

Michael Gilson

List of Publications by Year in descending order

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133
papers

18,527
citations

20817

60
h-index

12946

131
g-index

166
all docs

166
docs citations

166
times ranked

13395
citing authors

#	ARTICLE	IF	CITATIONS
1	Stimuli Induced Uptake of Protein-Like Peptide Brush Polymers. <i>Chemistry - A European Journal</i> , 2022, 28, .	3.3	6
2	CACHE (Critical Assessment of Computational Hit-finding Experiments): A public-private partnership benchmarking initiative to enable the development of computational methods for hit-finding. <i>Nature Reviews Chemistry</i> , 2022, 6, 287-295.	30.2	22
3	Experimental characterization of the association of β -cyclodextrin and eight novel cyclodextrin derivatives with two guest compounds. <i>Journal of Computer-Aided Molecular Design</i> , 2021, 35, 95-104.	2.9	9
4	Enhancing water sampling of buried binding sites using nonequilibrium candidate Monte Carlo. <i>Journal of Computer-Aided Molecular Design</i> , 2021, 35, 167-177.	2.9	22
5	Automation of absolute protein-ligand binding free energy calculations for docking refinement and compound evaluation. <i>Scientific Reports</i> , 2021, 11, 1116.	3.3	49
6	Mechanistic analysis of light-driven overcrowded alkene-based molecular motors by multiscale molecular simulations. <i>Physical Chemistry Chemical Physics</i> , 2021, 23, 8525-8540.	2.8	6
7	Alignment-Free Antimicrobial Peptide Predictors: Improving Performance by a Thorough Analysis of the Largest Available Data Set. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 3141-3157.	5.4	27
8	Development and Benchmarking of Open Force Field v1.0.0—the Parsley Small-Molecule Force Field. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 6262-6280.	5.3	80
9	Improving Structure-Based Virtual Screening with Ensemble Docking and Machine Learning. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 5362-5376.	5.4	27
10	Fast Equilibration of Water between Buried Sites and the Bulk by Molecular Dynamics with Parallel Monte Carlo Water Moves on Graphical Processing Units. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 7366-7372.	5.3	16
11	Data-Driven Mapping of Gas-Phase Quantum Calculations to General Force Field Lennard-Jones Parameters. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 1115-1127.	5.3	15
12	Accounting for the Central Role of Interfacial Water in Protein-Ligand Binding Free Energy Calculations. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 7883-7894.	5.3	24
13	Data-driven analysis of the number of Lennard-Jones types needed in a force field. <i>Communications Chemistry</i> , 2020, 3, .	4.5	6
14	D3R grand challenge 4: blind prediction of protein-ligand poses, affinity rankings, and relative binding free energies. <i>Journal of Computer-Aided Molecular Design</i> , 2020, 34, 99-119.	2.9	81
15	Enhanced Diffusion and Chemotaxis of Enzymes. <i>Annual Review of Biophysics</i> , 2020, 49, 87-105.	10.0	43
16	The SAMPL6 SAMPLing challenge: assessing the reliability and efficiency of binding free energy calculations. <i>Journal of Computer-Aided Molecular Design</i> , 2020, 34, 601-633.	2.9	86
17	Drug Design Data Resource, Grand Challenge 4, second of two issues. <i>Journal of Computer-Aided Molecular Design</i> , 2020, 34, 97-97.	2.9	0
18	Non-bonded force field model with advanced restrained electrostatic potential charges (RESP2). <i>Communications Chemistry</i> , 2020, 3, .	4.5	98

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19	Antitumor Activity of 1,18-Octadecanedioic Acid-Paclitaxel Complexed with Human Serum Albumin. <i>Journal of the American Chemical Society</i> , 2019, 141, 11765-11769.	13.7	61
20	A molecular reconstruction approach to site-based 3D-RISM and comparison to GIST hydration thermodynamic maps in an enzyme active site. <i>PLoS ONE</i> , 2019, 14, e0219473.	2.5	22
21	Continuous Evaluation of Ligand Protein Predictions: A Weekly Community Challenge for Drug Docking. <i>Structure</i> , 2019, 27, 1326-1335.e4.	3.3	39
22	Binding Thermodynamics of Host-Guest Systems with SMIRNOFF99Frosst 1.0.5 from the Open Force Field Initiative. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 6225-6242.	5.3	21
23	A Thermodynamic Limit on the Role of Self-Propulsion in Enhanced Enzyme Diffusion. <i>Biophysical Journal</i> , 2019, 116, 1898-1906.	0.5	17
24	Entropic effects enable life at extreme temperatures. <i>Science Advances</i> , 2019, 5, eaaw4783.	10.3	7
25	Simulating Water Exchange to Buried Binding Sites. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 2684-2691.	5.3	33
26	This issue: Drug Design Data Resource Grand Challenge 4, first of two issues. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 1009-1009.	2.9	0
27	D3R Grand Challenge 3: blind prediction of protein-ligand poses and affinity rankings. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 1-18.	2.9	104
28	Facile synthesis of a diverse library of mono-3-substituted β -cyclodextrin analogues. <i>Supramolecular Chemistry</i> , 2019, 31, 251-259.	1.2	8
29	Toward Learned Chemical Perception of Force Field Typing Rules. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 402-423.	5.3	30
30	Accounting for apparent deviations between calorimetric and van't Hoff enthalpies. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 692-704.	2.4	22
31	Substrate-driven chemotactic assembly in an enzyme cascade. <i>Nature Chemistry</i> , 2018, 10, 311-317.	13.6	121
32	Solvation Structure and Thermodynamic Mapping (SSTMap): An Open-Source, Flexible Package for the Analysis of Water in Molecular Dynamics Trajectories. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 418-425.	5.3	40
33	D3R Grand Challenge 2: blind prediction of protein-ligand poses, affinity rankings, and relative binding free energies. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 1-20.	2.9	156
34	Overview of the SAMPL6 host-guest binding affinity prediction challenge. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 937-963.	2.9	106
35	Discovering de novo peptide substrates for enzymes using machine learning. <i>Nature Communications</i> , 2018, 9, 5253.	12.8	55
36	Escaping Atom Types in Force Fields Using Direct Chemical Perception. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 6076-6092.	5.3	110

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37	Protein-ligand binding enthalpies from near-millisecond simulations: Analysis of a preorganization paradox. <i>Journal of Chemical Physics</i> , 2018, 149, 072311.	3.0	17
38	Motor-like Properties of Nonmotor Enzymes. <i>Biophysical Journal</i> , 2018, 114, 2174-2179.	0.5	13
39	Structural insights into the gating of DNA passage by the topoisomerase II DNA-gate. <i>Nature Communications</i> , 2018, 9, 3085.	12.8	47
40	Toward Expanded Diversity of Host-Guest Interactions via Synthesis and Characterization of Cyclodextrin Derivatives. <i>Journal of Solution Chemistry</i> , 2018, 47, 1597-1608.	1.2	14
41	Bind3P: Optimization of a Water Model Based on Host-Guest Binding Data. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 3621-3632.	5.3	23
42	Dual Inhibitors of Cyclooxygenase-2 and Soluble Epoxide Hydrolase: Studies of Binding Modes at the Active Sites and Time-dependency of Inhibition, and Development of Water-soluble Prodrugs. <i>FASEB Journal</i> , 2018, 32, 558.2.	0.5	1
43	Predicting Binding Free Energies: Frontiers and Benchmarks. <i>Annual Review of Biophysics</i> , 2017, 46, 531-558.	10.0	265
44	Attractive Interactions between Heteroallenes and the Cucurbituril Portal. <i>Journal of the American Chemical Society</i> , 2017, 139, 8138-8145.	13.7	22
45	Testing inhomogeneous solvation theory in structure-based ligand discovery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6839-E6846.	7.1	65
46	HYDROPHOBE Challenge: A Joint Experimental and Computational Study on the Host-Guest Binding of Hydrocarbons to Cucurbiturils, Allowing Explicit Evaluation of Guest Hydration Free-Energy Contributions. <i>Journal of Physical Chemistry B</i> , 2017, 121, 11144-11162.	2.6	62
47	Evaluating Force Field Performance in Thermodynamic Calculations of Cyclodextrin Host-Guest Binding: Water Models, Partial Charges, and Host Force Field Parameters. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 4253-4269.	5.3	51
48	Overview of the SAMPL5 host-guest challenge: Are we doing better?. <i>Journal of Computer-Aided Molecular Design</i> , 2017, 31, 1-19.	2.9	140
49	Evaluation and Minimization of Uncertainty in ITC Binding Measurements: Heat Error, Concentration Error, Saturation, and Stoichiometry. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 485-498.	2.4	45
50	Lessons learned from comparing molecular dynamics engines on the SAMPL5 dataset. <i>Journal of Computer-Aided Molecular Design</i> , 2017, 31, 147-161.	2.9	187
51	Probing the orientation of inhibitor and epoxy-eicosatrienoic acid binding in the active site of soluble epoxide hydrolase. <i>Archives of Biochemistry and Biophysics</i> , 2017, 613, 1-11.	3.0	9
52	The SAMPL5 host-guest challenge: computing binding free energies and enthalpies from explicit solvent simulations by the attach-pull-release (APR) method. <i>Journal of Computer-Aided Molecular Design</i> , 2017, 31, 133-145.	2.9	33
53	Attach-Pull-Release Calculations of Ligand Binding and Conformational Changes on the First BRD4 Bromodomain. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 3260-3275.	5.3	49
54	Solvation thermodynamic mapping of molecular surfaces in AmberTools: GIST. <i>Journal of Computational Chemistry</i> , 2016, 37, 2029-2037.	3.3	95

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55	Enthalpic Breakdown of Water Structure on Protein Active-Site Surfaces. <i>Journal of Physical Chemistry B</i> , 2016, 120, 8743-8756.	2.6	33
56	D3R grand challenge 2015: Evaluation of protein–ligand pose and affinity predictions. <i>Journal of Computer-Aided Molecular Design</i> , 2016, 30, 651-668.	2.9	178
57	Blind prediction of cyclohexane–water distribution coefficients from the SAMPL5 challenge. <i>Journal of Computer-Aided Molecular Design</i> , 2016, 30, 927-944.	2.9	99
58	Parameterization of an effective potential for protein–ligand binding from host–guest affinity data. <i>Journal of Molecular Recognition</i> , 2016, 29, 10-21.	2.1	27
59	Improving the Efficiency and Activity of Electrocatalysts for the Reduction of CO ₂ through Supramolecular Assembly with Amino Acid-Modified Ligands. <i>Journal of the American Chemical Society</i> , 2016, 138, 8184-8193.	13.7	59
60	Evaluation of Representations and Response Models for Polarizable Force Fields. <i>Journal of Physical Chemistry B</i> , 2016, 120, 8668-8684.	2.6	6
61	Spatial Decomposition of Translational Water–Water Correlation Entropy in Binding Pockets. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 414-429.	5.3	34
62	BindingDB in 2015: A public database for medicinal chemistry, computational chemistry and systems pharmacology. <i>Nucleic Acids Research</i> , 2016, 44, D1045-D1053.	14.5	1,002
63	Connecting proteins with drug-like compounds: Open source drug discovery workflows with BindingDB and KNIME. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bav087.	3.0	15
64	Binding Enthalpy Calculations for a Neutral Host–Guest Pair Yield Widely Divergent Salt Effects across Water Models. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 4555-4564.	5.3	36
65	Toward Improved Force-Field Accuracy through Sensitivity Analysis of Host-Guest Binding Thermodynamics. <i>Journal of Physical Chemistry B</i> , 2015, 119, 10145-10155.	2.6	30
66	Computational Calorimetry: High-Precision Calculation of Host–Guest Binding Thermodynamics. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 4377-4394.	5.3	96
67	Blind prediction of SAMPL4 cucurbit[7]uril binding affinities with the mining minima method. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 463-474.	2.9	18
68	The SAMPL4 hydration challenge: evaluation of partial charge sets with explicit-water molecular dynamics simulations. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 277-287.	2.9	31
69	Dynamic architecture of a protein kinase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4623-31.	7.1	205
70	Bridging Calorimetry and Simulation through Precise Calculations of Cucurbituril–Guest Binding Enthalpies. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 4069-4078.	5.3	83
71	The SAMPL4 host–guest blind prediction challenge: an overview. <i>Journal of Computer-Aided Molecular Design</i> , 2014, 28, 305-317.	2.9	162
72	Thermodynamics of Water in an Enzyme Active Site: Grid-Based Hydration Analysis of Coagulation Factor Xa. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 2769-2780.	5.3	117

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73	Quantum Mechanical Calculation of Noncovalent Interactions: A Large-Scale Evaluation of PMx, DFT, and SAPT Approaches. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 1563-1575.	5.3	107
74	Calculation and Visualization of Atomistic Mechanical Stresses in Nanomaterials and Biomolecules. <i>PLoS ONE</i> , 2014, 9, e113119.	2.5	13
75	Overcoming dissipation in the calculation of standard binding free energies by ligand extraction. <i>Journal of Computational Chemistry</i> , 2013, 34, 2360-2371.	3.3	57
76	The electrostatic response of water to neutral polar solutes: Implications for continuum solvent modeling. <i>Journal of Chemical Physics</i> , 2013, 138, 224504.	3.0	19
77	Grid inhomogeneous solvation theory: Hydration structure and thermodynamics of the miniature receptor cucurbit[7]uril. <i>Journal of Chemical Physics</i> , 2012, 137, 044101.	3.0	258
78	Entropy-enthalpy transduction caused by conformational shifts can obscure the forces driving protein-ligand binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 20006-20011.	7.1	109
79	Force and Stress along Simulated Dissociation Pathways of Cucurbituril-Guest Systems. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 966-976.	5.3	14
80	Calculation of Host-Guest Binding Affinities Using a Quantum-Mechanical Energy Model. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 2023-2033.	5.3	60
81	Shouldn't enantiomeric purity be included in the 'minimum information about a bioactive entity? Response from the MIABE group. <i>Nature Reviews Drug Discovery</i> , 2012, 11, 730-730.	46.4	0
82	Public Domain Databases for Medicinal Chemistry. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 6987-7002.	6.4	81
83	Prediction of SAMPL3 host-guest binding affinities: evaluating the accuracy of generalized force-fields. <i>Journal of Computer-Aided Molecular Design</i> , 2012, 26, 517-525.	2.9	29
84	Blind prediction of host-guest binding affinities: a new SAMPL3 challenge. <i>Journal of Computer-Aided Molecular Design</i> , 2012, 26, 475-487.	2.9	117
85	Protein folding and binding: from biology to physics and back again. <i>Current Opinion in Structural Biology</i> , 2011, 21, 1-3.	5.7	49
86	New Ultrahigh Affinity Host-Guest Complexes of Cucurbit[7]uril with Bicyclo[2.2.2]octane and Adamantane Guests: Thermodynamic Analysis and Evaluation of M2 Affinity Calculations. <i>Journal of the American Chemical Society</i> , 2011, 133, 3570-3581.	13.7	306
87	Thermodynamic and Differential Entropy under a Change of Variables. <i>Entropy</i> , 2010, 12, 578-590.	2.2	37
88	Symmetry Numbers for Rigid, Flexible, and Fluxional Molecules: Theory and Applications. <i>Journal of Physical Chemistry B</i> , 2010, 114, 16304-16317.	2.6	65
89	Stress Analysis at the Molecular Level: A Forced Cucurbituril-Guest Dissociation Pathway. <i>Journal of Chemical Theory and Computation</i> , 2010, 6, 637-646.	5.3	12
90	Theory of Free Energy and Entropy in Noncovalent Binding. <i>Chemical Reviews</i> , 2009, 109, 4092-4107.	47.7	334

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91	Host-Guest Complexes with Protein-Ligand-like Affinities: Computational Analysis and Design. <i>Journal of the American Chemical Society</i> , 2009, 131, 4012-4021.	13.7	108
92	A synthetic host-guest system achieves avidin-biotin affinity by overcoming enthalpy-entropy compensation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 20737-20742.	7.1	534
93	Biological Applications of Electrostatic Calculations and Brownian Dynamics Simulations. <i>Reviews in Computational Chemistry</i> , 2007, , 229-267.	1.5	70
94	Extraction of configurational entropy from molecular simulations via an expansion approximation. <i>Journal of Chemical Physics</i> , 2007, 127, 024107.	3.0	161
95	BindingDB: a web-accessible database of experimentally determined protein-ligand binding affinities. <i>Nucleic Acids Research</i> , 2007, 35, D198-D201.	14.5	1,493
96	Calculation of Protein-Ligand Binding Affinities. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2007, 36, 21-42.	18.3	807
97	Sensitivity Analysis and Charge-Optimization for Flexible Ligands: Applicability to Lead Optimization. <i>Journal of Chemical Theory and Computation</i> , 2006, 2, 259-270.	5.3	11
98	Virtual Screening of Molecular Databases Using a Support Vector Machine. <i>Journal of Chemical Information and Modeling</i> , 2005, 45, 549-561.	5.4	241
99	Free Energy, Entropy, and Induced Fit in Host-Guest Recognition: Calculations with the Second-Generation Mining Minima Algorithm. <i>Journal of the American Chemical Society</i> , 2004, 126, 13156-13164.	13.7	211
100	Identification of Symmetries in Molecules and Complexes. <i>Journal of Chemical Information and Computer Sciences</i> , 2004, 44, 1301-1313.	2.8	42
101	On the Theory of Noncovalent Binding. <i>Biophysical Journal</i> , 2004, 87, 23-36.	0.5	51
102	Calculation of Cyclodextrin Binding Affinities: Energy, Entropy, and Implications for Drug Design. <i>Biophysical Journal</i> , 2004, 87, 3035-3049.	0.5	217
103	Tork: Conformational analysis method for molecules and complexes. <i>Journal of Computational Chemistry</i> , 2003, 24, 1987-1998.	3.3	102
104	Fast Assignment of Accurate Partial Atomic Charges: An Electronegativity Equalization Method that Accounts for Alternate Resonance Forms. <i>Journal of Chemical Information and Computer Sciences</i> , 2003, 43, 1982-1997.	2.8	84
105	Calculation of Molecular Configuration Integrals. <i>Journal of Physical Chemistry B</i> , 2003, 107, 1048-1055.	2.6	76
106	The Binding Database: data management and interface design. <i>Bioinformatics</i> , 2002, 18, 130-139.	4.1	142
107	The bioinformatics of molecular recognition. <i>Journal of Molecular Recognition</i> , 2002, 15, 1-1.	2.1	2
108	Editorial: Molecular recognition databases. <i>Biopolymers</i> , 2001, 61, 97-98.	2.4	2

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109	The binding database: Overview and user's guide. <i>Biopolymers</i> , 2001, 61, 127-141.	2.4	69
110	Ligand-receptor docking with the Mining Minima optimizer. <i>Journal of Computer-Aided Molecular Design</i> , 2001, 15, 157-171.	2.9	51
111	BindingDB: A Web-Accessible Molecular Recognition Database. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2001, 4, 719-725.	1.1	172
112	Comparison of generalized born and poisson models: Energetics and dynamics of HIV protease. <i>Journal of Computational Chemistry</i> , 2000, 21, 295-309.	3.3	98
113	Thermodynamic linkage between the binding of protons and inhibitors to HIV protease. <i>Protein Science</i> , 1999, 8, 180-195.	7.6	55
114	Theoretical and Experimental Analysis of Ionization Equilibria in Ovomuroid Third Domain. <i>Biochemistry</i> , 1998, 37, 8643-8652.	2.5	63
115	pKaShifts in Small Molecules and HIV Protease: Electrostatics and Conformation. <i>Journal of the American Chemical Society</i> , 1998, 120, 6138-6146.	13.7	55
116	The statistical-thermodynamic basis for computation of binding affinities: a critical review. <i>Biophysical Journal</i> , 1997, 72, 1047-1069.	0.5	1,087
117	Direct Computation of Conformational Free Energy. <i>Journal of Physical Chemistry A</i> , 1997, 101, 1609-1618.	2.5	124
118	Responsibility of Co-Authors. <i>Science</i> , 1997, 275, 11e-14.	12.6	11
119	The Determinants of pKas in Proteins. <i>Biochemistry</i> , 1996, 35, 7819-7833.	2.5	439
120	Electrostatics and diffusion of molecules in solution: simulations with the University of Houston Brownian Dynamics program. <i>Computer Physics Communications</i> , 1995, 91, 57-95.	7.5	622
121	Molecular dynamics simulation with a continuum electrostatic model of the solvent. <i>Journal of Computational Chemistry</i> , 1995, 16, 1081-1095.	3.3	96
122	Prediction of Ph-dependent Properties of Proteins. <i>Journal of Molecular Biology</i> , 1994, 238, 415-436.	4.2	807
123	Open "back door" in a molecular dynamics simulation of acetylcholinesterase. <i>Science</i> , 1994, 263, 1276-1278.	12.6	277
124	Acetylcholinesterase: Effects of Ionic Strength and Dimerization on the Rate Constants. <i>Israel Journal of Chemistry</i> , 1994, 34, 151-158.	2.3	21
125	Multiple-site titration and molecular modeling: Two rapid methods for computing energies and forces for ionizable groups in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 15, 266-282.	2.6	273
126	The inclusion of electrostatic hydration energies in molecular mechanics calculations. <i>Journal of Computer-Aided Molecular Design</i> , 1991, 5, 5-20.	2.9	95

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127	Destabilization of an alpha-helix-bundle protein by helix dipoles.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 1524-1528.	7.1	68
128	Calculating the electrostatic potential of molecules in solution: Method and error assessment. Journal of Computational Chemistry, 1988, 9, 327-335.	3.3	1,017
129	Energetics of charge-charge interactions in proteins. Proteins: Structure, Function and Bioinformatics, 1988, 3, 32-52.	2.6	277
130	Calculation of the total electrostatic energy of a macromolecular system: Solvation energies, binding energies, and conformational analysis. Proteins: Structure, Function and Bioinformatics, 1988, 4, 7-18.	2.6	794
131	Calculation of electrostatic potentials in an enzyme active site. Nature, 1987, 330, 84-86.	27.8	458
132	The dielectric constant of a folded protein. Biopolymers, 1986, 25, 2097-2119.	2.4	455
133	Continuous Evaluation of Ligand Protein Predictions: A Weekly Community Challenge for Drug Docking. SSRN Electronic Journal, 0, , .	0.4	0