Peter G Stockley

List of Publications by Year
in descending order

156 papers	6,895 citations	57758 44 h-index	74163 75 g-index
167 all docs	167 docs citations	167 times ranked	6023 citing authors

#	Article	IF	Citations
1	An age-structured model of hepatitis B viral infection highlights the potential of different therapeutic strategies. Scientific Reports, 2022, 12, 1252.	3.3	9
2	Dysregulation of Hepatitis B Virus Nucleocapsid Assembly in vitro by RNA-binding Small Ligands. Journal of Molecular Biology, 2022, 434, 167557.	4.2	6
3	Dataset of high-throughput ligand screening against the RNA Packaging Signals regulating Hepatitis B Virus nucleocapsid formation. Data in Brief, 2022, 42, 108206.	1.0	0
4	Genome Packaging. , 2021, , 488-494.		0
5	Single-Stranded RNA Bacterial Viruses. , 2021, , 21-25.		0
6	Evolution of a virus-like architecture and packaging mechanism in a repurposed bacterial protein. Science, 2021, 372, 1220-1224.	12.6	53
7	Comparing antiviral strategies against COVID-19 via multiscale within-host modelling. Royal Society Open Science, 2021, 8, 210082.	2.4	17
8	An Intracellular Model of Hepatitis B Viral Infection: An In Silico Platform for Comparing Therapeutic Strategies. Viruses, 2021, 13, 11.	3.3	13
9	In vitro functional analysis of gRNA sites regulating assembly of hepatitis B virus. Communications Biology, 2021, 4, 1407.	4.4	6
10	Therapeutic interfering particles exploiting viral replication and assembly mechanisms show promising performance: a modelling study. Scientific Reports, 2021, 11, 23847.	3.3	1
11	Viral Genome Conformations and Contacts across Different Lifecycle Stages. Proceedings (mdpi), 2020, 50, .	0.2	0
12	Conservation of Genetically-Embedded Virus Assembly Instructions: A Novel Route to Antiviral Therapy. Proceedings (mdpi), 2020, 50, 87.	0.2	0
13	Broadly Neutralizing Bovine Antibodies: Highly Effective New Tools against Evasive Pathogens?. Viruses, 2020, 12, 473.	3.3	10
14	Assembly of infectious enteroviruses depends on multiple, conserved genomic RNA-coat protein contacts. PLoS Pathogens, 2020, 16, e1009146.	4.7	31
15	Structural characterization of genomic RNA-coat protein contacts in single-stranded RNA viruses by high-resolution cryo-EM. Access Microbiology, 2020, 2, .	0.5	0
16	Cut-and-Run: A Distinct Mechanism by which V(D)J Recombination Causes Genome Instability. Molecular Cell, 2019, 74, 584-597.e9.	9.7	20
17	RNA-Mediated Virus Assembly: Mechanisms and Consequences for Viral Evolution and Therapy. Annual Review of Biophysics, 2019, 48, 495-514.	10.0	54
18	A modelling paradigm for RNA virus assembly. Current Opinion in Virology, 2018, 31, 74-81.	5.4	62

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19	Hamiltonian path analysis of viral genomes. Nature Communications, 2018, 9, 2021.	12.8	30
20	HBV RNA pre-genome encodes specific motifs that mediate interactions with the viral core protein that promote nucleocapsid assembly. Nature Microbiology, 2017, 2, 17098.	13.3	69
21	Genomic RNA folding mediates assembly of human parechovirus. Nature Communications, 2017, 8, 5.	12.8	67
22	Rewriting natureâ€™s assembly manual for a ssRNA virus. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12255-12260.	7.1	47
23	Direct Evidence for Packaging Signal-Mediated Assembly of Bacteriophage MS2. Journal of Molecular Biology, 2016, 428, 431-448.	4.2	80
24	Sizes of Long RNA Molecules Are Determined by the Branching Patterns of Their Secondary Structures. Biophysical Journal, 2016, 111, 2077-2085.	0.5	53
25	Bacteriophage MS2 genomic RNA encodes an assembly instruction manual for its capsid. Bacteriophage, 2016, 6, e1157666.	1.9	38
26	Mutations in RNA Polymerase Bridge Helix and Switch Regions Affect Active-Site Networks and Transcript-Assisted Hydrolysis. Journal of Molecular Biology, 2015, 427, 3516-3526.	4.2	6
27	Evidence that avian reovirus ÏƒNS is an RNA chaperone: implications for genome segment assortment. Nucleic Acids Research, 2015, 43, 7044-7057.	14.5	26
28	Trivalent Gd-DOTA reagents for modification of proteins. RSC Advances, 2015, 5, 96194-96200.	3.6	9
29	Revealing the density of encoded functions in a viral RNA. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2227-2232.	7.1	64
30	Asymmetric Genome Organization in an RNA Virus Revealed via Graph-Theoretical Analysis of Tomographic Data. PLoS Computational Biology, 2015, 11, e1004146.	3.2	12
31	The Influence of Twoâ€Dimensional Organization on Peptide Conformation. Angewandte Chemie - International Edition, 2015, 54, 974-978.	13.8	20
32	Revised Morning Loops of the Arabidopsis Circadian Clock Based on Analyses of Direct Regulatory Interactions. PLoS ONE, 2015, 10, e0143943.	2.5	90
33	Distinguishing Closely Related Amyloid Precursors Using an RNA Aptamer. Journal of Biological Chemistry, 2014, 289, 26859-26871.	3.4	7
34	Domain movements of the enhancer-dependent sigma factor drive DNA delivery into the RNA polymerase active site: insights from single molecule studies. Nucleic Acids Research, 2014, 42, 5177-5190.	14.5	24
35	Solving a Levinthal's paradox for virus assembly identifies a unique antiviral strategy. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 5361-5366.	7.1	102
36	Oncogene dependency and the potential of targeted RNAi-based anti-cancer therapy. Biochemical Journal, 2014, 461, 1-13.	3.7	18

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37	Limits of Structural Plasticity in a Picornavirus Capsid Revealed by a Massively Expanded Equine Rhinitis A Virus Particle. Journal of Virology, 2014, 88, 6093-6099.	3.4	20
38	Packaging signals in single-stranded RNA viruses: natureâ€™s alternative to a purely electrostatic assembly mechanism. Journal of Biological Physics, 2013, 39, 277-287.	1.5	86
39	Packaging Signals in Two Single-Stranded RNA Viruses Imply a Conserved Assembly Mechanism and Geometry of the Packaged Genome. Journal of Molecular Biology, 2013, 425, 3235-3249.	4.2	80
40	Sequence-Specific, RNAâ€"Protein Interactions Overcome Electrostatic Barriers Preventing Assembly of Satellite Tobacco Necrosis Virus Coat Protein. Journal of Molecular Biology, 2013, 425, 1050-1064.	4.2	50
41	The Asymmetric Structure of an Icosahedral Virus Bound to Its Receptor Suggests a Mechanism for Genome Release. Structure, 2013, 21, 1225-1234.	3.3	61
42	A new paradigm for the roles of the genome in ssRNA viruses. Future Virology, 2013, 8, 531-543.	1.8	18
43	MS2 Viruslike Particles: A Robust, Semisynthetic Targeted Drug Delivery Platform. Molecular Pharmaceutics, 2013, 10, 59-68.	4.6	113
44	Assessing the causes and consequences of co-polymerization in amyloid formation. Prion, 2013, 7, 359-368.	1.8	42
45	Expanding the Repertoire of Amyloid Polymorphs by Co-polymerization of Related Protein Precursors. Journal of Biological Chemistry, 2013, 288, 7327-7337.	3.4	36
46	Structural constraints on the three-dimensional geometry of simple viruses: case studies of a new predictive tool. Acta Crystallographica Section A: Foundations and Advances, 2013, 69, 140-150.	0.3	25
47	Building a viral capsid in the presence of genomic RNA. Physical Review E, 2013, 87, 022717.	2.1	45
48	A two-stage mechanism of viral RNA compaction revealed by single molecule fluorescence. RNA Biology, 2013, 10, 481-489.	3.1	47
49	Evidence that viral RNAs have evolved for efficient, two-stage packaging. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 15769-15774.	7.1	131
50	Directed surface attachment of nanomaterials via coiled-coil-driven self-assembly. Nanotechnology, 2012, 23, 495304.	2.6	7
51	Toggled RNA Aptamers Against Aminoglycosides Allowing Facile Detection of Antibiotics Using Gold Nanoparticle Assays. Analytical Chemistry, 2012, 84, 6595-6602.	6.5	85
52	Isolation of an Asymmetric RNA Uncoating Intermediate for a Single-Stranded RNA Plant Virus. Journal of Molecular Biology, 2012, 417, 65-78.	4.2	30
53	CHAPTER 6. Therapeutic Applications of Nucleic Acid Aptamer Conjugates. RSC Biomolecular Sciences, 2012, , 140-165.	0.4	0
54	On-Surface Assembly of Coiled-Coil Heterodimers. Langmuir, 2012, 28, 13877-13882.	3.5	7

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55	Design, synthesis and in vitro evaluation of novel bivalent S-adenosylmethionine analogues. Bioorganic and Medicinal Chemistry Letters, 2012, 22, 278-284.	2.2	9
56	Development of smart nanoparticleâ€"aptamer sensing technology. Faraday Discussions, 2011, 149, 319-332.	3.2	25
57	Visualising a Viral RNA Genome Poised for Release from Its Receptor Complex. Journal of Molecular Biology, 2011, 408, 408-419.	4.2	36
58	Construction and Crystal Structure of Recombinant STNV Capsids. Journal of Molecular Biology, 2011, 413, 41-50.	4.2	38
59	Degenerate RNA Packaging Signals in the Genome of Satellite Tobacco Necrosis Virus: Implications for the Assembly of a T= 1 Capsid. Journal of Molecular Biology, 2011, 413, 51-65.	4.2	65
60	Determining the topology of virus assembly intermediates using ion mobility spectrometryâ€"mass spectrometry. Rapid Communications in Mass Spectrometry, 2010, 24, 3033-3042.	1.5	81
61	The physics of virus assembly. Physical Biology, 2010, 7, 040301.	1.8	1
62	Viral Genomic Single-Stranded RNA Directs the Pathway Toward a T=3 Capsid. Journal of Molecular Biology, 2010, 395, 924-936.	4.2	60
63	Mutually-induced Conformational Switching of RNA and Coat Protein Underpins Efficient Assembly of a Viral Capsid. Journal of Molecular Biology, 2010, 401, 309-322.	4.2	37
64	The Impact of Viral RNA on Assembly Pathway Selection. Journal of Molecular Biology, 2010, 401, 298-308.	4.2	64
65	Development of aptamer therapeutics. Current Opinion in Pharmacology, 2010, 10, 557-562.	3.5	130
66	RNA-induced conformational changes in a viral coat protein studied by hydrogen/deuterium exchange mass spectrometry. Physical Chemistry Chemical Physics, 2010, 12, 13468.	2.8	18
67	Emerging Topics in Physical Virology. , 2010, , .		15
68	Cryo-Electron Microscopy of Viruses. , 2010, , 1-33.		1
69	Characterization of RNA aptamers that disrupt the RUNX1â€"CBFÎ²/DNA complex. Nucleic Acids Research, 2009, 37, 6818-6830.	14.5	20
70	Conformational flexibility and molecular interactions of an archaeal homologue of the Shwachman-Bodian-Diamond syndrome protein. BMC Structural Biology, 2009, 9, 32.	2.3	27
71	Filter-Binding Assays. Methods in Molecular Biology, 2009, 543, 1-14.	0.9	17
72	Synthesis, molecular structure and evaluation of new organometallic ruthenium anticancer agents. Dalton Transactions, 2009, , 10914.	3.3	45

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73	Identification of stable S-adenosylmethionine (SAM) analogues derivatised with bioorthogonal tags: effect of ligands on the affinity of the E. colimethionine repressor, MetJ, for its operator DNA. Organic and Biomolecular Chemistry, 2009, 7, 635-638.	2.8	18
74	Surface Plasmon Resonance Assays of DNA-Protein Interactions. Methods in Molecular Biology, 2009, 543, 653-669.	0.9	23
75	Ethylation Interference Footprinting of DNA-Protein Complexes. Methods in Molecular Biology, 2009, 543, 105-120.	0.9	4
76	Insights into virus capsid assembly from nonâ€covalent mass spectrometry. Mass Spectrometry Reviews, 2008, 27, 575-595.	5.4	47
77	Modus operandi of the bacterial RNA polymerase containing the Ïƒ⁵⁴ promoterâ€specificity factor. Molecular Microbiology, 2008, 68, 538-546.	2.5	118
78	Structural Insights into the Polymorphism of Amyloid-Like Fibrils Formed by Region 20âˆ'29 of Amylin Revealed by Solid-State NMR and X-ray Fiber Diffraction. Journal of the American Chemical Society, 2008, 130, 14990-15001.	13.7	177
79	The Three-dimensional Structure of Genomic RNA in Bacteriophage MS2: Implications for Assembly. Journal of Molecular Biology, 2008, 375, 824-836.	4.2	105
80	Structure and Function of the Arginine Repressor-Operator Complex from Bacillus subtilis. Journal of Molecular Biology, 2008, 379, 284-298.	4.2	29
81	Single-Molecule Fluorescence Resonance Energy Transfer Assays Reveal Heterogeneous Folding Ensembles in a Simple RNA Stemâ€"Loop. Journal of Molecular Biology, 2008, 384, 264-278.	4.2	28
82	RNA Packing Specificity and Folding during Assembly of the Bacteriophage MS2. Computational and Mathematical Methods in Medicine, 2008, 9, 339-349.	1.3	12
83	Visualizing the organization and reorganization of transcription complexes for gene expression. Biochemical Society Transactions, 2008, 36, 776-779.	3.4	4
84	A Simple, RNA-Mediated Allosteric Switch Controls the Pathway to Formation of a T=3 Viral Capsid. Journal of Molecular Biology, 2007, 369, 541-552.	4.2	128
85	Production and Characterization of RNA Aptamers Specific for Amyloid Fibril Epitopes. Journal of Biological Chemistry, 2007, 282, 34500-34509.	3.4	37
86	Scanning conformational space with a library of stereo- and regiochemically diverse aminoglycoside derivatives: the discovery of new ligands for RNA hairpin sequences. Organic and Biomolecular Chemistry, 2007, 5, 1081.	2.8	22
87	A high-resolution structure of the DNA-binding domain of AhrC, the arginine repressor/activator protein fromBacillus subtilis. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 914-917.	0.7	15
88	Structure of the C-terminal effector-binding domain of AhrC bound to its corepressor<scp>L</scp>-arginine. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 918-921.	0.7	16
89	The Organization of Aromatic Side Groups in an Amyloid Fibril Probed by Solid-State 2H and 19F NMR Spectroscopy. Journal of the American Chemical Society, 2006, 128, 8098-8099.	13.7	37
90	New Insights into the Interaction of Ribosomal Protein L1 with RNA. Journal of Molecular Biology, 2006, 355, 747-759.	4.2	40

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91	Transcript analysis reveals an extended regulon and the importance of proteinâ€"protein co-operativity for the Escherichia coli methionine repressor. Biochemical Journal, 2006, 396, 227-234.	3.7	43
92	Aptamers come of age â€" at last. Nature Reviews Microbiology, 2006, 4, 588-596.	28.6	662
93	Structural Basis of RNA Binding Discrimination between Bacteriophages QÎ² and MS2. Structure, 2006, 14, 487-495.	3.3	47
94	Delivery of antisense oligonucleotides to leukemia cells by RNA bacteriophage capsids. Nanomedicine: Nanotechnology, Biology, and Medicine, 2005, 1, 67-76.	3.3	78
95	Engineering Thermal Stability in RNA Phage Capsids via Disulphide Bonds. Journal of Nanoscience and Nanotechnology, 2005, 5, 2034-2041.	0.9	64
96	Mathematical Virology. Journal of Theoretical Medicine, 2005, 6, 67-68.	0.5	1
97	Asymmetric double ring-opening of a C2h-symmetric bis-epoxide: improved enantiomeric excess of the product through enantioselective desymmetrisation and â€˜proof-readingâ€™ steps. Organic and Biomolecular Chemistry, 2005, 3, 2350.	2.8	6
98	Synthesis of a library of stereo- and regiochemically diverse aminoglycoside derivatives. Organic and Biomolecular Chemistry, 2005, 3, 2776.	2.8	16
99	The crystal structure of a high affinity RNA stem-loop complexed with the bacteriophage MS2 capsid: Further challenges in the modeling of ligand-RNA interactions. Rna, 2004, 10, 1776-1782.	3.5	56
100	New tertiary constraints between the RNA components of active yeast spliceosomes: A photo-crosslinking study. Rna, 2004, 10, 1251-1265.	3.5	18
101	Kinetic analysis of operator binding by theE. colimethionine repressor highlights the role(s) of electrostatic interactions. FEBS Letters, 2004, 564, 136-142.	2.8	12
102	A biaryl peptide crosslink in a MetJ peptide model confers cooperative, nonspecific binding to DNA that ablates both repressor binding and In vitro transcription. Bioorganic and Medicinal Chemistry, 2003, 11, 811-816.	3.0	5
103	Investigating the structural basis of purine specificity in the structures of MS2 coat protein RNA translational operator hairpins. Nucleic Acids Research, 2002, 30, 2678-2685.	14.5	34
104	RNA Bacteriophage Capsid-Mediated Drug Delivery and Epitope Presentation. Intervirology, 2002, 45, 371-380.	2.8	89
105	Structural and Functional Studies of an Intermediate on the Pathway to Operator Binding by Escherichia coli MetJ. Journal of Molecular Biology, 2002, 320, 39-53.	4.2	18
106	An improved Western blotting technique effectively reduces background. Electrophoresis, 2002, 23, 2373-2376.	2.4	66
107	An improved Western blotting technique effectively reduces background. , 2002, 23, 2373.		1
108	Filter-Binding Assays. , 2001, 148, 001-011.		3

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109	Probing the kinetics of formation of the bacteriophage MS2 translational operator complex: identification of a protein conformer unable to bind RNA. Journal of Molecular Biology, 2001, 305, 1131-1144.	4.2	45
110	Ethylation Interference. , 2001, 148, 229-243.		0
111	Ribosome-mediated refolding of partially-unfolded ricin A-chain. Biochemical Society Transactions, 2000, 28, A68-A68.	3.4	0
112	Ribosome-mediated Folding of Partially Unfolded Ricin A-chain. Journal of Biological Chemistry, 2000, 275, 9263-9269.	3.4	105
113	[34] Use of fusions to viral coat proteins as antigenic carriers for vaccine development. Methods in Enzymology, 2000, 326, 551-569.	1.0	8
114	RNA aptamers for the MS2 bacteriophage coat protein and the wild-type RNA operator have similar solution behaviour. Nucleic Acids Research, 2000, 28, 489-497.	14.5	32
115	Crystallographic studies of RNA hairpins in complexes with recombinant MS2 capsids: Implications for binding requirements. Rna, 1999, 5, 131-138.	3.5	34
116	Secondary Structure Mapping of an RNA Ligand That Has High Affinity for the MetJ Repressor Protein and Interference Modification Analysis of the Protein-RNA Complex. Journal of Biological Chemistry, 1999, 274, 2255-2262.	3.4	12
117	Expression and immunogenicity of a liver stage malaria epitope presented as a foreign peptide on the surface of RNA-free MS2 bacteriophage capsids. Vaccine, 1999, 18, 251-258.	3.8	27
118	Probing Activation of the Prokaryotic Arginine Transcriptional Regulator Using Chimeric Proteins. Journal of Molecular Biology, 1999, 289, 707-727.	4.2	28
119	Crystal structures of a series of RNA aptamers complexed to the same protein target. Nature Structural Biology, 1998, 5, 970-975.	9.7	103
120	Crystal structure of an RNA aptamerâ€"protein complex at 2.8 Ã… resolution. Nature Structural Biology, 1998, 5, 133-139.	9.7	134
121	Dissecting the molecular details of prokaryotic transcriptional control by surface plasmon resonance: the methionine and arginine repressor proteins. Biosensors and Bioelectronics, 1998, 13, 637-650.	10.1	37
122	Specific cytotoxicity against cells bearing HIV1 gp120 antigen by bacteriophage-encapsidated ricin A chain: implications for cell specific drug delivery. Biochemical Society Transactions, 1997, 25, 158S-158S.	3.4	3
123	Analysis of phage MS2 coat protein mutants expressed from a reconstituted phagemid reveals that proline 78 is essential for viral infectivity 1 1 Edited by J.Karn. Journal of Molecular Biology, 1997, 266, 1-7.	4.2	28
124	The three-dimensional structures of two complexes between recombinant MS2 capsids and RNA operator fragments reveal sequence-specific protein-RNA interactions. Journal of Molecular Biology, 1997, 270, 724-738.	4.2	206
125	Operator interactions by the Bacillus subtilis arginine repressor/activator, AhrC: novel positioning and DNAâ€mediated assembly of a transcriptional activator at catabolic sites. Molecular Microbiology, 1997, 26, 37-48.	2.5	79
126	Quantitation of theEscherichia coliMethionine Repressorâ€"Operator Interaction by Surface Plasmon Resonance Is Not Affected by the Presence of a Dextran Matrix. Analytical Biochemistry, 1997, 254, 82-87.	2.4	26

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127	In VitroEvolution of the DNA Binding Sites ofEscherichia coliMethionine Repressor, MetJ. Journal of Molecular Biology, 1996, 255, 55-66.	4.2	44
128	Crystal Structures of MS2 Capsids with Mutations in the Subunit FG Loop. Journal of Molecular Biology, 1996, 256, 330-339.	4.2	49
129	Molecular interactions in the RNA bacteriophage MS2. Biochemical Society Transactions, 1996, 24, 412S-412S.	3.4	7
130	DEVELOPMENT OF A NOVEL DRUG-DELIVERY SYSTEM USING BACTERIOPHAGE MS2 CAPSIDS. Biochemical Society Transactions, 1996, 24, 413S-413S.	3.4	6
131	Biomolecular interaction analysis. Trends in Biotechnology, 1996, 14, 39-41.	9.3	1
132	Effects of systematic variation of the minimal Escherichia coli met consensus operator site: in vivo and in vitromet repressor binding. Molecular Microbiology, 1996, 21, 1125-1135.	2.5	17
133	Phage presentation. Molecular Microbiology, 1996, 20, 685-692.	2.5	32
134	A binding site for activation by theBacillus subtilis AhrC protein, a repressor/activator of arginine metabolism. Molecular Genetics and Genomics, 1995, 248, 329-340.	2.4	42
135	Incorporation of 6-thioinosine into oligoribonucleotides. Tetrahedron Letters, 1995, 36, 4637-4640.	1.4	6
136	Probing the molecular mechanism of action of co-repressor in theE.colimethionine repressor-operator complex using surface plasmon resonance (SPR). Nucleic Acids Research, 1995, 23, 211-216.	14.5	63
137	Cell-Specific Delivery of Bacteriophage-Encapsidated Ricin A Chain. Bioconjugate Chemistry, 1995, 6, 587-595.	3.6	92
138	Probing sequence-specific RNA recognition by the bacteriophage MS2 coat protien. Nucleic Acids Research, 1995, 23, 2512-2518.	14.5	65
139	Ethylation Interference. , 1994, 30, 125-140.		8
140	A convenient synthesis of S-cyanoethyl-protected 4-thiouridine and its incorporation into oligoribonucleotides. Tetrahedron Letters, 1994, 35, 765-768.	1.4	34
141	Incorporation of a fluorescent nucleotide into oligoribonucleotides. Tetrahedron Letters, 1994, 35, 1597-1600.	1.4	24
142	Similarity of met and trp repressors. Nature, 1994, 368, 106-106.	27.8	10
143	Crystal structure of an RNA bacteriophage coat proteinâ€"operator complex. Nature, 1994, 371, 623-626.	27.8	375
144	Filter-Binding Assays. , 1994, 30, 251-262.		2

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145	Calorimetric studies of the energetics of protein-DNA interactions in theE. colimethionine repressor (MetJ) system. FEBS Letters, 1994, 348, 41-45.	2.8	41
146	Modeling and solution structure probing of the HIV-1 TAR stem-loop. Journal of Molecular Graphics, 1993, 11, 92-97.	1.1	13
147	Molecular mechanism of RNA-phage morphogenesis. Biochemical Society Transactions, 1993, 21, 627-634.	3.4	28
148	Viral protein-nucleic acid interactions. Current Opinion in Structural Biology, 1992, 2, 143-149.	5.7	3
149	Differential scanning calorimetry of thermal unfolding of the methionine repressor protein (MetJ) from Escherichia coli. Biochemistry, 1992, 31, 9717-9724.	2.5	37
150	Probing met represserâ€“operator recognition in solution. Nature, 1992, 359, 431-433.	27.8	35
151	Regulation of methionine biosynthesis in the enterobacteriaceae. Progress in Biophysics and Molecular Biology, 1991, 56, 145-185.	2.9	60
152	Hyperreactivity of adenines and conformational flexibility of a translational repression site. FEBS Letters, 1991, 283, 159-164.	2.8	9
153	Modeling loop structures in proteins and nucleic acids: an RNA stem-loop. Journal of Molecular Graphics, 1989, 7, 186-195.	1.1	9
154	Cooperative tandem binding of met repressor of Escherichia coli. Nature, 1989, 341, 711-715.	27.8	122
155	A nucleosome-like particle containing an octamer of the arginine-rich histones H3 and H4. FEBS Letters, 1979, 99, 129-135.	2.8	43
156	Equipping a Research Scale Fermentation Laboratory for Production of Membrane Proteins. , 0, , 37-67.		3