

36028

97
g-index

177
all docs

177
docs citations

177
times ranked

7588
citing authors

#	ARTICLE	IF	CITATIONS
1	X-ray Crystallographic Structure of the Norwalk Virus Capsid. <i>Science</i> , 1999, 286, 287-290.	12.6	820
2	Three-dimensional structure of rotavirus. <i>Journal of Molecular Biology</i> , 1988, 199, 269-275.	4.2	363
3	The Stereochemistry of Peptides Containing Î±-Aminoisobutyric Aci. <i>Critical Reviews in Biochemistry</i> , 1984, 16, 307-348.	7.5	332
4	Cell attachment protein VP8* of a human rotavirus specifically interacts with A-type histo-blood group antigen. <i>Nature</i> , 2012, 485, 256-259.	27.8	283
5	Localization of VP4 neutralization sites in rotavirus by three-dimensional cryo-electron microscopy. <i>Nature</i> , 1990, 343, 476-479.	27.8	246
6	Atomic resolution structural characterization of recognition of histo-blood group antigens by Norwalk virus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 9175-9180.	7.1	236
7	Visualization of ordered genomic RNA and localization of transcriptional complexes in rotavirus. <i>Nature</i> , 1996, 382, 471-473.	27.8	219
8	Three-dimensional structure of a membrane-containing virus.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 9095-9099.	7.1	205
9	Structural rearrangements in the membrane penetration protein of a non-enveloped virus. <i>Nature</i> , 2004, 430, 1053-1058.	27.8	200
10	Three-dimensional visualization of mRNA release from actively transcribing rotavirus particles. <i>Nature Structural Biology</i> , 1997, 4, 118-121.	9.7	195
11	Protein Subunit Structures in the Herpes Simplex Virus A-capsid Determined from 400 kV Spot-scan Electron Cryomicroscopy. <i>Journal of Molecular Biology</i> , 1994, 242, 456-469.	4.2	187
12	Noroviruses everywhere: has something changed?. <i>Current Opinion in Infectious Diseases</i> , 2006, 19, 467-474.	3.1	182
13	Structural Requirements for the Assembly of Norwalk Virus-Like Particles. <i>Journal of Virology</i> , 2002, 76, 4044-4055.	3.4	175
14	Atomic structure of the major capsid protein of rotavirus: implications for the architecture of the virion. <i>EMBO Journal</i> , 2001, 20, 1485-1497.	7.8	172
15	Three-dimensional structure of the HSV1 nucleocapsid. <i>Cell</i> , 1989, 56, 651-660.	28.9	164
16	Three-dimensional Transformation of Capsids Associated with Genome Packaging in a Bacterial Virus. <i>Journal of Molecular Biology</i> , 1993, 231, 65-74.	4.2	163
17	X-ray structure of a native calicivirus: Structural insights into antigenic diversity and host specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8048-8053.	7.1	159
18	Three-dimensional visualization of the rotavirus hemagglutinin structure. <i>Cell</i> , 1993, 74, 693-701.	28.9	151

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19	Inhibition of rotavirus replication by a non-neutralizing, rotavirus VP6-specific IgA mAb. <i>Journal of Clinical Investigation</i> , 2002, 109, 1203-1213.	8.2	148
20	Selective Inhibitors of Histone Methyltransferase DOT1L: Design, Synthesis, and Crystallographic Studies. <i>Journal of the American Chemical Society</i> , 2011, 133, 16746-16749.	13.7	144
21	Structural Analysis of Histo-Blood Group Antigen Binding Specificity in a Norovirus GII.4 Epidemic Variant: Implications for Epochal Evolution. <i>Journal of Virology</i> , 2011, 85, 8635-8645.	3.4	138
22	X-ray structure of NS1 from a highly pathogenic H5N1 influenza virus. <i>Nature</i> , 2008, 456, 985-988.	27.8	132
23	Human milk oligosaccharides, milk microbiome and infant gut microbiome modulate neonatal rotavirus infection. <i>Nature Communications</i> , 2018, 9, 5010.	12.8	130
24	The structure of a cyovirus and the functional organization of dsRNA viruses. <i>Nature Structural Biology</i> , 1999, 6, 565-568.	9.7	129
25	Trypsin Cleavage Stabilizes the Rotavirus VP4 Spike. <i>Journal of Virology</i> , 2001, 75, 6052-6061.	3.4	128
26	Rotavirus Proteins: Structure and Assembly. , 2006, 309, 189-219.		128
27	Principles of Virus Structural Organization. <i>Advances in Experimental Medicine and Biology</i> , 2012, 726, 17-47.	1.6	124
28	Inter- and Intragenus Structural Variations in Caliciviruses and Their Functional Implications. <i>Journal of Virology</i> , 2004, 78, 6469-6479.	3.4	122
29	X-Ray Structures of the N- and C-Terminal Domains of a Coronavirus Nucleocapsid Protein: Implications for Nucleocapsid Formation. <i>Journal of Virology</i> , 2006, 80, 6612-6620.	3.4	120
30	Norwalk Virus Assembly and Stability Monitored by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1742-1751.	3.8	118
31	Emerging themes in rotavirus cell entry, genome organization, transcription and replication. <i>Virus Research</i> , 2004, 101, 67-81.	2.2	116
32	Norwalk Virus Minor Capsid Protein VP2 Associates within the VP1 Shell Domain. <i>Journal of Virology</i> , 2013, 87, 4818-4825.	3.4	115
33	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
34	Human Milk Contains Novel Glycans That Are Potential Decoy Receptors for Neonatal Rotaviruses. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2944-2960.	3.8	113
35	Three-dimensional Structure of Calicivirus. <i>Journal of Molecular Biology</i> , 1994, 240, 256-264.	4.2	108
36	Rotavirus Architecture at Subnanometer Resolution. <i>Journal of Virology</i> , 2009, 83, 1754-1766.	3.4	106

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37	Three-dimensional Structure of Scaffolding-containing Phage P22 Procapsids by Electron Cryo-microscopy. <i>Journal of Molecular Biology</i> , 1996, 260, 85-98.	4.2	97
38	Structure of the catalytic domain of the colistin resistance enzyme MCR-1. <i>BMC Biology</i> , 2016, 14, 81.	3.8	95
39	Rotavirus protein involved in genome replication and packaging exhibits a HIT-like fold. <i>Nature</i> , 2002, 417, 311-315.	27.8	93
40	X-ray structure of influenza virus NS1 effector domain. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 559-560.	8.2	93
41	Interactions between the Inner and Outer Capsids of Bluetongue Virus. <i>Journal of Virology</i> , 2004, 78, 8059-8067.	3.4	91
42	The structure of aquareovirus shows how the different geometries of the two layers of the capsid are reconciled to provide symmetrical interactions and stabilization. <i>Structure</i> , 1996, 4, 957-967.	3.3	89
43	X-Ray Crystallographic Structure of the Norwalk Virus Protease at 1.5-Å Resolution. <i>Journal of Virology</i> , 2006, 80, 5050-5058.	3.4	88
44	Cyclic peptide disulfides. Solution and solid-state conformation of Boc-Cys-Pro-Aib-Cys-NHMe with a disulfide bridge from Cys to Cys, a disulfide-bridged peptide helix. <i>Journal of the American Chemical Society</i> , 1983, 105, 105-109.	13.7	85
45	Mechanism of genome transcription in segmented dsRNA viruses. <i>Advances in Virus Research</i> , 2000, 55, 185-229.	2.1	82
46	Sequence comparison of single-stranded DNA binding proteins and its structural implications. <i>Journal of Molecular Biology</i> , 1987, 193, 579-584.	4.2	80
47	Evolutionary Trace Residues in Noroviruses: Importance in Receptor Binding, Antigenicity, Virion Assembly, and Strain Diversity. <i>Journal of Virology</i> , 2005, 79, 554-568.	3.4	80
48	High-Resolution Molecular and Antigen Structure of the VP8* Core of a Sialic Acid-Independent Human Rotavirus Strain. <i>Journal of Virology</i> , 2006, 80, 1513-1523.	3.4	77
49	The VP8* Domain of Neonatal Rotavirus Strain G10P[11] Binds to Type II Precursor Glycans. <i>Journal of Virology</i> , 2013, 87, 7255-7264.	3.4	74
50	Diversity in Rotavirus-Host Glycan Interactions: A "Sweet" Spectrum. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2016, 2, 263-273.	4.5	72
51	Structure and mechanism of human diacylglycerol O-acyltransferase 1. <i>Nature</i> , 2020, 581, 329-332.	27.8	72
52	Crystal and molecular structure of benzyloxycarbonyl- β -aminoisobutyryl-L-prolyl methylamide: The observation of an X ₂ -Pro ₃ Type III β -Turn. <i>Biopolymers</i> , 1979, 18, 1635-1646.	2.4	70
53	Crystallographic Investigation and Selective Inhibition of Mutant Isocitrate Dehydrogenase. <i>ACS Medicinal Chemistry Letters</i> , 2013, 4, 542-546.	2.8	70
54	The Influenza A Virus Protein NS1 Displays Structural Polymorphism. <i>Journal of Virology</i> , 2014, 88, 4113-4122.	3.4	69

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55	Differential active site requirements for NDM-1 β -lactamase hydrolysis of carbapenem versus penicillin and cephalosporin antibiotics. <i>Nature Communications</i> , 2018, 9, 4524.	12.8	67
56	Characterization of Rotavirus VP2 Particles. <i>Virology</i> , 1994, 201, 55-65.	2.4	66
57	Cryoelectron Microscopy Structures of Rotavirus NSP2-NSP5 and NSP2-RNA Complexes: Implications for Genome Replication. <i>Journal of Virology</i> , 2006, 80, 10829-10835.	3.4	66
58	Structure of Rotavirus. <i>Current Topics in Microbiology and Immunology</i> , 1994, 185, 9-29.	1.1	66
59	Proposed mechanisms for binding of apo[a] kringle type 9 to apo B-100 in human lipoprotein[a]. <i>Biophysical Journal</i> , 1993, 64, 686-700.	0.5	65
60	Rotavirus non-structural proteins: structure and function. <i>Current Opinion in Virology</i> , 2012, 2, 380-388.	5.4	63
61	Glycan recognition in globally dominant human rotaviruses. <i>Nature Communications</i> , 2018, 9, 2631.	12.8	63
62	Inhibition of 1-Deoxy- α -Xylulose-5-Phosphate Reductoisomerase by Lipophilic Phosphonates: SAR, QSAR, and Crystallographic Studies. <i>Journal of Medicinal Chemistry</i> , 2011, 54, 4721-4734.	6.4	59
63	Conformational Changes in the Capsid of a Calicivirus upon Interaction with Its Functional Receptor. <i>Journal of Virology</i> , 2010, 84, 5550-5564.	3.4	57
64	A Novel Form of Rotavirus NSP2 and Phosphorylation-Dependent NSP2-NSP5 Interactions Are Associated with Viroplasm Assembly. <i>Journal of Virology</i> , 2014, 88, 786-798.	3.4	57
65	Trypsin-Induced Structural Transformation in Aquareovirus. <i>Journal of Virology</i> , 2000, 74, 6546-6555.	3.4	55
66	Prestress Strengthens the Shell of Norwalk Virus Nanoparticles. <i>Nano Letters</i> , 2011, 11, 4865-4869.	9.1	55
67	A Case Study of the Conformation of Poly(α -aminoisobutyric acid): α - or β -Helix. <i>Macromolecules</i> , 1979, 12, 1107-1110.	4.8	53
68	Conformational analysis of small disulfide loops. Spectroscopic and theoretical studies on a synthetic cyclic tetrapeptide containing cystine. <i>Biochemistry</i> , 1982, 21, 5502-5509.	2.5	51
69	Molecular Basis for the Catalytic Specificity of the CTX-M Extended-Spectrum β -Lactamases. <i>Biochemistry</i> , 2015, 54, 447-457.	2.5	50
70	Structural basis of glycan specificity in neonate-specific bovine-human reassortant rotavirus. <i>Nature Communications</i> , 2015, 6, 8346.	12.8	50
71	Structural Localization of the E3 Glycoprotein in Attenuated Sindbis Virus Mutants. <i>Journal of Virology</i> , 1998, 72, 1534-1541.	3.4	50
72	Structure-Function Analysis of Rotavirus NSP2 Octamer by Using a Novel Complementation System. <i>Journal of Virology</i> , 2006, 80, 7984-7994.	3.4	49

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73	A Triple Mutant in the $\hat{\text{C}}$ -loop of TEM-1 $\hat{\text{I}}^2$ -Lactamase Changes the Substrate Profile via a Large Conformational Change and an Altered General Base for Catalysis. <i>Journal of Biological Chemistry</i> , 2015, 290, 10382-10394.	3.4	49
74	Structural Basis of Substrate Specificity and Protease Inhibition in Norwalk Virus. <i>Journal of Virology</i> , 2013, 87, 4281-4292.	3.4	47
75	Structural Analysis of Determinants of Histo-Blood Group Antigen Binding Specificity in Genogroup I Noroviruses. <i>Journal of Virology</i> , 2014, 88, 6168-6180.	3.4	47
76	The reversible condensation and expansion of the rotavirus genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 1381-1386.	7.1	46
77	Structural and Biochemical Evidence That a TEM-1 $\hat{\text{I}}^2$ -Lactamase N170G Active Site Mutant Acts via Substrate-assisted Catalysis. <i>Journal of Biological Chemistry</i> , 2009, 284, 33703-33712.	3.4	45
78	Comparative structural analysis of transcriptionally competent and incompetent rotavirus-antibody complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 5428-5433.	7.1	44
79	Type II β -turn conformation of pivaloyl-L-prolyl- β -aminoisobutyryl-N-methylamide: Theoretical, spectroscopic, and X-ray studies. <i>Biopolymers</i> , 1982, 21, 1261-1273.	2.4	43
80	Structural Studies of Recombinant Norwalk Capsids. <i>Journal of Infectious Diseases</i> , 2000, 181, S317-S321.	4.0	41
81	Structural basis for norovirus neutralization by an HBGA blocking human IgA antibody. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5830-E5837.	7.1	41
82	Automated Software Package for Icosahedral Virus Reconstruction. <i>Journal of Structural Biology</i> , 1996, 116, 209-215.	2.8	40
83	X-Pro peptides. A theoretical study of the hydrogen bonded conformations of ($\hat{\text{I}}^{\pm}$ -aminoisobutyryl-l-prolyl) $_n$ sequences. <i>International Journal of Biological Macromolecules</i> , 1982, 4, 99-102.	7.5	39
84	Crystallographic and Biochemical Analysis of Rotavirus NSP2 with Nucleotides Reveals a Nucleoside Diphosphate Kinase-Like Activity. <i>Journal of Virology</i> , 2007, 81, 12272-12284.	3.4	39
85	Phosphorylation cascade regulates the formation and maturation of rotaviral replication factories. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E12015-E12023.	7.1	39
86	Rotavirus Cell Entry. <i>Current Topics in Microbiology and Immunology</i> , 2010, 343, 121-148.	1.1	37
87	Role of the Histidine Triad-like Motif in Nucleotide Hydrolysis by the Rotavirus RNA-packaging Protein NSP2. <i>Journal of Biological Chemistry</i> , 2004, 279, 10624-10633.	3.4	36
88	Structural Basis for Different Substrate Profiles of Two Closely Related Class D $\hat{\text{I}}^2$ -Lactamases and Their Inhibition by Halogens. <i>Biochemistry</i> , 2015, 54, 3370-3380.	2.5	35
89	Antiviral targets of human noroviruses. <i>Current Opinion in Virology</i> , 2016, 18, 117-125.	5.4	35
90	A Monoclonal Antibody Specific for Reovirus Outer-Capsid Protein $\hat{\text{I}}_3$ Inhibits $\hat{\text{I}}_1$ -Mediated Hemagglutination by Steric Hindrance. <i>Journal of Virology</i> , 2001, 75, 6625-6634.	3.4	33

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91	Functional Maturation of the Human Antibody Response to Rotavirus. <i>Journal of Immunology</i> , 2008, 180, 3980-3989.	0.8	33
92	Structural basis of glycan interaction in gastroenteric viral pathogens. <i>Current Opinion in Virology</i> , 2014, 7, 119-127.	5.4	32
93	Human VP8* mAbs neutralize rotavirus selectively in human intestinal epithelial cells. <i>Journal of Clinical Investigation</i> , 2019, 129, 3839-3851.	8.2	32
94	pH-Induced Conformational Change of the Rotavirus VP4 Spike: Implications for Cell Entry and Antibody Neutralization. <i>Journal of Virology</i> , 2005, 79, 8572-8580.	3.4	30
95	A New Crucial Protein Interaction Element That Targets the Adenovirus E4-ORF1 Oncoprotein to Membrane Vesicles. <i>Journal of Virology</i> , 2007, 81, 4787-4797.	3.4	30
96	Structural and functional dissection of reovirus capsid folding and assembly by the prefoldin-TRiC/CCT chaperone network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	30
97	Probing the Sites of Interactions of Rotaviral Proteins Involved in Replication. <i>Journal of Virology</i> , 2014, 88, 12866-12881.	3.4	29
98	Structural Basis for 2'-5'-Oligoadenylate Binding and Enzyme Activity of a Viral RNase L Antagonist. <i>Journal of Virology</i> , 2015, 89, 6633-6645.	3.4	28
99	Multiple oligomeric structures of a bacterial small heat shock protein. <i>Scientific Reports</i> , 2016, 6, 24019.	3.3	28
100	The Drug-Resistant Variant P167S Expands the Substrate Profile of CTX-M β -Lactamases for Oxyimino-Cephalosporin Antibiotics by Enlarging the Active Site upon Acylation. <i>Biochemistry</i> , 2017, 56, 3443-3453.	2.5	28
101	Identifying Oxacillinase-48 Carbapenemase Inhibitors Using DNA-Encoded Chemical Libraries. <i>ACS Infectious Diseases</i> , 2020, 6, 1214-1227.	3.8	27
102	Frequent Use of the IgA Isotype in Human B Cells Encoding Potent Norovirus-Specific Monoclonal Antibodies That Block HBGA Binding. <i>PLoS Pathogens</i> , 2016, 12, e1005719.	4.7	27
103	The crystal structure of benzyloxycarbonyl-(\pm -aminoisobutyryl) ₂ -L-alanyl methyl ester. <i>Acta Crystallographica Section B: Structural Crystallography and Crystal Chemistry</i> , 1980, 36, 107-110.	0.4	26
104	Multiple conformational states of a Pro-Pro peptide. Solid-state and solution conformations of Boc-Aib-Pro-Pro-NHMe. <i>Journal of the American Chemical Society</i> , 1983, 105, 4065-4071.	13.7	25
105	Crystallographic Analysis of Rotavirus NSP2-RNA Complex Reveals Specific Recognition of 5' GG Sequence for RTPase Activity. <i>Journal of Virology</i> , 2012, 86, 10547-10557.	3.4	25
106	Identification of the activator-binding residues in the second cysteine-rich regulatory domain of protein kinase C δ (PKC δ). <i>Biochemical Journal</i> , 2013, 451, 33-44.	3.7	25
107	Structural features of glycan recognition among viral pathogens. <i>Current Opinion in Structural Biology</i> , 2017, 44, 211-218.	5.7	25
108	A Single Mutation in the Carboxy Terminus of Reovirus Outer-Capsid Protein σ 3 Confers Enhanced Kinetics of σ 3 Proteolysis, Resistance to Inhibitors of Viral Disassembly, and Alterations in σ 3 Structure. <i>Journal of Virology</i> , 2002, 76, 9832-9843.	3.4	24

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109	Enterococcal Adherence to Human Heparan Sulfate Proteoglycans Drives Segment and Host Specific Responses to Infection. <i>PLoS Pathogens</i> , 2020, 16, e1008851.	4.7	24
110	Structures of Rotavirus Reassortants Demonstrate Correlation of Altered Conformation of the VP4 Spike and Expression of Unexpected VP4-Associated Phenotypes. <i>Journal of Virology</i> , 2003, 77, 3291-3296.	3.4	23
111	Mutagenesis of Zinc Ligand Residue Cys221 Reveals Plasticity in the IMP-1 Metallo- β -Lactamase Active Site. <i>Antimicrobial Agents and Chemotherapy</i> , 2012, 56, 5667-5677.	3.2	22
112	Antibody Responses to Norovirus Genogroup GI.1 and GII.4 Proteases in Volunteers Administered Norwalk Virus. <i>Vaccine Journal</i> , 2012, 19, 1980-1983.	3.1	22
113	Structural Plasticity of the Coiled-Coil Domain of Rotavirus NSP4. <i>Journal of Virology</i> , 2014, 88, 13602-13612.	3.4	22
114	Broadly cross-reactive human antibodies that inhibit genogroup I and II noroviruses. <i>Nature Communications</i> , 2021, 12, 4320.	12.8	21
115	Structural Studies on Gastroenteritis Viruses. <i>Novartis Foundation Symposium</i> , 2008, 238, 26-46.	1.1	20
116	Removal of the Side Chain at the Active-Site Serine by a Glycine Substitution Increases the Stability of a Wide Range of Serine β -Lactamases by Relieving Steric Strain. <i>Biochemistry</i> , 2016, 55, 2479-2490.	2.5	20
117	Synergistic effects of functionally distinct substitutions in β -lactamase variants shed light on the evolution of bacterial drug resistance. <i>Journal of Biological Chemistry</i> , 2018, 293, 17971-17984.	3.4	20
118	TrkA undergoes a tetramer-to-dimer conversion to open TrkH which enables changes in membrane potential. <i>Nature Communications</i> , 2020, 11, 547.	12.8	20
119	Expression of Tobacco Ringspot Virus Capsid Protein and Satellite RNA in Insect Cells and Three-Dimensional Structure of Tobacco Ringspot Virus-like Particles. <i>Virology</i> , 1995, 213, 472-481.	2.4	19
120	Atomic structure of the predominant GII.4 human norovirus capsid reveals novel stability and plasticity. <i>Nature Communications</i> , 2022, 13, 1241.	12.8	19
121	NANOG prion-like assembly mediates DNA bridging to facilitate chromatin reorganization and activation of pluripotency. <i>Nature Cell Biology</i> , 2022, 24, 737-747.	10.3	19
122	Reovirus Variants Selected for Resistance to Ammonium Chloride Have Mutations in Viral Outer-Capsid Protein σ 3. <i>Journal of Virology</i> , 2006, 80, 671-681.	3.4	18
123	Analysis of the Binding Forces Driving the Tight Interactions between β -Lactamase Inhibitory Protein-II (BLIP-II) and Class A β -Lactamases. <i>Journal of Biological Chemistry</i> , 2011, 286, 32723-32735.	3.4	18
124	Mechanistic Basis of OXA-48-like β -Lactamases'™ Hydrolysis of Carbapenems. <i>ACS Infectious Diseases</i> , 2021, 7, 445-460.	3.8	18
125	Synthesis, activity and structure-activity relationship of noroviral protease inhibitors. <i>MedChemComm</i> , 2013, 4, 1354.	3.4	17
126	Reovirus Nonstructural Protein σ NS Acts as an RNA Stability Factor Promoting Viral Genome Replication. <i>Journal of Virology</i> , 2018, 92, .	3.4	17

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127	A cytoskeletal function for PBRM1 reading methylated microtubules. <i>Science Advances</i> , 2021, 7, .	10.3	17
128	Structural basis of the stereoselective formation of the spirooxindole ring in the biosynthesis of citrinadins. <i>Nature Communications</i> , 2021, 12, 4158.	12.8	17
129	Rotavirus structure: interactions between the structural proteins. , 1996, 12, 21-27.		16
130	Identification and Characterization of a Transcription Pause Site in Rotavirus. <i>Journal of Virology</i> , 2001, 75, 1632-1642.	3.4	16
131	Crystallization and preliminary crystallographic analysis of San Miguel sea lion virus: An animal calicivirus. <i>Journal of Structural Biology</i> , 2003, 141, 143-148.	2.8	16
132	2.7 Å... cryo-EM structure of rotavirus core protein VP3, a unique capping machine with a helicase activity. <i>Science Advances</i> , 2020, 6, eaay6410.	10.3	16
133	Glycan Recognition in Human Norovirus Infections. <i>Viruses</i> , 2021, 13, 2066.	3.3	15
134	Crystal structures of diketopiperazines containing β -aminoisobutyric acid: Cyclo(Aib-Aib) and cyclo(Aib-L-Ile). <i>Biopolymers</i> , 1982, 21, 1847-1855.	2.4	14
135	Functionally distinct monomers and trimers produced by a viral oncoprotein. <i>Oncogene</i> , 2008, 27, 1412-1420.	5.9	14
136	Strain-Specific Virolysis Patterns of Human Noroviruses in Response to Alcohols. <i>PLoS ONE</i> , 2016, 11, e0157787.	2.5	14
137	Antagonism between substitutions in β -lactamase explains a path not taken in the evolution of bacterial drug resistance. <i>Journal of Biological Chemistry</i> , 2020, 295, 7376-7390.	3.4	14
138	Local interactions with the Glu166 base and the conformation of an active site loop play key roles in carbapenem hydrolysis by the KPC-2 β -lactamase. <i>Journal of Biological Chemistry</i> , 2021, 296, 100799.	3.4	14
139	A drug-resistant β -lactamase variant changes the conformation of its active-site proton shuttle to alter substrate specificity and inhibitor potency. <i>Journal of Biological Chemistry</i> , 2020, 295, 18239-18255.	3.4	14
140	Molecular structure of a cyclic tetrapeptide disulfide. A novel 310 helical conformation with an S-S bridge. <i>Biochemical and Biophysical Research Communications</i> , 1981, 103, 1138-1144.	2.1	12
141	Teaching electron diffraction and imaging of macromolecules. <i>Biophysical Journal</i> , 1993, 64, 1610-1625.	0.5	12
142	Electron Cryomicroscopy and Computer Image Processing Techniques: Use in Structure-Function Studies of Rotavirus. , 2000, 34, 9-31.		12
143	Carbohydrate-Binding Module and Linker Allow Cold Adaptation and Salt Tolerance of Maltopentaose-Forming Amylase From Marine Bacterium <i>Saccharophagus degradans</i> 2-40T. <i>Frontiers in Microbiology</i> , 2021, 12, 708480.	3.5	12
144	Influenza A Virus Protein NS1 Exhibits Strain-Independent Conformational Plasticity. <i>Journal of Virology</i> , 2019, 93, .	3.4	11

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145	GII.4 Norovirus Protease Shows pH-Sensitive Proteolysis with a Unique Arg-His Pairing in the Catalytic Site. <i>Journal of Virology</i> , 2019, 93, .	3.4	10
146	High-Resolution Mapping of Human Norovirus Antigens via Genomic Phage Display Library Selections and Deep Sequencing. <i>Journal of Virology</i> , 2020, 95, .	3.4	10
147	Novel fold of rotavirus glycan-binding domain predicted by AlphaFold2 and determined by X-ray crystallography. <i>Communications Biology</i> , 2022, 5, 419.	4.4	10
148	Estimation of allowable errors for tilt parameter determination in protein electron crystallography. <i>Ultramicroscopy</i> , 1990, 33, 281-285.	1.9	9
149	Viral Genome Organization. <i>Advances in Protein Chemistry</i> , 2003, 64, 219-258.	4.4	9
150	Serological Responses to a Norovirus Nonstructural Fusion Protein after Vaccination and Infection. <i>Vaccine Journal</i> , 2016, 23, 181-183.	3.1	9
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