BVVenkataram Prasad

List of Publications by Year
in descending order

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	Atomic structure of the predominant GII.4 human norovirus capsid reveals novel stability and plasticity. Nature Communications, 2022, 13, 1241.	12.8	19
2	Antiviral Activity of Olanexidine-Containing Hand Rub against Human Noroviruses. MBio, 2022, 13, e0284821.	4.1	9
3	NANOG prion-like assembly mediates DNA bridging to facilitate chromatin reorganization and activation of pluripotency. Nature Cell Biology, 2022, 24, 737-747.	10.3	19
4	Novel fold of rotavirus glycan-binding domain predicted by AlphaFold2 and determined by X-ray crystallography. Communications Biology, 2022, 5, 419.	4.4	10
5	Cryo-EM Structure of Rotavirus VP3 Reveals Novel Insights into Its Role in RNA Capping and Endogenous Transcription. Springer Proceedings in Materials, 2021, , 211-220.	0.3	0
6	Local interactions with the Glu166 base and the conformation of an active site loop play key roles in carbapenem hydrolysis by the KPC-2 Î²-lactamase. Journal of Biological Chemistry, 2021, 296, 100799.	3.4	14
7	Reoviruses (Reoviridae) and Their Structural Relatives. , 2021, , 303-317.		1
8	Structural and functional dissection of reovirus capsid folding and assembly by the prefoldin-TRiC/CCT chaperone network. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	30
9	A cytoskeletal function for PBRM1 reading methylated microtubules. Science Advances, 2021, 7, .	10.3	17
10	Bile Goes Viral. Viruses, 2021, 13, 998.	3.3	7
11	Broadly cross-reactive human antibodies that inhibit genogroup I and II noroviruses. Nature Communications, 2021, 12, 4320.	12.8	21
12	Carbohydrate-Binding Module and Linker Allow Cold Adaptation and Salt Tolerance of Maltopentaose-Forming Amylase From Marine Bacterium Saccharophagus degradans 2-40T. Frontiers in Microbiology, 2021, 12, 708480.	3.5	12
13	Structural basis of the stereoselective formation of the spirooxindole ring in the biosynthesis of citrinadins. Nature Communications, 2021, 12, 4158.	12.8	17
14	Mechanistic Basis of OXA-48-like Î²-Lactamasesâ€™ Hydrolysis of Carbapenems. ACS Infectious Diseases, 2021, 7, 445-460.	3.8	18
15	Glycan Recognition in Human Norovirus Infections. Viruses, 2021, 13, 2066.	3.3	15
16	Norovirus Protease Structure and Antivirals Development. Viruses, 2021, 13, 2069.	3.3	3
17	Unique Diacidic Fragments Inhibit the OXA-48 Carbapenemase and Enhance the Killing of <i>Escherichia coli</i> Producing OXA-48. ACS Infectious Diseases, 2021, 7, 3345-3354.	3.8	3
18	High-Resolution Mapping of Human Norovirus Antigens via Genomic Phage Display Library Selections and Deep Sequencing. Journal of Virology, 2020, 95, .	3.4	10

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19	Enteroaggregative E. coli Adherence to Human Heparan Sulfate Proteoglycans Drives Segment and Host Specific Responses to Infection. PLoS Pathogens, 2020, 16, e1008851.	4.7	24
20	Structure and mechanism of human diacylglycerol O-acyltransferaseÂ1. Nature, 2020, 581, 329-332.	27.8	72
21	Identifying Oxacillinase-48 Carbapenemase Inhibitors Using DNA-Encoded Chemical Libraries. ACS Infectious Diseases, 2020, 6, 1214-1227.	3.8	27
22	TrkA undergoes a tetramer-to-dimer conversion to open TrkH which enables changes in membrane potential. Nature Communications, 2020, 11, 547.	12.8	20
23	Antagonism between substitutions in Î²-lactamase explains a path not taken in the evolution of bacterial drug resistance. Journal of Biological Chemistry, 2020, 295, 7376-7390.	3.4	14
24	2.7 Ã… cryo-EM structure of rotavirus core protein VP3, a unique capping machine with a helicase activity. Science Advances, 2020, 6, eaay6410.	10.3	16
25	A drug-resistant Î²-lactamase variant changes the conformation of its active-site proton shuttle to alter substrate specificity and inhibitor potency. Journal of Biological Chemistry, 2020, 295, 18239-18255.	3.4	14
26	Title is missing!. , 2020, 16, e1008851.		0
27	Title is missing!. , 2020, 16, e1008851.		0
28	Title is missing!. , 2020, 16, e1008851.		0
29	Title is missing!. , 2020, 16, e1008851.		0
30	Influenza A Virus Protein NS1 Exhibits Strain-Independent Conformational Plasticity. Journal of Virology, 2019, 93, .	3.4	11
31	GII.4 Norovirus Protease Shows pH-Sensitive Proteolysis with a Unique Arg-His Pairing in the Catalytic Site. Journal of Virology, 2019, 93, .	3.4	10
32	Human VP8* mAbs neutralize rotavirus selectively in human intestinal epithelial cells. Journal of Clinical Investigation, 2019, 129, 3839-3851.	8.2	32
33	Human milk oligosaccharides, milk microbiome and infant gut microbiome modulate neonatal rotavirus infection. Nature Communications, 2018, 9, 5010.	12.8	130
34	Phosphorylation cascade regulates the formation and maturation of rotaviral replication factories. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E12015-E12023.	7.1	39
35	Synergistic effects of functionally distinct substitutions in Î²-lactamase variants shed light on the evolution of bacterial drug resistance. Journal of Biological Chemistry, 2018, 293, 17971-17984.	3.4	20
36	Differential active site requirements for NDM-1 Î²-lactamase hydrolysis of carbapenem versus penicillin and cephalosporin antibiotics. Nature Communications, 2018, 9, 4524.	12.8	67

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37	Reovirus Nonstructural Protein ÏƒNS Acts as an RNA Stability Factor Promoting Viral Genome Replication. Journal of Virology, 2018, 92, .	3.4	17
38	Glycan recognition in globally dominant human rotaviruses. Nature Communications, 2018, 9, 2631.	12.8	63
39	The Drug-Resistant Variant P167S Expands the Substrate Profile of CTX-M Î²-Lactamases for Oxyimino-Cephalosporin Antibiotics by Enlarging the Active Site upon Acylation. Biochemistry, 2017, 56, 3443-3453.	2.5	28
40	Structural features of glycan recognition among viral pathogens. Current Opinion in Structural Biology, 2017, 44, 211-218.	5.7	25
41	Structural Biology of Noroviruses. , 2016, , 329-354.		6
42	Strain-Specific Virolysis Patterns of Human Noroviruses in Response to Alcohols. PLoS ONE, 2016, 11, e0157787.	2.5	14
43	Multiple oligomeric structures of a bacterial small heat shock protein. Scientific Reports, 2016, 6, 24019.	3.3	28
44	Removal of the Side Chain at the Active-Site Serine by a Glycine Substitution Increases the Stability of a Wide Range of Serine Î²-Lactamases by Relieving Steric Strain. Biochemistry, 2016, 55, 2479-2490.	2.5	20
45	Structure of the catalytic domain of the colistin resistance enzyme MCR-1. BMC Biology, 2016, 14, 81.	3.8	95
46	Structural basis for norovirus neutralization by an HBGA blocking human IgA antibody. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5830-E5837.	7.1	41
47	Antiviral targets of human noroviruses. Current Opinion in Virology, 2016, 18, 117-125.	5.4	35
48	Diversity in Rotavirusâ€"Host Glycan Interactions: A â€œSweetâ€• Spectrum. Cellular and Molecular Gastroenterology and Hepatology, 2016, 2, 263-273.	4.5	72
49	Serological Responses to a Norovirus Nonstructural Fusion Protein after Vaccination and Infection. Vaccine Journal, 2016, 23, 181-183.	3.1	9
50	Frequent Use of the IgA Isotype in Human B Cells Encoding Potent Norovirus-Specific Monoclonal Antibodies That Block HBGA Binding. PLoS Pathogens, 2016, 12, e1005719.	4.7	27
51	Structural Basis for 2â€²-5â€²-Oligoadenylate Binding and Enzyme Activity of a Viral RNase L Antagonist. Journal of Virology, 2015, 89, 6633-6645.	3.4	28
52	Molecular Basis for the Catalytic Specificity of the CTX-M Extended-Spectrum Î²-Lactamases. Biochemistry, 2015, 54, 447-457.	2.5	50
53	A Triple Mutant in the Î©-loop of TEM-1 Î²-Lactamase Changes the Substrate Profile via a Large Conformational Change and an Altered General Base for Catalysis. Journal of Biological Chemistry, 2015, 290, 10382-10394.	3.4	49
54	Structural Basis for Different Substrate Profiles of Two Closely Related Class D Î²-Lactamases and Their Inhibition by Halogens. Biochemistry, 2015, 54, 3370-3380.	2.5	35

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55	Structural basis of glycan specificity in neonate-specific bovine-human reassortant rotavirus. Nature Communications, 2015, 6, 8346.	12.8	50
56	Quelling an innate response to dsRNA. Oncotarget, 2015, 6, 28535-28536.	1.8	1
57	Editorial overview: virusâ€"glycan interactions and pathogenesis. Current Opinion in Virology, 2014, 7, v-vi.	5.4	0
58	Human Milk Contains Novel Glycans That Are Potential Decoy Receptors for Neonatal Rotaviruses. Molecular and Cellular Proteomics, 2014, 13, 2944-2960.	3.8	113
59	The Influenza A Virus Protein NS1 Displays Structural Polymorphism. Journal of Virology, 2014, 88, 4113-4122.	3.4	69
60	A Novel Form of Rotavirus NSP2 and Phosphorylation-Dependent NSP2-NSP5 Interactions Are Associated with Viroplasm Assembly. Journal of Virology, 2014, 88, 786-798.	3.4	57
61	Development of a Gaussia Luciferase-Based Human Norovirus Protease Reporter System: Cell Type-Specific Profile of Norwalk Virus Protease Precursors and Evaluation of Inhibitors. Journal of Virology, 2014, 88, 10312-10326.	3.4	8
62	Probing the Sites of Interactions of Rotaviral Proteins Involved in Replication. Journal of Virology, 2014, 88, 12866-12881.	3.4	29
63	Structural basis of glycan interaction in gastroenteric viral pathogens. Current Opinion in Virology, 2014, 7, 119-127.	5.4	32
64	Structural Plasticity of the Coiled-Coil Domain of Rotavirus NSP4. Journal of Virology, 2014, 88, 13602-13612.	3.4	22
65	Structural Analysis of Determinants of Histo-Blood Group Antigen Binding Specificity in Genogroup I Noroviruses. Journal of Virology, 2014, 88, 6168-6180.	3.4	47
66	Synthesis, activity and structureâ€"activity relationship of noroviral protease inhibitors. MedChemComm, 2013, 4, 1354.	3.4	17
67	Crystallographic Investigation and Selective Inhibition of Mutant Isocitrate Dehydrogenase. ACS Medicinal Chemistry Letters, 2013, 4, 542-546.	2.8	70
68	Identification of the activator-binding residues in the second cysteine-rich regulatory domain of protein kinase CÎ¸ (PKCÎ¸). Biochemical Journal, 2013, 451, 33-44.	3.7	25
69	Structural Basis of Substrate Specificity and Protease Inhibition in Norwalk Virus. Journal of Virology, 2013, 87, 4281-4292.	3.4	47
70	Norwalk Virus Minor Capsid Protein VP2 Associates within the VP1 Shell Domain. Journal of Virology, 2013, 87, 4818-4825.	3.4	115
71	The VP8* Domain of Neonatal Rotavirus Strain G10P[11] Binds to Type II Precursor Glycans. Journal of Virology, 2013, 87, 7255-7264.	3.4	74
72	Mutagenesis of Zinc Ligand Residue Cys221 Reveals Plasticity in the IMP-1 Metallo-Î²-Lactamase Active Site. Antimicrobial Agents and Chemotherapy, 2012, 56, 5667-5677.	3.2	22

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73	Antibody Responses to Norovirus Genogroup GI.1 and GII.4 Proteases in Volunteers Administered Norwalk Virus. Vaccine Journal, 2012, 19, 1980-1983.	3.1	22
74	Crystallographic Analysis of Rotavirus NSP2-RNA Complex Reveals Specific Recognition of 5â€² GG Sequence for RTPase Activity. Journal of Virology, 2012, 86, 10547-10557.	3.4	25
75	Principles of Virus Structural Organization. Advances in Experimental Medicine and Biology, 2012, 726, 17-47.	1.6	124
76	Rotavirus non-structural proteins: structure and function. Current Opinion in Virology, 2012, 2, 380-388.	5.4	63
77	Cell attachment protein VP8* of a human rotavirus specifically interacts with A-type histo-blood group antigen. Nature, 2012, 485, 256-259.	27.8	283
78	Prestress Strengthens the Shell of Norwalk Virus Nanoparticles. Nano Letters, 2011, 11, 4865-4869.	9.1	55
79	Selective Inhibitors of Histone Methyltransferase DOT1L: Design, Synthesis, and Crystallographic Studies. Journal of the American Chemical Society, 2011, 133, 16746-16749.	13.7	144
80	Inhibition of 1-Deoxy-<scp>d</scp>-Xylulose-5-Phosphate Reductoisomerase by Lipophilic Phosphonates: SAR, QSAR, and Crystallographic Studies. Journal of Medicinal Chemistry, 2011, 54, 4721-4734.	6.4	59
81	Structural Analysis of Histo-Blood Group Antigen Binding Specificity in a Norovirus GII.4 Epidemic Variant: Implications for Epochal Evolution. Journal of Virology, 2011, 85, 8635-8645.	3.4	138
82	Analysis of the Binding Forces Driving the Tight Interactions between Î²-Lactamase Inhibitory Protein-II (BLIP-II) and Class A Î²-Lactamases. Journal of Biological Chemistry, 2011, 286, 32723-32735.	3.4	18
83	Norwalk Virus Assembly and Stability Monitored by Mass Spectrometry. Molecular and Cellular Proteomics, 2010, 9, 1742-1751.	3.8	118
84	Conformational Changes in the Capsid of a Calicivirus upon Interaction with Its Functional Receptor. Journal of Virology, 2010, 84, 5550-5564.	3.4	57
85	Rotavirus Cell Entry. Current Topics in Microbiology and Immunology, 2010, 343, 121-148.	1.1	37
86	Rotavirus Architecture at Subnanometer Resolution. Journal of Virology, 2009, 83, 1754-1766.	3.4	106
87	Structural and Biochemical Evidence That a TEM-1 Î²-Lactamase N170G Active Site Mutant Acts via Substrate-assisted Catalysis. Journal of Biological Chemistry, 2009, 284, 33703-33712.	3.4	45
88	X-ray structure of NS1 from a highly pathogenic H5N1 influenza virus. Nature, 2008, 456, 985-988.	27.8	132
89	Functionally distinct monomers and trimers produced by a viral oncoprotein. Oncogene, 2008, 27, 1412-1420.	5.9	14
90	Functional Maturation of the Human Antibody Response to Rotavirus. Journal of Immunology, 2008, 180, 3980-3989.	0.8	33

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91	Atomic resolution structural characterization of recognition of histo-blood group antigens by Norwalk virus. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9175-9180.	7.1	236
92	Structural Studies on Gastroenteritis Viruses. Novartis Foundation Symposium, 2008, 238, 26-46.	1.1	20
93	A New Crucial Protein Interaction Element That Targets the Adenovirus E4-ORF1 Oncoprotein to Membrane Vesicles. Journal of Virology, 2007, 81, 4787-4797.	3.4	30
94	Crystallographic and Biochemical Analysis of Rotavirus NSP2 with Nucleotides Reveals a Nucleoside Diphosphate Kinase-Like Activity. Journal of Virology, 2007, 81, 12272-12284.	3.4	39
95	Rotavirus Proteins: Structure and Assembly. , 2006, 309, 189-219.		128
96	Noroviruses everywhere: has something changed?. Current Opinion in Infectious Diseases, 2006, 19, 467-474.	3.1	182
97	X-ray structure of influenza virus NS1 effector domain. Nature Structural and Molecular Biology, 2006, 13, 559-560.	8.2	93
98	Cryoelectron Microscopy Structures of Rotavirus NSP2-NSP5 and NSP2-RNA Complexes: Implications for Genome Replication. Journal of Virology, 2006, 80, 10829-10835.	3.4	66
99	X-Ray Crystallographic Structure of the Norwalk Virus Protease at 1.5-AÌŠ Resolution. Journal of Virology, 2006, 80, 5050-5058.	3.4	88
100	Reovirus Variants Selected for Resistance to Ammonium Chloride Have Mutations in Viral Outer-Capsid Protein Ïƒ3. Journal of Virology, 2006, 80, 671-681.	3.4	18
101	Structure-Function Analysis of Rotavirus NSP2 Octamer by Using a Novel Complementation System. Journal of Virology, 2006, 80, 7984-7994.	3.4	49
102	X-Ray Structures of the N- and C-Terminal Domains of a Coronavirus Nucleocapsid Protein: Implications for Nucleocapsid Formation. Journal of Virology, 2006, 80, 6612-6620.	3.4	120
103	High-Resolution Molecular and Antigen Structure of the VP8* Core of a Sialic Acid-Independent Human Rotavirus Strain. Journal of Virology, 2006, 80, 1513-1523.	3.4	77
104	X-ray structure of a native calicivirus: Structural insights into antigenic diversity and host specificity. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 8048-8053.	7.1	159
105	pH-Induced Conformational Change of the Rotavirus VP4 Spike: Implications for Cell Entry and Antibody Neutralization. Journal of Virology, 2005, 79, 8572-8580.	3.4	30
106	Evolutionary Trace Residues in Noroviruses: Importance in Receptor Binding, Antigenicity, Virion Assembly, and Strain Diversity. Journal of Virology, 2005, 79, 554-568.	3.4	80
107	Inter- and Intragenus Structural Variations in Caliciviruses and Their Functional Implications. Journal of Virology, 2004, 78, 6469-6479.	3.4	122
108	Role of the Histidine Triad-like Motif in Nucleotide Hydrolysis by the Rotavirus RNA-packaging Protein NSP2. Journal of Biological Chemistry, 2004, 279, 10624-10633.	3.4	36

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109	Interactions between the Inner and Outer Capsids of Bluetongue Virus. Journal of Virology, 2004, 78, 8059-8067.	3.4	91
110	Structural rearrangements in the membrane penetration protein of a non-enveloped virus. Nature, 2004, 430, 1053-1058.	27.8	200
111	Macromolecular assemblages â€" putting the pieces together. Current Opinion in Structural Biology, 2004, 14, 117-120.	5.7	4
112	Emerging themes in rotavirus cell entry, genome organization, transcription and replication. Virus Research, 2004, 101, 67-81.	2.2	116
113	Viral Genome Organization. Advances in Protein Chemistry, 2003, 64, 219-258.	4.4	9
114	II, 1. Structural organization of the genome in rotavirus. Perspectives in Medical Virology, 2003, 9, 115-127.	0.1	5
115	Crystallization and preliminary crystallographic analysis of San Miguel sea lion virus: An animal calicivirus. Journal of Structural Biology, 2003, 141, 143-148.	2.8	16
116	Structures of Rotavirus Reassortants Demonstrate Correlation of Altered Conformation of the VP4 Spike and Expression of Unexpected VP4-Associated Phenotypes. Journal of Virology, 2003, 77, 3291-3296.	3.4	23
117	IV, 1. Structure of norwalk virus: the prototype human calicivirus. Perspectives in Medical Virology, 2003, 9, 455-466.	0.1	2
118	A Single Mutation in the Carboxy Terminus of Reovirus Outer-Capsid Protein Ïƒ3 Confers Enhanced Kinetics of Ïƒ3 Proteolysis, Resistance to Inhibitors of Viral Disassembly, and Alterations in Ïƒ3 Structure. Journal of Virology, 2002, 76, 9832-9843.	3.4	24
119	Structural Requirements for the Assembly of Norwalk Virus-Like Particles. Journal of Virology, 2002, 76, 4044-4055.	3.4	175
120	Rotavirus protein involved in genome replication and packaging exhibits a HIT-like fold. Nature, 2002, 417, 311-315.	27.8	93
121	Inhibition of rotavirus replication by a non-neutralizing, rotavirus VP6â€"specific IgA mAb. Journal of Clinical Investigation, 2002, 109, 1203-1213.	8.2	148
122	Atomic structure of the major capsid protein of rotavirus: implications for the architecture of the virion. EMBO Journal, 2001, 20, 1485-1497.	7.8	172
123	A Monoclonal Antibody Specific for Reovirus Outer-Capsid Protein Ï,3 Inhibits Ï,1-Mediated Hemagglutination by Steric Hindrance. Journal of Virology, 2001, 75, 6625-6634.	3.4	33
124	The reversible condensation and expansion of the rotavirus genome. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 1381-1386.	7.1	46
125	Identification and Characterization of a Transcription Pause Site in Rotavirus. Journal of Virology, 2001, 75, 1632-1642.	3.4	16
126	Trypsin Cleavage Stabilizes the Rotavirus VP4 Spike. Journal of Virology, 2001, 75, 6052-6061.	3.4	128

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127	Trypsin-Induced Structural Transformation in Aquareovirus. Journal of Virology, 2000, 74, 6546-6555.	3.4	55
128	Structural Studies of Recombinant Norwalk Capsids. Journal of Infectious Diseases, 2000, 181, S317-S321.	4.0	41
129	Mechanism of genome transcription in segmented dsRNA viruses. Advances in Virus Research, 2000, 55, 185-229.	2.1	82
130	Electron Cryomicroscopy and Computer Image Processing Techniques: Use in Structure-Function Studies of Rotavirus. , 2000, 34, 9-31.		12
131	Comparative structural analysis of transcriptionally competent and incompetent rotavirus-antibody complexes. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 5428-5433.	7.1	44
132	The structure of a cypovirus and the functional organization of dsRNA viruses. Nature Structural Biology, 1999, 6, 565-568.	9.7	129
133	X-ray Crystallographic Structure of the Norwalk Virus Capsid. Science, 1999, 286, 287-290.	12.6	820
134	Towards Understanding the Structural Requirements for Endogenous Transcription in Rotavirus. Microscopy and Microanalysis, 1998, 4, 1050-1051.	0.4	0
135	Structural Localization of the E3 Glycoprotein in Attenuated Sindbis Virus Mutants. Journal of Virology, 1998, 72, 1534-1541.	3.4	50
136	Towards Understanding the Structural Basis of Endogenous Transcription in dsRNA Viruses. Microscopy and Microanalysis, 1997, 3, 89-90.	0.4	0
137	Three-dimensional visualization of mRNA release from actively transcribing rotavirus particles. Nature Structural Biology, 1997, 4, 118-121.	9.7	195
138	An atomic model of the outer layer of the bluetongue virus core derived from X-ray crystallography and electron cryomicroscopy. Structure, 1997, 5, 885-893.	3.3	114
139	Three-dimensional Structure of Scaffolding-containing Phage P22 Procapsids by Electron Cryo-microscopy. Journal of Molecular Biology, 1996, 260, 85-98.	4.2	97
140	Automated Software Package for Icosahedral Virus Reconstruction. Journal of Structural Biology, 1996, 116, 209-215.	2.8	40
141	The structure of aquareovirus shows how the different geometries of the two layers of the capsid are reconciled to provide symmetrical interactions and stabilization. Structure, 1996, 4, 957-967.	3.3	89
142	Visualization of ordered genomic RNA and localization of transcriptional complexes in rotavirus. Nature, 1996, 382, 471-473.	27.8	219
143	Rotavirus structure: interactions between the structural proteins. , 1996, 12, 21-27.		16
144	Expression of Tobacco Ringspot Virus Capsid Protein and Satellite RNA in Insect Cells and Three-Dimensional Structure of Tobacco Ringspot Virus-like Particles. Virology, 1995, 213, 472-481.	2.4	19

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145	Characterization of Rotavirus VP2 Particles. Virology, 1994, 201, 55-65.	2.4	66
146	Three-dimensional Structure of Calicivirus. Journal of Molecular Biology, 1994, 240, 256-264.	4.2	108
147	Protein Subunit Structures in the Herpes Simplex Virus A-capsid Determined from 400 kV Spot-scan Electron Cryomicroscopy. Journal of Molecular Biology, 1994, 242, 456-469.	4.2	187
148	Structure of Rotavirus. Current Topics in Microbiology and Immunology, 1994, 185, 9-29.	1.1	66
149	Three-dimensional Transformation of Capsids Associated with Genome Packaging in a Bacterial Virus. Journal of Molecular Biology, 1993, 231, 65-74.	4.2	163
150	Three-dimensional visualization of the rotavirus hemagglutinin structure. Cell, 1993, 74, 693-701.	28.9	151
151	Proposed mechanisms for binding of apo[a] kringle type 9 to apo B-100 in human lipoprotein[a]. Biophysical Journal, 1993, 64, 686-700.	0.5	65
152	Teaching electron diffraction and imaging of macromolecules. Biophysical Journal, 1993, 64, 1610-1625.	0.5	12
153	Three-dimensional structure of a membrane-containing virus.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 9095-9099.	7.1	205
154	Visualization and Characterization of Tobacco Mosaic Virus Movement Protein Binding to Single-Stranded Nucleic Acids. Plant Cell, 1992, 4, 397.	6.6	2
155	Method for calculating 3-D coordinates from molecular stereograms. The Protein Journal, 1992, 11, 653-656.	1.1	1
156	Localization of VP4 neutralization sites in rotavirus by three-dimensional cryo-electron microscopy. Nature, 1990, 343, 476-479.	27.8	246
157	Estimation of allowable errors for tilt parameter determination in protein electron crystallography. Ultramicroscopy, 1990, 33, 281-285.	1.9	9
158	Three-dimensional structure of the HSV1 nucleocapsid. Cell, 1989, 56, 651-660.	28.9	164
159	Three-dimensional structure of rotavirus. Journal of Molecular Biology, 1988, 199, 269-275.	4.2	363
160	Sequence comparison of single-stranded DNA binding proteins and its structural implications. Journal of Molecular Biology, 1987, 193, 579-584.	4.2	80
161	Cryo electron microscopy of spherical viruses: An application to rotaviruses. Micron and Microscopica Acta, 1987, 18, 327-331.	0.2	3
162	Potential for High-Resolution Electron Crystallography at Intermediate High Voltage. Annals of the New York Academy of Sciences, 1986, 483, 149-156.	3.8	7

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163	The Stereochemistry of Peptides Containing Î±-Aminoisobutyric Aci. Critical Reviews in Biochemistry, 1984, 16, 307-348.	7.5	332
164	Acyclic peptides as conformational models. International Journal of Peptide and Protein Research, 1984, 24, 135-140.	0.1	3
165	Multiple conformational states of a Pro-Pro peptide. Solid-state and solution conformations of Boc-Aib-Pro-Pro-NHMe. Journal of the American Chemical Society, 1983, 105, 4065-4071.	13.7	25
166	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. Journal of the American Chemical Society, 1983, 105, 105-109.	13.7	85
167	X-Pro peptides. A theoretical study of the hydrogen bonded conformations of (Î±-aminoisobutyryl-l-prolyl)n sequences. International Journal of Biological Macromolecules, 1982, 4, 99-102.	7.5	39
168	Conformational analysis of small disulfide loops. Spectroscopic and theoretical studies on a synthetic cyclic tetrapeptide containing cystine. Biochemistry, 1982, 21, 5502-5509.	2.5	51
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170	Crystal structures of diketopiperazines containing ?-aminoisobutyric acid: Cyclo(Aib-Aib) and cyclo(Aib-L-Ile). Biopolymers, 1982, 21, 1847-1855.	2.4	14
171	Molecular structure of a cyclic tetrapeptide disulfide. A novel 310 helical conformation with an S-S bridge. Biochemical and Biophysical Research Communications, 1981, 103, 1138-1144.	2.1	12
172	The crystal structure of benzyloxycarbonyl-(Î±-aminoisobutyryl)2-L-alanyl methyl ester. Acta Crystallographica Section B: Structural Crystallography and Crystal Chemistry, 1980, 36, 107-110.	0.4	26
173	Crystal and molecular structure of benzyloxycarbonyl-?-aminoisobutyryl-L-prolyl methylamide: The observation of anX2-Pro3 Type III ?-Turn. Biopolymers, 1979, 18, 1635-1646.	2.4	70
174	A Case Study of the Conformation of Poly(Î±-aminoisobutyric acid): Î±- or 310-Helix. Macromolecules, 1979, 12, 1107-1110.	4.8	53