Michael Levitt

List of Publications by Year
in descending order

172	23,901	13099 68	7745 150
papers	citations	h-index	g-index

186	186	186	14560
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Structural patterns in globular proteins. Nature, 1976, 261, 552-558.	27.8	1,288
2	Conformations of immunoglobulin hypervariable regions. Nature, 1989, 342, 877-883.	27.8	1,199
3	A simplified representation of protein conformations for rapid simulation of protein folding. Journal of Molecular Biology, 1976, 104, 59-107.	4.2	1,057
4	Computer simulation of protein folding. Nature, 1975, 253, 694-698.	27.8	978
5	Conformation of amino acid side-chains in proteins. Journal of Molecular Biology, 1978, 125, 357-386.	4.2	783
6	Protein normal-mode dynamics: Trypsin inhibitor, crambin, ribonuclease and lysozyme. Journal of Molecular Biology, 1985, 181, 423-447.	4.2	692
7	Aromatic rings act as hydrogen bond acceptors. Journal of Molecular Biology, 1988, 201, 751-754.	4.2	672
8	Conformational preferences of amino acids in globular proteins. Biochemistry, 1978, 17, 4277-4285.	2.5	670
9	Accurate modeling of protein conformation by automatic segment matching. Journal of Molecular Biology, 1992, 226, 507-533.	4.2	555
10	Helix to helix packing in proteins. Journal of Molecular Biology, 1981, 145, 215-250.	4.2	543
11	Automatic identification of secondary structure in globular proteins. Journal of Molecular Biology, 1977, 114, 181-239.	4.2	509
12	Calibration and Testing of a Water Model for Simulation of the Molecular Dynamics of Proteins and Nucleic Acids in Solution. Journal of Physical Chemistry B, 1997, 101, 5051-5061.	2.6	503
13	The ASTRAL Compendium in 2004. Nucleic Acids Research, 2004, 32, 189D-192.	14.5	480
14	Refinement of protein conformations using a macromolecular energy minimization procedure. Journal of Molecular Biology, 1969, 46, 269-279.	4.2	433
15	The ASTRAL compendium for protein structure and sequence analysis. Nucleic Acids Research, 2000, 28, 254-256.	14.5	432
16	Potential energy function and parameters for simulations of the molecular dynamics of proteins and nucleic acids in solution. Computer Physics Communications, 1995, 91, 215-231.	7.5	431
17	Detailed Molecular Model for Transfer Ribonucleic Acid. Nature, 1969, 224, 759-763.	27.8	411
18	Energy Functions that Discriminate X-ray and Near-native Folds from Well-constructed Decoys. Journal of Molecular Biology, 1996, 258, 367-392.	4.2	375

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19	Protein folding by restrained energy minimization and molecular dynamics. Journal of Molecular Biology, 1983, 170, 723-764.	4.2	349
20	Molecular dynamics of native protein. Journal of Molecular Biology, 1983, 168, 595-617.	4.2	348
21	Within the twilight zone: a sensitive profile-profile comparison tool based on information theory. Journal of Molecular Biology, 2002, 315, 1257-1275.	4.2	267
22	Super-resolution biomolecular crystallography with low-resolution data. Nature, 2010, 464, 1218-1222.	27.8	267
23	Comprehensive Evaluation of Protein Structure Alignment Methods: Scoring by Geometric Measures. Journal of Molecular Biology, 2005, 346, 1173-1188.	4.2	260
24	Energy refinement of hen egg-white lysozyme. Journal of Molecular Biology, 1974, 82, 393-420.	4.2	259
25	Nature of the protein universe. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 11079-11084.	7.1	254
26	The Volume of Atoms on the Protein Surface: Calculated from Simulation, using Voronoi Polyhedra. Journal of Molecular Biology, 1995, 249, 955-966.	4.2	243
27	Molecular dynamics simulations of helix denaturation. Journal of Molecular Biology, 1992, 223, 1121-1138.	4.2	231
28	Water: now you see it, now you don't. Structure, 1993, 1, 223-226.	3.3	231
29	Extreme conformational flexibility of the furanose ring in DNA and RNA. Journal of the American Chemical Society, 1978, 100, 2607-2613.	13.7	225
30	Structural Basis of Transcription: Backtracked RNA Polymerase II at 3.4 Angstrom Resolution. Science, 2009, 324, 1203-1206.	12.6	225
31	The complexity and accuracy of discrete state models of protein structure. Journal of Molecular Biology, 1995, 249, 493-507.	4.2	222
32	Decoys â€˜Râ€™ Us: A database of incorrect conformations to improve protein structure prediction. Protein Science, 2000, 9, 1399-1401.	7.6	215
33	Combining Efficient Conformational Sampling with a Deformable Elastic Network Model Facilitates Structure Refinement at Low Resolution. Structure, 2007, 15, 1630-1641.	3.3	213
34	Mechanism of folding chamber closure in a group II chaperonin. Nature, 2010, 463, 379-383.	27.8	196
35	Molecular dynamics of native protein. Journal of Molecular Biology, 1983, 168, 621-657.	4.2	195
36	Comprehensive assessment of automatic structural alignment against a manual standard, the scop classification of proteins. Protein Science, 1998, 7, 445-456.	7.6	190

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37	Accurate prediction of the stability and activity effects of site-directed mutagenesis on a protein core. Nature, 1991, 352, 448-451.	27.8	188
38	PROTEIN FOLDING:The Endgame. Annual Review of Biochemistry, 1997, 66, 549-579.	11.1	184
39	Protein Unfolding Pathways Explored Through Molecular Dynamics Simulations. Journal of Molecular Biology, 1993, 232, 600-619.	4.2	178
40	Small Libraries of Protein Fragments Model Native Protein Structures Accurately. Journal of Molecular Biology, 2002, 323, 297-307.	4.2	170
41	Ab initio construction of protein tertiary structures using a hierarchical approach. Journal of Molecular Biology, 2000, 300, 171-185.	4.2	162
42	Factors affecting the ability of energy functions to discriminate correct from incorrect folds. Journal of Molecular Biology, 1997, 266, 831-846.	4.2	159
43	Subunit order of eukaryotic TRiC/CCT chaperonin by cross-linking, mass spectrometry, and combinatorial homology modeling. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2884-2889.	7.1	158
44	Exploring conformational space with a simple lattice model for protein structure. Journal of Molecular Biology, 1994, 243, 668-682.	4.2	153
45	Effect of proline residues on protein folding. Journal of Molecular Biology, 1981, 145, 251-263.	4.2	146
46	Growth of novel protein structural data. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3183-3188.	7.1	145
47	Architecture of an RNA Polymerase II Transcription Pre-Initiation Complex. Science, 2013, 342, 1238724.	12.6	143
48	Nonpolar solutes enhance water structure within hydration shells while reducing interactions between them. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 6777-6782.	7.1	141
49	Recognizing Native Folds by the Arrangement of Hydrophobic and Polar Residues. Journal of Molecular Biology, 1995, 252, 709-720.	4.2	134
50	Near-native structure refinement using in vacuo energy minimization. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3177-3182.	7.1	134
51	Millisecond dynamics of RNA polymerase II translocation at atomic resolution. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7665-7670.	7.1	127
52	KoBaMIN: a knowledge-based minimization web server for protein structure refinement. Nucleic Acids Research, 2012, 40, W323-W328.	14.5	124
53	De novo protein design. I. in search of stability and specificity 1 1Edited by F. E. Cohen. Journal of Molecular Biology, 1999, 293, 1161-1181.	4.2	122
54	ASTRAL compendium enhancements. Nucleic Acids Research, 2002, 30, 260-263.	14.5	117

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55	Alignment of the amino acid sequences of distantly related proteins using variable gap penalties. Protein Engineering, Design and Selection, 1986, 1, 77-78.	2.1	108
56	Can Morphing Methods Predict Intermediate Structures?. Journal of Molecular Biology, 2009, 385, 665-674.	4.2	104
57	The birth of computational structural biology. , 2001, 8, 392-393.		101
58	Solvent dramatically affects protein structure refinement. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20239-20244.	7.1	99
59	Keeping the shape but changing the charges: A simulation study of urea and its isoâ€steric analogs. Journal of Chemical Physics, 1996, 104, 9417-9430.	3.0	95
60	Protein topology and stability define the space of allowed sequences. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1280-1285.	7.1	94
61	Hierarchy of structure loss in MD simulations of src SH3 domain unfolding. Journal of Molecular Biology, 1999, 291, 215-225.	4.2	91
62	Birth and Future of Multiscale Modeling for Macromolecular Systems (Nobel Lecture). Angewandte Chemie - International Edition, 2014, 53, 10006-10018.	13.8	91
63	Simulating protein evolution in sequence and structure space. Current Opinion in Structural Biology, 2004, 14, 202-207.	5.7	89
64	Modeling nucleic acids. Current Opinion in Structural Biology, 2012, 22, 273-278.	5.7	85
65	A Novel Approach to Decoy Set Generation: Designing a Physical Energy Function Having Local Minima with Native Structure Characteristics. Journal of Molecular Biology, 2003, 329, 159-174.	4.2	83
66	Fully differentiable coarse-grained and all-atom knowledge-based potentials for RNA structure evaluation. Rna, 2011, 17, 1066-1075.	3.5	81
67	Symmetry-free cryo-EM structures of the chaperonin TRiC along its ATPase-driven conformational cycle. EMBO Journal, 2012, 31, 720-730.	7.8	80
68	Finite-difference solution of the Poisson-Boltzmann equation: Complete elimination of self-energy. Journal of Computational Chemistry, 1996, 17, 1344-1351.	3.3	77
69	De novo protein design. II. plasticity in sequence space 1 1Edited by F. E. Cohen. Journal of Molecular Biology, 1999, 293, 1183-1193.	4.2	74
70	Induced peptide conformations in different antibody complexes: molecular modeling of the three-dimensional structure of peptide-antibody complexes using NMR-derived distance restraints. Biochemistry, 1992, 31, 6884-6897.	2.5	73
71	On the Universe of Protein Folds. Annual Review of Biophysics, 2013, 42, 559-582.	10.0	73
72	RNA polymerase II trigger loop residues stabilize and position the incoming nucleotide triphosphate in transcription. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 15745-15750.	7.1	70

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73	Folding and stability of helical proteins: Carp myogen. Journal of Molecular Biology, 1976, 106, 421-437.	4.2	69
74	Using a Hydrophobic Contact Potential to Evaluate Native and Near-native Folds Generated by Molecular Dynamics Simulations. Journal of Molecular Biology, 1996, 257, 716-725.	4.2	68
75	Competitive assessment of protein fold recognition and alignment accuracy. Proteins: Structure, Function and Bioinformatics, 1997, 29, 92-104.	2.6	68
76	Ab initio protein structure prediction using a combined hierarchical approach. Proteins: Structure, Function and Bioinformatics, 1999, 37, 194-198.	2.6	66
77	Diffusion of nucleoside triphosphates and role of the entry site to the RNA polymerase II active center. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 17361-17364.	7.1	66
78	Roles of mutation and recombination in the evolution of protein thermodynamics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 10382-10387.	7.1	63
79	Molecular dynamics of hydrogen bonds in bovine pancreatic trypsin inhibitor protein. Nature, 1981, 294, 379-380.	27.8	61
80	Future of fundamental discovery in US biomedical research. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 6498-6503.	7.1	61
81	How Hydrophobic Buckminsterfullerene Affects Surrounding Water Structure. Journal of Physical Chemistry B, 2008, 112, 2981-2990.	2.6	60
82	An Atomic Environment Potential for use in Protein Structure Prediction. Journal of Molecular Biology, 2005, 352, 986-1001.	4.2	59
83	The Crystal Structures of the Eukaryotic Chaperonin CCT Reveal Its Functional Partitioning. Structure, 2013, 21, 540-549.	3.3	59
84	Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predicted structures, and observed antibody-antigen interactions in complexes of two antipeptide antibodies. Biochemistry, 1989, 28, 7168-7175.	2.5	58
85	Sequence Variations within Protein Families are Linearly Related to Structural Variations. Journal of Molecular Biology, 2002, 323, 551-562.	4.2	57
86	Detailed Hydration Maps of Benzene and Cyclohexane Reveal Distinct Water Structures. Journal of Physical Chemistry B, 2004, 108, 13492-13500.	2.6	57
87	Simulating Water and the Molecules of Life. Scientific American, 1998, 279, 100-105.	1.0	56
88	Improved protein structure selection using decoy-dependent discriminatory functions. BMC Structural Biology, 2004, 4, 8.	2.3	56
89	Protein foldingâ†"unfolding dynamics. Current Opinion in Structural Biology, 1994, 4, 291-295.	5.7	55
90	Evidence of turn and salt bridge contributions to Î²-hairpin stability: MD simulations of C-terminal fragment from the B1 domain of protein G. Biophysical Chemistry, 2002, 101-102, 187-201.	2.8	55

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91	Generalized ensemble methods for de novo structure prediction. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1415-1420.	7.1	52
92	Cryo-EM Structure of a Group II Chaperonin in the Prehydrolysis ATP-Bound State Leading to Lid Closure. Structure, 2011, 19, 633-639.	3.3	52
93	Insights on cross-species transmission of SARS-CoV-2 from structural modeling. PLoS Computational Biology, 2020, 16, e1008449.	3.2	52
94	The PRESAGE database for structural genomics. Nucleic Acids Research, 1999, 27, 251-253.	14.5	48
95	WeFold: A coopetition for protein structure prediction. Proteins: Structure, Function and Bioinformatics, 2014, 82, 1850-1868.	2.6	48
96	A comprehensive analysis of 40 blind protein structure predictions. , 2002, 2, 3.		47
97	Consistent refinement of submitted models at CASP using a knowledgeâ€based potential. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2668-2678.	2.6	46
98	NMR-derived model for a peptide-antibody complex. Biochemistry, 1990, 29, 10032-10041.	2.5	45
99	Emerging Î²-Sheet Rich Conformations in Supercompact Huntingtin Exon-1 Mutant Structures. Journal of the American Chemical Society, 2017, 139, 8820-8827.	13.7	43
100	Accuracy of side-chain prediction upon near-native protein backbones generated by ab initio folding methods. , 1998, 33, 204-217.		42
101	Modeling and design by hierarchical natural moves. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2890-2895.	7.1	42
102	Contribution of tryptophan residues to the combining site of a monoclonal anti-dinitrophenyl spin-label antibody. Biochemistry, 1987, 26, 6058-6064.	2.5	41
103	Simulating the minimum core for hydrophobic collapse in globular proteins. Protein Science, 1997, 6, 2606-2616.	7.6	40
104	Optimized Torsion-Angle Normal Modes Reproduce Conformational Changes More Accurately Than Cartesian Modes. Biophysical Journal, 2011, 101, 2966-2969.	0.5	37
105	Improving the Accuracy of Macromolecular Structure Refinement at 7ÂÃ… Resolution. Structure, 2012, 20, 957-966.	3.3	37
106	Constructing side chains on near-native main chains for ab initio protein structure prediction. Protein Engineering, Design and Selection, 2000, 13, 453-457.	2.1	36
107	Probing Protein Fold Space with a Simplified Model. Journal of Molecular Biology, 2008, 375, 920-933.	4.2	36
108	Comparison of pandemic excess mortality in 2020â€“2021 across different empirical calculations. Environmental Research, 2022, 213, 113754.	7.5	36

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109	Protein folding. Current Opinion in Structural Biology, 1991, 1, 224-229.	5.7	35
110	The solution structure of monomeric <scp>CCL</scp>5 in complex with a doubly sulfated Nâ€terminal segment of <scp>CCR</scp>5. FEBS Journal, 2018, 285, 1988-2003.	4.7	35
111	From Structure to Sequence and Back Again. Journal of Molecular Biology, 1996, 258, 201-209.	4.2	34
112	Funnel sculpting for in silico assembly of secondary structure elements of proteins. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 10700-10705.	7.1	34
113	A COMBINED APPROACH FOR AB INITIO CONSTRUCTION OF LOW RESOLUTION PROTEIN TERTIARY STRUCTURES FROM SEQUENCE. , 1998, , 505-16.		34
114	Funnel-like organization in sequence space determines the distributions of protein stability and folding rate preferred by evolution. Proteins: Structure, Function and Bioinformatics, 2004, 55, 107-114.	2.6	33
115	Inhibition Mechanism of the Acetylcholine Receptor by Î±-Neurotoxins as Revealed by Normal-Mode Dynamics. Biochemistry, 2008, 47, 4065-4070.	2.5	33
116	Protein segment finder: an online search engine for segment motifs in the PDB. Nucleic Acids Research, 2009, 37, D224-D228.	14.5	33
117	The normal modes of a protein: Native bovine pancreatic trypsin inhibitor. International Journal of Quantum Chemistry, 1983, 24, 181-199.	2.0	33
118	Multiscale natural moves refine macromolecules using single-particle electron microscopy projection images. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 9845-9850.	7.1	32
119	On the importance of accounting for nuclear quantum effects in ab initio calibrated force fields in biological simulations. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8878-8882.	7.1	32
120	Describing RNA Structure by Libraries of Clustered Nucleotide Doublets. Journal of Molecular Biology, 2005, 351, 26-38.	4.2	31
121	Simulations of RNA base pairs in a nanodroplet reveal solvation-dependent stability. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 12336-12340.	7.1	31
122	Proteomic analysis of monolayer-integrated proteins on lipid droplets identifies amphipathic interfacial Î±-helical membrane anchors. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8172-E8180.	7.1	31
123	A Novel Method for Sampling Alpha-helical Protein Backbones. Journal of Molecular Biology, 2001, 305, 191-201.	4.2	29
124	Deformable elastic network refinement for low-resolution macromolecular crystallography. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 2241-2255.	2.5	29
125	The language of the protein universe. Current Opinion in Genetics and Development, 2015, 35, 50-56.	3.3	27
126	Ab initio protein structure prediction using a combined hierarchical approach. Proteins: Structure, Function and Bioinformatics, 1999, 37, 194-198.	2.6	27

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127	Extracting knowledge-based energy functions from protein structures by error rate minimization: Comparison of methods using lattice model. Journal of Chemical Physics, 2000, 113, 9318-9330.	3.0	26
128	Application of DEN refinement and automated model building to a difficult case of molecular-replacement phasing: the structure of a putative succinyl-diaminopimelate desuccinylase from Corynebacterium glutamicum. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 391-403.	2.5	26
129	Remarkable patterns of surface water ordering around polarized buckminsterfullerene. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 14455-14460.	7.1	25
130	Clustering to identify RNA conformations constrained by secondary structure. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3590-3595.	7.1	25
131	Training-free atomistic prediction of nucleosome occupancy. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 6293-6298.	7.1	25
132	Structural and kinetic studies of the Fab fragment of a monoclonal anti-spin label antibody by nuclear magnetic resonance. Journal of Molecular Biology, 1991, 221, 257-270.	4.2	24
133	A molecular dynamics simulation of the C-terminal fragment of the L7/L12 ribosomal protein in solution. Chemical Physics, 1991, 158, 501-512.	1.9	24
134	Design of an optimal Chebyshev-expanded discrimination function for globular proteins. Protein Science, 2002, 11, 2010-2021.	7.6	24
135	Conformational Optimization with Natural Degrees of Freedom: A Novel Stochastic Chain Closure Algorithm. Journal of Computational Biology, 2010, 17, 993-1010.	1.6	23
136	Sequential allosteric mechanism of ATP hydrolysis by the CCT/TRiC chaperone is revealed through Arrhenius analysis. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5189-5194.	7.1	23
137	Real-time interactive frequency filtering of molecular dynamics trajectories. Journal of Molecular Biology, 1991, 220, 1-4.	4.2	22
138	Normal Modes of Prion Proteins: From Native to Infectious Particle. Biochemistry, 2011, 50, 2243-2248.	2.5	22
139	The Area Derivative of a Space-Filling Diagram. Discrete and Computational Geometry, 2004, 32, 293.	0.6	21
140	Integrating the equations of motion. Journal of Molecular Biology, 1983, 168, 617-620.	4.2	20
141	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. Scientific Reports, 2018, 8, 9939.	3.3	19
142	Improved recognition of native-like protein structures using a family of designed sequences. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 691-696.	7.1	18
143	HYDROGEN BOND AND INTERNAL SOLVENT DYNAMICS OF BPTI PROTEIN. Annals of the New York Academy of Sciences, 1981, 367, 162-181.	3.8	14
144	Evolutionarily consistent families in SCOP: sequence, structure and function. BMC Structural Biology, 2012, 12, 27.	2.3	14

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145	Comparative modeling and proteinâ€like features of hydrophobicâ€“polar models on a twoâ€dimensional lattice. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1683-1693.	2.6	14
146	Accurate determination of solvation free energies of neutral organic compounds from first principles. Nature Communications, 2022, 13, 414.	12.8	14
147	Spatial Regulation and the Rate of Signal Transduction Activation. PLoS Computational Biology, 2006, 2, e44.	3.2	12
148	Redundancy-weighting for better inference of protein structural features. Bioinformatics, 2014, 30, 2295-2301.	4.1	12
149	Simulation of protein-folding pathways: lost in (conformational) space?. Trends in Biotechnology, 1995, 13, 23-27.	9.3	11
150	Unique function words characterize genomic proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6703-6708.	7.1	10
151	MOTIF-EM: an automated computational tool for identifying conserved regions in CryoEM structures. Bioinformatics, 2010, 26, i301-i309.	4.1	9
152	Orientation of double-helical segments in crystals of yeast phenylalanine transfer RNA. Journal of Molecular Biology, 1973, 80, 255-263.	4.2	8
153	Structural diversity in a conserved cholera toxin epitope involved in ganglioside binding. Protein Science, 1995, 4, 841-848.	7.6	8
154	Theory and simulation through the breach. Current Opinion in Structural Biology, 1996, 6, 193-194.	5.7	7
155	A unified sequence-structure classification of protein sequences. , 2000, , .		7
156	EVALUATING MIXTURE MODELS FOR BUILDING RNA KNOWLEDGE-BASED POTENTIALS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1241010.	0.8	7
157	Theory and simulation. Current Opinion in Structural Biology, 2006, 16, 139-141.	5.7	5
158	Solving the structure of Lgl2, a difficult blind test of unsupervised structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10819-10823.	7.1	5
159	Finiteâ€difference solution of the Poissonâ€“Boltzmann equation: Complete elimination of selfâ€energy. Journal of Computational Chemistry, 1996, 17, 1344-1351.	3.3	5
160	Probing Interplays between Human XBP1u Translational Arrest Peptide and 80S Ribosome. Journal of Chemical Theory and Computation, 2022, 18, 1905-1914.	5.3	5
161	INSIGHTS INTO THE INTRA-RING SUBUNIT ORDER OF TRIC/CCT:. , 2009, , 252-259.		4
162	Unsupervised determination of protein crystal structures. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10813-10818.	7.1	4

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163	Simulating Protein Dynamics in Solution: Bovine Pancreatic Trypsin Inhibitor. , 1987, , 197-205.		4
164	Foreword by the Guest Editors of this Issue. Israel Journal of Chemistry, 1986, 27, 119-120.	2.3	3
165	Discussion of â€œEqui-energy samplerâ€•by Kou, Zhou and Wong. Annals of Statistics, 2006, 34, .	2.6	3
166	Molecular Dynamics of the DNA Double Helix. , 1984, , 43-57.		1
167	Folding of Nucleic Acids. Novartis Foundation Symposium, 1972, 7, 147-171.	1.1	1
168	Probing structure-function relationships of the DNA polymerase alpha-associated zinc-finger protein using computational approaches. , 1999, , 179-90.		1
169	Geburt und Zukunft der Multiskalenmodellierung von makromolekularen Systemen (Nobelâ€Aufsatz). Angewandte Chemie, 2014, 126, 10168-10181.	2.0	0
170	Automatic Inference of Sequence from Low-Resolution Crystallographic Data. Structure, 2018, 26, 1546-1554.e2.	3.3	0
171	Computer Simulations in Service of Biology. Frontiers for Young Minds, 0, 8, .	0.8	0
172	Simulating the Dynamics of the DNA Double Helix in Solution. , 1996, , 173-191.		0