

Jonathan King

List of Publications by Year in descending order

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148
papers

10,583
citations

20817

60
h-index

36028

97
g-index

149
all docs

149
docs citations

149
times ranked

4758
citing authors

#	ARTICLE	IF	CITATIONS
1	Polypeptides of the tail fibres of bacteriophage T4. <i>Journal of Molecular Biology</i> , 1971, 62, 465-477.	4.2	970
2	Mechanism of head assembly and DNA encapsulation in Salmonella phage P22. <i>Journal of Molecular Biology</i> , 1973, 80, 669-695.	4.2	313
3	Cyanobacterial photosynthesis in the oceans: the origins and significance of divergent light-harvesting strategies. <i>Trends in Microbiology</i> , 2002, 10, 134-142.	7.7	305
4	Specific aggregation of partially folded polypeptide chains: The molecular basis of inclusion body composition. <i>Nature Biotechnology</i> , 1996, 14, 1283-1287.	17.5	301
5	Assembly of the tau of bacteriophage T4. <i>Journal of Molecular Biology</i> , 1968, 32, 231-262.	4.2	283
6	Structure of epsilon15 bacteriophage reveals genome organization and DNA packaging/injection apparatus. <i>Nature</i> , 2006, 439, 612-616.	27.8	280
7	Protein Folding Intermediates and Inclusion Body Formation.. <i>Nature Biotechnology</i> , 1989, 7, 690-697.	17.5	273
8	Mechanism of head assembly and DNA encapsulation in Salmonella phage P22. <i>Journal of Molecular Biology</i> , 1973, 80, 697-731.	4.2	236
9	Catalytic head assembling protein in virus morphogenesis. <i>Nature</i> , 1974, 251, 112-119.	27.8	218
10	Backbone structure of the infectious μ 15 virus capsid revealed by electron cryomicroscopy. <i>Nature</i> , 2008, 451, 1130-1134.	27.8	204
11	Scaffolding protein regulates the polymerization of P22 coat subunits into icosahedral shells in vitro. <i>Journal of Molecular Biology</i> , 1988, 202, 743-757.	4.2	186
12	P22 morphogenesis I: Catalytic scaffolding protein in capsid assembly. <i>Journal of Supramolecular Structure</i> , 1974, 2, 202-224.	2.3	173
13	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
14	Genomic and structural analysis of Syn9, a cyanophage infecting marine <i>Prochlorococcus</i> and <i>Synechococcus</i> . <i>Environmental Microbiology</i> , 2007, 9, 1675-1695.	3.8	158
15	In vitro unfolding, refolding, and polymerization of human gammaD crystallin, a protein involved in cataract formation. <i>Protein Science</i> , 2003, 12, 480-490.	7.6	156
16	Thermolabile folding intermediates: inclusion body precursors and chaperonin substrates. <i>FASEB Journal</i> , 1996, 10, 57-66.	0.5	151
17	Cryo-EM Asymmetric Reconstruction of Bacteriophage P22 Reveals Organization of its DNA Packaging and Infecting Machinery. <i>Structure</i> , 2006, 14, 1073-1082.	3.3	149
18	Genetic control of bacteriophage T4 baseplate morphogenesis. <i>Journal of Molecular Biology</i> , 1975, 99, 695-716.	4.2	142

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19	Genetic control of bacteriophage T4 baseplate morphogenesis. <i>Journal of Molecular Biology</i> , 1975, 99, 645-672.	4.2	123
20	Zernike Phase Contrast Cryo-Electron Microscopy and Tomography for Structure Determination at Nanometer and Subnanometer Resolutions. <i>Structure</i> , 2010, 18, 903-912.	3.3	118
21	Temperature-sensitive mutants blocked in the folding or subunit assembly of the bacteriophage P22 tail spike protein. <i>Journal of Molecular Biology</i> , 1981, 145, 633-651.	4.2	117
22	Structure of phage P22 coat protein aggregates formed in the absence of the scaffolding protein. <i>Journal of Molecular Biology</i> , 1978, 126, 721-747.	4.2	115
23	Molecular reorganization in the hexagon to star transition of the baseplate of bacteriophage T4. <i>Journal of Molecular Biology</i> , 1977, 116, 489-523.	4.2	112
24	Glutamine Deamidation Destabilizes Human $\hat{1}^3$ D-Crystallin and Lowers the Kinetic Barrier to Unfolding. <i>Journal of Biological Chemistry</i> , 2006, 281, 30782-30793.	3.4	108
25	Bacteriophage T4 tail assembly: Proteins of the sheath, core and baseplate. <i>Journal of Molecular Biology</i> , 1973, 75, 339-358.	4.2	106
26	Aggregation of granulocyte-colony stimulating factor in vitro involves a conformationally altered monomeric state. <i>Protein Science</i> , 2005, 14, 2246-2257.	7.6	102
27	Genetic control of bacteriophage T4 baseplate morphogenesis. <i>Journal of Molecular Biology</i> , 1975, 99, 673-694.	4.2	98
28	Bacteriophage T4 tail assembly: Structural proteins and their genetic identification. <i>Journal of Molecular Biology</i> , 1973, 75, 315-337.	4.2	97
29	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
30	Functions of two new genes in Salmonella phage P22 assembly. <i>Virology</i> , 1977, 76, 725-739.	2.4	93
31	Contributions of hydrophobic domain interface interactions to the folding and stability of human \hat{A}^D -crystallin. <i>Protein Science</i> , 2005, 14, 569-581.	7.6	93
32	Bacteriophage T4 tail assembly: Four steps in core formation. <i>Journal of Molecular Biology</i> , 1971, 58, 693-709.	4.2	92
33	Probing folding and fluorescence quenching in human $\hat{1}^3$ D crystallin Greek key domains using triple tryptophan mutant proteins. <i>Protein Science</i> , 2004, 13, 2223-2235.	7.6	92
34	Interdomain side-chain interactions in human $\hat{1}^3$ D crystallin influencing folding and stability. <i>Protein Science</i> , 2005, 14, 2030-2043.	7.6	92
35	Genome Sequence, Structural Proteins, and Capsid Organization of the Cyanophage Syn5: A "Horned" Bacteriophage of Marine Synechococcus. <i>Journal of Molecular Biology</i> , 2007, 368, 966-981.	4.2	92
36	Role of the Scaffolding Protein in P22 Procapsid Size Determination Suggested by T=4 and T=7 Procapsid Structures. <i>Biophysical Journal</i> , 1998, 74, 559-568.	0.5	90

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37	Distinct cysteine sulfhydryl environments detected by analysis of Raman S-H markers of Cys ¹¹ Ser mutant proteins ¹¹ Edited by P. E. Wright. Journal of Molecular Biology, 2001, 307, 899-911.	4.2	90
38	Cataract. Nature Reviews Disease Primers, 2015, 1, 15014.	30.5	90
39	Mechanism of the Highly Efficient Quenching of Tryptophan Fluorescence in Human ¹³ D-Crystallin. Biochemistry, 2006, 45, 11552-11563.	2.5	86
40	Steps in the stabilization of newly packaged DNA during phage P22 Morphogenesis. Journal of Molecular Biology, 1984, 172, 523-543.	4.2	84
41	Mechanism of the Very Efficient Quenching of Tryptophan Fluorescence in Human ¹³ D- and ¹³ S-Crystallins: The ¹³ -Crystallin Fold May Have Evolved To Protect Tryptophan Residues from Ultraviolet Photodamage. Biochemistry, 2009, 48, 3708-3716.	2.5	84
42	Purification and organization of the gene 1 portal protein required for phage P22 DNA packaging. Biochemistry, 1988, 27, 1849-1856.	2.5	83
43	Polymerization mechanism of polypeptide chain aggregation. , 1997, 54, 333-343.		83
44	Frequencies of amino acid strings in globular protein sequences indicate suppression of blocks of consecutive hydrophobic residues. Protein Science, 2001, 10, 1023-1031.	7.6	83
45	Temperature-sensitive mutants blocked in the folding or subunit assembly of the bacteriophage P22 tail spike protein. Journal of Molecular Biology, 1981, 145, 653-676.	4.2	81
46	Multimeric intermediates in the pathway to the aggregated inclusion body state for P22 tailspike polypeptide chains. Protein Science, 1995, 4, 900-908.	7.6	81
47	Intracellular visualization of precursor capsids in phage P22 mutant infected cells. Virology, 1975, 68, 182-199.	2.4	79
48	Assembly of bacteriophage T4 tail fibers: The sequence of gene product interaction. Journal of Molecular Biology, 1969, 39, 583-601.	4.2	78
49	Initiation of P22 procapsid assembly in vivo. Journal of Molecular Biology, 1988, 202, 77-86.	4.2	76
50	There's a right way and a wrong way: in vivo and in vitro folding, misfolding and subunit assembly of the P22 tailspike. Structure, 1999, 7, R131-R139.	3.3	76
51	Effects of Oxygen on Recombinant Protein Expression. Biotechnology Progress, 1998, 14, 393-409.	2.6	73
52	A Newly Synthesized, Ribosome-bound Polypeptide Chain Adopts Conformations Dissimilar from Early in Vitro Refolding Intermediates. Journal of Biological Chemistry, 2001, 276, 25411-25420.	3.4	71
53	Formation of Amyloid Fibrils In Vitro from Partially Unfolded Intermediates of Human ¹³ C-Crystallin. , 2010, 51, 672.		70
54	Nature and distribution of sites of temperature-sensitive folding mutations in the gene for the P22 Tailspike polypeptide chain. Journal of Molecular Biology, 1988, 204, 607-619.	4.2	68

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55	Visualization of the maturation transition in bacteriophage P22 by electron cryomicroscopy. <i>Journal of Molecular Biology</i> , 2000, 297, 615-626.	4.2	68
56	TEMPERATURE-SENSITIVE MUTANTS BLOCKED IN THE FOLDING OR SUBUNIT ASSMBLY OF THE BACTERIOPHAGE P22 TAILSPIKE PROTEIN. I. FINE-STRUCTURE MAPPING. <i>Genetics</i> , 1980, 96, 331-352.	2.9	68
57	Thermal unfolding pathway for the thermostable P22 tailspike endorhamnosidase. <i>Biochemistry</i> , 1991, 30, 6260-6269.	2.5	67
58	Secondary structure and thermostability of the phage P22 tailspike. <i>Journal of Molecular Biology</i> , 1988, 199, 491-502.	4.2	66
59	Inhibition of viral capsid assembly by 1,1'-bis(4-anilinonaphthalene-5-sulfonic acid). <i>Biochemistry</i> , 1993, 32, 10658-10665.	2.5	66
60	Purification of the coat and scaffolding proteins from procapsids of bacteriophage P22. <i>Virology</i> , 1981, 112, 529-547.	2.4	65
61	Assembly in vitro of bacteriophage P22 procapsids from purified coat and scaffolding subunits. <i>Journal of Molecular Biology</i> , 1982, 156, 633-665.	4.2	65
62	Conformation of P22 tailspike folding and aggregation intermediates probed by monoclonal antibodies. <i>Protein Science</i> , 1997, 6, 99-108.	7.6	65
63	Partially Folded Aggregation Intermediates of Human β D-, β C-, and β S-Crystallin Are Recognized and Bound by Human I β B-Crystallin Chaperone. <i>Journal of Molecular Biology</i> , 2010, 401, 134-152.	4.2	61
64	Formation of amyloid fibrils in vitro by human gammaD-crystallin and its isolated domains. <i>Molecular Vision</i> , 2008, 14, 81-9.	1.1	61
65	Scaffolding Mutants Identifying Domains Required for P22 Procapsid Assembly and Maturation. <i>Virology</i> , 1996, 225, 82-96.	2.4	60
66	Control of the synthesis of phage p22 scaffolding protein is coupled to capsid assembly. <i>Cell</i> , 1978, 15, 551-560.	28.9	57
67	Folding of the phage P22 coat protein in vitro. <i>Biochemistry</i> , 1993, 32, 10839-10847.	2.5	57
68	Disulphide-bonded intermediate on the folding and assembly pathway of a non-disulphide bonded protein. <i>Nature Structural Biology</i> , 1997, 4, 450-455.	9.7	57
69	Homotrimeric, β 2-Stranded Viral Adhesins and Tail Proteins. <i>Journal of Bacteriology</i> , 2003, 185, 4022-4030.	2.2	57
70	The Structure of the Cataract-Causing P23T Mutant of Human β D-Crystallin Exhibits Distinctive Local Conformational and Dynamic Changes. <i>Biochemistry</i> , 2009, 48, 2597-2609.	2.5	57
71	[13]Mutational analysis of protein folding pathways: The P22 tailspike endorhamnosidase. <i>Methods in Enzymology</i> , 1986, 131, 250-266.	1.0	55
72	Mechanism of the Efficient Tryptophan Fluorescence Quenching in Human β D-Crystallin Studied by Time-Resolved Fluorescence. <i>Biochemistry</i> , 2008, 47, 10705-10721.	2.5	54

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73	Binding of Scaffolding Subunits within the P22 Procapsid Lattice. <i>Virology</i> , 1994, 205, 188-197.	2.4	51
74	Hydrophobic Core Mutations Associated with Cataract Development in Mice Destabilize Human $\hat{1}^3$ D-Crystallin. <i>Journal of Biological Chemistry</i> , 2009, 284, 33285-33295.	3.4	50
75	Amino acid substitutions influencing intracellular protein folding pathways. <i>FEBS Letters</i> , 1992, 307, 20-25.	2.8	49
76	Tryptophan Cluster Protects Human $\hat{1}^3$ D-Crystallin from Ultraviolet Radiation-Induced Photoaggregation <i>in Vitro</i> . <i>Photochemistry and Photobiology</i> , 2013, 89, 1106-1115.	2.5	49
77	Prevalence of temperature sensitive folding mutations in the parallel beta coil domain of the phage P22 tailspike endorhamnosidase. <i>Journal of Molecular Biology</i> , 1997, 267, 88-102.	4.2	48
78	Femtosecond Fluorescence Spectra of Tryptophan in Human $\hat{1}^3$ -Crystallin Mutants: Site-Dependent Ultrafast Quenching. <i>Journal of the American Chemical Society</i> , 2009, 131, 16751-16757.	13.7	44
79	Structural studies of P22 phage, precursor particles, and proteins by laser Raman spectroscopy. <i>Biochemistry</i> , 1982, 21, 3866-3878.	2.5	42
80	Frequencies of hydrophobic and hydrophilic runs and alternations in proteins of known structure. <i>Protein Science</i> , 2006, 15, 102-112.	7.6	42
81	Contributions of aromatic pairs to the folding and stability of long-lived human $\hat{1}^3$ D-crystallin. <i>Protein Science</i> , 2011, 20, 513-528.	7.6	41
82	Conformational stability of P22 tailspike proteins carrying temperature-sensitive folding mutations. <i>Biochemistry</i> , 1990, 29, 4181-4187.	2.5	39
83	Mutational Effects on Inclusion Body Formation. <i>Advances in Protein Chemistry</i> , 1997, 50, 243-264.	4.4	39
84	Predicting the Beta-Helix Fold from Protein Sequence Data. <i>Journal of Computational Biology</i> , 2002, 9, 261-276.	1.6	37
85	Structural studies of bacteriophage lambda heads and proheads by small angle X-ray diffraction. <i>Journal of Molecular Biology</i> , 1979, 134, 575-594.	4.2	36
86	Genetic Analysis of Protein Folding Pathways. <i>Nature Biotechnology</i> , 1986, 4, 297-303.	17.5	36
87	Cold rescue of the thermolabile tailspike intermediate at the junction between productive folding and off-pathway aggregation. <i>Protein Science</i> , 1998, 7, 1516-1523.	7.6	36
88	Conformational states of the bacteriophage P22 capsid subunit in relation to self-assembly. <i>Biochemistry</i> , 1990, 29, 5626-5633.	2.5	34
89	Solution X-Ray Scattering-Based Estimation of Electron Cryomicroscopy Imaging Parameters for Reconstruction of Virus Particles. <i>Biophysical Journal</i> , 1999, 76, 2249-2261.	0.5	34
90	Identification of Sites Influencing the Folding and Subunit Assembly of the P22 Tailspike Polypeptide Chain Using Nonsense Mutations. <i>Genetics</i> , 1987, 117, 157-171.	2.9	33

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91	Phycobiliprotein genes of the marine photosynthetic prokaryote <i>Prochlorococcus</i> : evidence for rapid evolution of genetic heterogeneity. <i>Microbiology (United Kingdom)</i> , 2001, 147, 3171-3182.	1.8	33
92	Folding and assembly of oligomeric proteins in <i>Escherichia coli</i> . <i>Current Opinion in Biotechnology</i> , 1992, 3, 468-473.	6.6	32
93	In vitro folding of phage P22 coat protein with amino acid substitutions that confer in vivo temperature sensitivity. <i>Biochemistry</i> , 1995, 34, 6815-6826.	2.5	32
94	The interdigitated beta-helix domain of the P22 tailspike protein acts as a molecular clamp in trimer stabilization. <i>Protein Science</i> , 2002, 11, 820-830.	7.6	32
95	The size of the bacteriophage T4 head in solution with comments about the dimension of virus particles as visualized by electron microscopy. <i>Journal of Molecular Biology</i> , 1978, 122, 247-253.	4.2	30
96	DNA injection proteins are targets of acridine-sensitized photoinactivation of bacteriophage P22. <i>Journal of Molecular Biology</i> , 1984, 180, 837-863.	4.2	30
97	Ubiquitin Proteasome Pathway-Mediated Degradation of Proteins: Effects Due to Site-Specific Substrate Deamidation. , 2010, 51, 4164.		30
98	An elongated spine of buried core residues necessary for in vivo folding of the parallel beta-helix of P22 tailspike adhesin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 3575-3580.	7.1	29
99	Novel second-site suppression of a cold-sensitive defect in phage P22 procapsid assembly. <i>Journal of Molecular Biology</i> , 1990, 216, 701-716.	4.2	28
100	Role for cysteine residues in the in vivo folding and assembly of the phage P22 tailspike. <i>Protein Science</i> , 2001, 10, 397-410.	7.6	28
101	Stability of Wild-type and Temperature-sensitive Protein Subunits of the Phage P22 Capsid. <i>Journal of Biological Chemistry</i> , 1995, 270, 16595-16601.	3.4	27
102	Tyrosine/Cysteine Cluster Sensitizing Human β -Crystallin to Ultraviolet Radiation-Induced Photoaggregation in Vitro. <i>Biochemistry</i> , 2014, 53, 979-990.	2.5	25
103	Isolation and characterization of precursors in T4 baseplate assembly the complex of gene 10 and gene 11 products. <i>Journal of Molecular Biology</i> , 1978, 124, 469-486.	4.2	24
104	β -Helix core packing within the triple-stranded oligomerization domain of the P22 tailspike. <i>Protein Science</i> , 2000, 9, 2338-2343.	7.6	24
105	Fold recognition and accurate sequence-structure alignment of sequences directing β -sheet proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 976-985.	2.6	24
106	Regulation of Structural Protein Interactions as Revealed in Phage Morphogenesis. , 1980, , 101-132.		23
107	The DNA Injection Apparatus of Phage P22. <i>Biophysical Journal</i> , 1986, 49, 24-26.	0.5	22
108	Characterization of the Protrimer Intermediate in the Folding Pathway of the Interdigitated β -Helix Tailspike Protein. <i>Biochemistry</i> , 2002, 41, 5093-5103.	2.5	22

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109	[22] Detection of early aggregation intermediates by native gel electrophoresis and native Western blotting. <i>Methods in Enzymology</i> , 1999, 309, 333-350.	1.0	21
110	Scaffolding Proteins and the Genetic Control of Virus Shell Assembly. <i>Quarterly Review of Biology</i> , 1980, 55, 369-393.	0.1	20
111	Mechanisms of Inclusion Body Formation. <i>ACS Symposium Series</i> , 1991, , 35-49.	0.5	19
112	Monitoring the refolding pathway for a large multimeric protein using capillary zone electrophoresis. <i>Journal of Chromatography A</i> , 1997, 769, 315-323.	3.7	19
113	In Vitro Unfolding/Refolding of Wild Type Phage P22 Scaffolding Protein Reveals Capsid-binding Domain. <i>Journal of Biological Chemistry</i> , 1999, 274, 16135-16140.	3.4	19
114	Protein Folding Failure Sets High-Temperature Limit on Growth of Phage P22 in <i>Salmonella enterica</i> Serovar Typhimurium. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4840-4847.	3.1	17
115	Assembly of the tail of bacteriophage T4. <i>Journal of Supramolecular Structure</i> , 1975, 3, 24-38.	2.3	16
116	Buried hydrophobic side-chains essential for the folding of the parallel \hat{I}^2 -helix domains of the P22 tailspike. <i>Protein Science</i> , 2004, 13, 2291-2303.	7.6	16
117	Genetic Control of Complex Bacteriophage Assembly. , 1979, , 581-633.		15
118	Identification of the 9-aminoacridine/DNA complex responsible for photodynamic inactivation of P22. <i>Biochemistry</i> , 1986, 25, 5858-5864.	2.5	13
119	Harvard XYY study. <i>Science</i> , 1975, 187, 298-299.	12.6	10
120	Antigenic gene products of bacteriophage T4 baseplates. <i>Virology</i> , 1978, 86, 312-328.	2.4	10
121	Monoclonal Antibody Epitope Mapping Describes Tailspike \hat{I}^2 -Helix Folding and Aggregation Intermediates. <i>Journal of Biological Chemistry</i> , 2005, 280, 23032-23040.	3.4	10
122	Hydro-epidemiological modelling of bacterial transport and decay in nearshore coastal waters. <i>Water Research</i> , 2021, 196, 117049.	11.3	10
123	Genetic and biochemical analysis of in vivo protein folding and subunit assembly. <i>Biopolymers</i> , 1983, 22, 125-129.	2.4	9
124	Folding and Stability of Mutant Scaffolding Proteins Defective in P22 Capsid Assembly. <i>Journal of Biological Chemistry</i> , 1999, 274, 16141-16146.	3.4	8
125	Wrap-and-Pack: A New Paradigm for Beta Structural Motif Recognition with Application to Recognizing Beta Trefoils. <i>Journal of Computational Biology</i> , 2005, 12, 777-795.	1.6	8
126	A late gene product of phage P22 affecting virus infectivity. <i>Virology</i> , 1985, 143, 368-379.	2.4	7

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127	Investigation of secondary structures and macromolecular interactions in bacteriophage p22 by laser raman spectroscopy. <i>Biophysical Journal</i> , 1980, 32, 234-237.	0.5	6
128	A green light for protein folding. <i>Nature Biotechnology</i> , 1999, 17, 637-638.	17.5	6
129	Stalled Folding Mutants in the Triple α -Helix Domain of the Phage P22 Tailspike Adhesin. <i>Journal of Molecular Biology</i> , 2005, 354, 1103-1117.	4.2	6
130	Aggregate formation from thermolabile intermediates in the maturation of the thermostable P22 tailspike. <i>Biochemical Society Transactions</i> , 1988, 16, 105-108.	3.4	4
131	Genetic Analysis of Polypeptide Chain Folding and Misfolding in Vivo. , 1990, , 59-78.		4
132	Genetic Identification of Amino Acid Sequences Influencing Protein Folding. , 1973, , 275-291.		4
133	Pathway for the Thermal Unfolding of Wild Type and Mutant Forms of the Thermostable P22 Tailspike Endorhamnosidase. <i>ACS Symposium Series</i> , 1991, , 119-132.	0.5	3
134	Refolding with a piece of the ring. <i>Nature Biotechnology</i> , 1997, 15, 514-515.	17.5	3
135	The C-terminal cysteine annulus participates in auto-chaperone function for Salmonellaphage P22 tailspike folding and assembly. <i>Bacteriophage</i> , 2012, 2, 36-49.	1.9	3
136	Amino Acid Sequence Determinants of Polypeptide Chain Folding and Inclusion Body Formation. <i>ACS Symposium Series</i> , 1993, , 24-37.	0.5	2
137	Unexpected pathways to protein stabilization. <i>Nature Biotechnology</i> , 1996, 14, 436-436.	17.5	2
138	Wrap-and-pack. , 2004, , .		2
139	Lattice Transformations and Subunit Conformational Changes in Phage Capsid Maturation. <i>Journal of Theoretical Medicine</i> , 2005, 6, 99-105.	0.5	1
140	Congressional Budget Responses to the Pandemic: Fund Health Care, Not Warfare. <i>American Journal of Public Health</i> , 2021, 111, 200-201.	2.7	1
141	Polymerization mechanism of polypeptide chain aggregation. <i>Biotechnology and Bioengineering</i> , 1997, 54, 333-343.	3.3	1
142	Mutations Affecting Protein Folding and Misfolding in Vivo. , 1991, , 129-136.		1
143	Introduction: From Genes to Organelles. <i>Quarterly Review of Biology</i> , 1980, 55, 329-333.	0.1	0
144	The Legal and Legislative Background. <i>Environment</i> , 1982, 24, 24-36.	1.4	0

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145	Amino Acid Sequence Control of the Folding of the Parallel β -Helix, the Simplest β -Sheet Fold. Lecture Notes in Computer Science, 2005, , 472-473.	1.3	0
146	Human β crystallins form fibrillar amyloid aggregates through a partially unfolded intermediate. FASEB Journal, 2008, 22, 1010.3.	0.5	0
147	Mutations associated with early cataract development in mice destabilize human gamma β -crystallin. FASEB Journal, 2008, 22, 232-232.	0.5	0
148	The Use of Salmonella Bacteriophage P22 to Study the Multiple Mechanisms of Acridine-Induced Damage. , 1983, , 79-109.		0