

Dimitrios Morikis

List of Publications by Year in descending order

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137
papers

4,195
citations

117625

34
h-index

133252

59
g-index

181
all docs

181
docs citations

181
times ranked

3606
citing authors

#	ARTICLE	IF	CITATIONS
1	SPARC coordinates extracellular matrix remodeling and efficient recruitment to and migration of antigen-specific T cells in the brain following infection. <i>Scientific Reports</i> , 2021, 11, 4549.	3.3	5
2	Role of Electrostatic Hotspots in the Selectivity of Complement Control Proteins Toward Human and Bovine Complement Inhibition. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 618068.	3.5	1
3	Systems Biology Modeling of the Complement System Under Immune Susceptible Pathogens. <i>Frontiers in Physics</i> , 2021, 9, .	2.1	4
4	Factor H-Inspired Design of Peptide Biomarkers of the Complement C3d Protein. <i>ACS Medicinal Chemistry Letters</i> , 2020, 11, 1054-1059.	2.8	3
5	Editorial: ImmunoPhysics and ImmunoEngineering. <i>Frontiers in Physics</i> , 2020, 8, .	2.1	0
6	Crosslinked flagella as a stabilized vaccine adjuvant scaffold. <i>BMC Biotechnology</i> , 2019, 19, 48.	3.3	6
7	Characterization, Dynamics, and Mechanism of CXCR4 Antagonists on a Constitutively Active Mutant. <i>Cell Chemical Biology</i> , 2019, 26, 662-673.e7.	5.2	20
8	Molecular Mechanisms of Macular Degeneration Associated with the Complement Factor H Y402H Mutation. <i>Biophysical Journal</i> , 2019, 116, 215-226.	0.5	8
9	Immunophysical Evaluation of the Initiating Step in the Formation of the Membrane Attack Complex. <i>Frontiers in Physics</i> , 2018, 6, .	2.1	4
10	A computational model for the evaluation of complement system regulation under homeostasis, disease, and drug intervention. <i>PLoS ONE</i> , 2018, 13, e0198644.	2.5	23
11	M13 bacteriophage spheroids as scaffolds for directed synthesis of spiky gold nanostructures. <i>Nanoscale</i> , 2018, 10, 13055-13063.	5.6	16
12	Virtual Screening of Chemical Compounds for Discovery of Complement C3 Ligands. <i>ACS Omega</i> , 2018, 3, 6427-6438.	3.5	15
13	Dissecting Distinct Roles of NEDDylation E1 Ligase Heterodimer APPBP1 and UBA3 Reveals Potential Evolution Process for Activation of Ubiquitin-related Pathways. <i>Scientific Reports</i> , 2018, 8, 10108.	3.3	12
14	Detection of Side Chain Rearrangements Mediating the Motions of Transmembrane Helices in Molecular Dynamics Simulations of G Protein-Coupled Receptors. <i>Computational and Structural Biotechnology Journal</i> , 2017, 15, 131-137.	4.1	16
15	AESOP: A Python Library for Investigating Electrostatics in Protein Interactions. <i>Biophysical Journal</i> , 2017, 112, 1761-1766.	0.5	18
16	Conformational heterogeneity in CCR7 undergoes transitions to specific states upon ligand binding. <i>Journal of Molecular Graphics and Modelling</i> , 2017, 74, 352-358.	2.4	5
17	Ionic tethering contributes to the conformational stability and function of complement C3b. <i>Molecular Immunology</i> , 2017, 85, 137-147.	2.2	5
18	Ligand-Specific Conformational Changes in CCR7 Coupled to Selecting Different Signaling Pathways upon CCL19 And CCL21 Ligand Binding. <i>Biophysical Journal</i> , 2016, 110, 361a.	0.5	0

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19	Synergy of Putative Binding Modes in the Factor H (CCP 19-20) and C3d Complex. <i>Biophysical Journal</i> , 2016, 110, 44a.	0.5	0
20	Interplay between Ionic Strength, Association Rates and Electrostatic Interaction in the C3d:CR2 Complex. <i>Biophysical Journal</i> , 2016, 110, 43a.	0.5	1
21	Discovery of functionally selective C5aR2 ligands: novel modulators of C5a signalling. <i>Immunology and Cell Biology</i> , 2016, 94, 787-795.	2.3	68
22	Molecular Mechanism of Biased Ligand Conformational Changes in CC Chemokine Receptor 7. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1808-1822.	5.4	13
23	Electrostatic Steering Accelerates C3d:CR2 Association. <i>Journal of Physical Chemistry B</i> , 2016, 120, 8416-8423.	2.6	15
24	Endosidin2 targets conserved exocyst complex subunit EXO70 to inhibit exocytosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E41-50.	7.1	129
25	Quantitative Modeling of the Alternative Pathway of the Complement System. <i>PLoS ONE</i> , 2016, 11, e0152337.	2.5	42
26	Peptide redesign for inhibition of the complement system: Targeting age-related macular degeneration. <i>Molecular Vision</i> , 2016, 22, 1280-1290.	1.1	6
27	Electrostatic Interactions between Complement Regulator CD46(SCR1-2) and Adenovirus Ad11/Ad21 Fiber Protein Knob. <i>Molecular Biology International</i> , 2015, 2015, 1-15.	1.7	1
28	A theoretical view of the C3d:CR2 binding controversy. <i>Molecular Immunology</i> , 2015, 64, 112-122.	2.2	21
29	New Compstatin Peptides Containing N-Terminal Extensions and Non-Natural Amino Acids Exhibit Potent Complement Inhibition and Improved Solubility Characteristics. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 814-826.	6.4	17
30	Energetic evaluation of binding modes in the C3d and Factor H (CCP 19-20) complex. <i>Protein Science</i> , 2015, 24, 789-802.	7.6	17
31	Discovery of Small Molecules for Fluorescent Detection of Complement Activation Product C3d. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 9535-9545.	6.4	10
32	Hybrid flagellin as a T cell independent vaccine scaffold. <i>BMC Biotechnology</i> , 2015, 15, 71.	3.3	20
33	Engineering pre-SUMO4 as efficient substrate of SENP2. <i>Protein Engineering, Design and Selection</i> , 2014, 27, 117-126.	2.1	8
34	Derivation of ligands for the complement C3a receptor from the C-terminus of C5a. <i>European Journal of Pharmacology</i> , 2014, 745, 176-181.	3.5	16
35	Insights into the mechanism of C5aR inhibition by PMX53 via implicit solvent molecular dynamics simulations and docking. <i>BMC Biophysics</i> , 2014, 7, 5.	4.4	21
36	Viral regulators of complement activation: Structure, function and evolution. <i>Molecular Immunology</i> , 2014, 61, 89-99.	2.2	31

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37	Molecular Analysis of the Interaction between Staphylococcal Virulence Factor Sbi-IV and Complement C3d. <i>Biophysical Journal</i> , 2014, 106, 1164-1173.	0.5	26
38	A Predictive Model for HIV Type 1 Coreceptor Selectivity. <i>AIDS Research and Human Retroviruses</i> , 2013, 29, 1386-1394.	1.1	3
39	Novel compstatin family peptides inhibit complement activation by drusen-like deposits in human retinal pigmented epithelial cell cultures. <i>Experimental Eye Research</i> , 2013, 116, 96-108.	2.6	25
40	The Two Sides of Complement C3d: Evolution of Electrostatics in a Link between Innate and Adaptive Immunity. <i>PLoS Computational Biology</i> , 2012, 8, e1002840.	3.2	32
41	De novo protein design of agonists and antagonists of C5a receptors. <i>Immunobiology</i> , 2012, 217, 1162-1163.	1.9	5
42	Computational and Experimental Analysis of the Interactions Between C3 and Compstatin Family Peptides. <i>Biophysical Journal</i> , 2012, 102, 62a.	0.5	0
43	Charge Discriminates Coreceptor Selectivity for HIV-1. <i>Biophysical Journal</i> , 2012, 102, 64a.	0.5	1
44	The Role of Electrostatics in the Function of Homologous Thioester Containing Proteins: Insights into the Evolution of the Complement C3d:Cr2 Interaction. <i>Biophysical Journal</i> , 2012, 102, 463a.	0.5	0
45	Exploring Protein-Protein and Protein-Ligand Interactions in the Immune System using Molecular Dynamics and Continuum Electrostatics. <i>Current Physical Chemistry</i> , 2012, 2, 324-343.	0.2	24
46	De Novo Peptide Design with C3a Receptor Agonist and Antagonist Activities: Theoretical Predictions and Experimental Validation. <i>Journal of Medicinal Chemistry</i> , 2012, 55, 4159-4168.	6.4	31
47	Molecular Dynamics in Drug Design: New Generations of Compstatin Analogs. <i>Chemical Biology and Drug Design</i> , 2012, 79, 703-718.	3.2	34
48	Clustering of HIV-1 Subtypes Based on gp120 V3 Loop electrostatic properties. <i>BMC Biophysics</i> , 2012, 5, 3.	4.4	19
49	Complement Inhibition by <i>Staphylococcus aureus</i> : Electrostatics of C3d α -EfbC and C3d α -Ehp Association. <i>Cellular and Molecular Bioengineering</i> , 2012, 5, 32-43.	2.1	20
50	Insights into the Structure, Correlated Motions, and Electrostatic Properties of Two HIV-1 gp120 V3 Loops. <i>PLoS ONE</i> , 2012, 7, e49925.	2.5	20
51	Exploring Protein-Protein and Protein-Ligand Interactions in the Immune System using Molecular Dynamics and Continuum Electrostatics. <i>Current Physical Chemistry</i> , 2012, 2, 324-343.	0.2	2
52	Title is missing!. , 2012, 7, e49925.		0
53	Is the rigid-body assumption reasonable?. <i>Journal of Non-Crystalline Solids</i> , 2011, 357, 707-716.	3.1	25
54	A New Generation of Potent Complement Inhibitors of the Compstatin Family. <i>Chemical Biology and Drug Design</i> , 2011, 77, 431-440.	3.2	14

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55	Electrostatic exploration of the C3dâ€‘FH4 interaction using a computational alanine scan. <i>Molecular Immunology</i> , 2011, 48, 1844-1850.	2.2	9
56	Electrostatic Clustering and Free Energy Calculations Provide a Foundation for Protein Design and Optimization. <i>Annals of Biomedical Engineering</i> , 2011, 39, 1252-1263.	2.5	53
57	The effect of electrostatics on factor H function and related pathologies. <i>Journal of Molecular Graphics and Modelling</i> , 2011, 29, 1047-1055.	2.4	20
58	Design of a modified mouse protein with ligand binding properties of its human analog by molecular dynamics simulations: The case of C3 inhibition by compstatin. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 3166-3179.	2.6	24
59	Electrostatic Similarity Determination Using Multiresolution Analysis. <i>Molecular Informatics</i> , 2011, 30, 733-746.	2.5	3
60	Automated computational framework for the analysis of electrostatic similarities of proteins. <i>Biotechnology Progress</i> , 2011, 27, 316-325.	2.6	25
61	An evaluation of poisson-boltzmann electrostatic free energy calculations through comparison with experimental mutagenesis data. <i>Biopolymers</i> , 2011, 95, n/a-n/a.	2.4	37
62	Contribution of Specific Amino Acid Changes in Penicillin Binding Protein 1 to Amoxicillin Resistance in Clinical <i>Helicobacter pylori</i> isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 101-109.	3.2	33
63	Solvation effects in calculated electrostatic association free energies for the C3dâ€‘CR2 complex and comparison with experimental data. <i>Biopolymers</i> , 2010, 93, 509-519.	2.4	19
64	Species specificity of the complement inhibitor compstatin investigated by all-atom molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2655-2667.	2.6	34
65	Influence of Electrostatics on the Complement Regulatory Functions of Kaposica, the Complement Inhibitor of Kaposiâ€™s Sarcoma-Associated Herpesvirus. <i>Journal of Immunology</i> , 2010, 184, 1956-1967.	0.8	33
66	A Gain-of-Function Mutation of <i>Arabidopsis</i> Lipid Transfer Protein 5 Disturbs Pollen Tube Tip Growth and Fertilization. <i>Plant Cell</i> , 2010, 21, 3902-3914.	6.6	106
67	A multifaceted study of stigma/style cysteine-rich adhesin (SCA)-like <i>Arabidopsis</i> lipid transfer proteins (LTPs) suggests diversified roles for these LTPs in plant growth and reproduction. <i>Journal of Experimental Botany</i> , 2010, 61, 4277-4290.	4.8	74
68	ADF/Cofilin Binds Phosphoinositides in a Multivalent Manner to Act as a PIP2-Density Sensor. <i>Biophysical Journal</i> , 2010, 98, 2327-2336.	0.5	73
69	New Compstatin Variants through Two De Novo Protein Design Frameworks. <i>Biophysical Journal</i> , 2010, 98, 2337-2346.	0.5	31
70	NMR evidence of charge-dependent interaction between various PND V3 and CCR5 N-terminal peptides. <i>Biopolymers</i> , 2009, 92, 94-109.	2.4	4
71	Computational studies of CXCR1, the receptor of IL8/CXCL8, using molecular dynamics and electrostatics. <i>Biopolymers</i> , 2008, 89, 52-61.	2.4	4
72	Structural study of Acâ€‘Pheâ€‘[Ornâ€‘Proâ€‘dChaâ€‘Trpâ€‘Arg], a potent C5a receptor antagonist, by NMR. <i>Biopolymers</i> , 2008, 90, 803-815.	2.4	8

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73	Native-state conformational dynamics of GART: A regulatory pH-dependent coil-helix transition examined by electrostatic calculations. <i>Protein Science</i> , 2008, 10, 2363-2378.	7.6	15
74	Proton transfer dynamics of GART: The pH-dependent catalytic mechanism examined by electrostatic calculations. <i>Protein Science</i> , 2008, 10, 2379-2392.	7.6	16
75	pH Dependence of Stability of the 10th Human Fibronectin Type III Domain: A Computational Study. <i>Biotechnology Progress</i> , 2008, 24, 48-55.	2.6	6
76	Toward Full-Sequence De Novo Protein Design with Flexible Templates for Human Beta-Defensin-2. <i>Biophysical Journal</i> , 2008, 94, 584-599.	0.5	45
77	Overcoming the Key Challenges in De Novo Protein Design: Enhancing Computational Efficiency and Incorporating True Backbone Flexibility. , 2008, , 133-183.		1
78	Two SCA (Stigma/Style Cysteine-rich Adhesin) Isoforms Show Structural Differences That Correlate with Their Levels of in Vitro Pollen Tube Adhesion Activity. <i>Journal of Biological Chemistry</i> , 2007, 282, 33845-33858.	3.4	33
79	Immunophysical Exploration of C3dâ€“CR2(CCP1-2) Interaction Using Molecular Dynamics and Electrostatics. <i>Journal of Molecular Biology</i> , 2007, 369, 567-583.	4.2	30
80	Solution Structure of a Bent Î±-Helix. <i>Biochemistry</i> , 2007, 46, 12959-12967.	2.5	4
81	Conformational analysis of compstatin analogues with molecular dynamics simulations in explicit water. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 26, 571-580.	2.4	12
82	Electrostatic modeling of peptides derived from the V3-loop of HIV-1 gp120: implications of the interaction with chemokine receptor CCR5. <i>International Journal of Molecular Medicine</i> , 2007, 19, 343-51.	4.0	14
83	Immunophysical Properties and Prediction of Activities for Vaccinia Virus Complement Control Protein and Smallpox Inhibitor of Complement Enzymes Using Molecular Dynamics and Electrostatics. <i>Biophysical Journal</i> , 2006, 90, 3106-3119.	0.5	47
84	An immunophysical study of the complement system: Examples for the pH dependence of protein binding and stability. <i>Journal of Non-Crystalline Solids</i> , 2006, 352, 4445-4450.	3.1	8
85	Characterization of the interaction between peptides derived from the gp120/V3 domain of HIV-1 and the amino terminal of the chemokine receptor CCR5 by NMR spectroscopy and light scattering. <i>Journal of Non-Crystalline Solids</i> , 2006, 352, 4451-4458.	3.1	10
86	Molecular thermodynamics for charged biomacromolecules. <i>Fluid Phase Equilibria</i> , 2006, 241, 317-333.	2.5	18
87	Applications of Molecular Dynamics Simulations in Immunology: A Useful Computational Method in Aiding Vaccine Design. <i>Current Proteomics</i> , 2006, 3, 259-270.	0.3	15
88	Structure-Based Integrative Computational and Experimental Approach for the Optimization of Drug Design. <i>Lecture Notes in Computer Science</i> , 2005, , 680-688.	1.3	10
89	Electrostatic Modeling Predicts the Activities of Orthopoxvirus Complement Control Proteins. <i>Journal of Immunology</i> , 2005, 174, 2143-2151.	0.8	73
90	Development of a Quasi-Dynamic Pharmacophore Model for Anti-Complement Peptide Analogues. <i>Journal of the American Chemical Society</i> , 2005, 127, 10967-10976.	13.7	26

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91	Design and NMR Characterization of Active Analogues of Compstatin Containing Non-Natural Amino Acids. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 274-286.	6.4	68
92	Structure, Dynamics, Activity, and Function of Compstatin and Design of More Potent Analogues. , 2005, , 317-340.		4
93	Structure, Dynamics, Activity, and Function of Compstatin and Design of More Potent Analogues. , 2005, , 317-340.		3
94	Structure of the Anaphylatoxins C3a and C5a. , 2005, , 161-177.		0
95	Structure of the Anaphylatoxins C3a and C5a. , 2005, , 161-178.		2
96	The Building Blocks of the Complement System. , 2005, , 1-18.		1
97	The Electrostatic Nature of C3d-Complement Receptor 2 Association. <i>Journal of Immunology</i> , 2004, 172, 7537-7547.	0.8	48
98	Thermodynamic Studies on the Interaction of the Third Complement Component and Its Inhibitor, Compstatin. <i>Journal of Biological Chemistry</i> , 2004, 279, 54987-54995.	3.4	24
99	Adaptation of inorganic quantum dots for stable molecular beacons. <i>Sensors and Actuators B: Chemical</i> , 2004, 102, 315-319.	7.8	128
100	Design of Peptide Analogues with Improved Activity Using a Novel de Novo Protein Design Approach. <i>Industrial & Engineering Chemistry Research</i> , 2004, 43, 3817-3826.	3.7	56
101	Physical methods for structure, dynamics and binding in immunological research. <i>Trends in Immunology</i> , 2004, 25, 700-707.	6.8	29
102	From atoms to systems: a cross-disciplinary approach to complement-mediated functions*1. <i>Molecular Immunology</i> , 2004, 41, 153-164.	2.2	10
103	Improvement of the anti-C3 activity of compstatin using rational and combinatorial approaches. <i>Biochemical Society Transactions</i> , 2004, 32, 28-32.	3.4	34
104	Hybrid Inorganic-Organic Molecular Beacons. <i>Sensor Letters</i> , 2004, 2, 85-90.	0.4	6
105	Synthetic small-molecule complement inhibitors. <i>Current Opinion in Investigational Drugs</i> , 2004, 5, 1164-73.	2.3	28
106	Complement. <i>Immunologic Research</i> , 2003, 27, 367-385.	2.9	53
107	The pH dependence of stability of the activation helix and the catalytic site of GART. <i>Biophysical Chemistry</i> , 2003, 105, 279-291.	2.8	7
108	Conformational interconversion in compstatin probed with molecular dynamics simulations. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 130-141.	2.6	23

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109	Related Protein-Protein Interaction Modules Present Drastically Different Surface Topographies Despite A Conserved Helical Platform. <i>Journal of Molecular Biology</i> , 2003, 330, 1117-1129.	4.2	57
110	Compstatin, a peptide inhibitor of complement, exhibits species-specific binding to complement component C3. <i>Molecular Immunology</i> , 2003, 39, 557-566.	2.2	81
111	Integrated Computational and Experimental Approach for Lead Optimization and Design of Compstatin Variants with Improved Activity. <i>Journal of the American Chemical Society</i> , 2003, 125, 8422-8423.	13.7	85
112	Studies of Structure-Activity Relations of Complement Inhibitor Compstatin. <i>Journal of Immunology</i> , 2003, 171, 1881-1890.	0.8	39
113	Structural aspects and design of low-molecular-mass complement inhibitors. <i>Biochemical Society Transactions</i> , 2002, 30, 1026-1036.	3.4	49
114	The Structural Basis of Compstatin Activity Examined by Structure-Function-based Design of Peptide Analogs and NMR. <i>Journal of Biological Chemistry</i> , 2002, 277, 14942-14953.	3.4	50
115	Electrostatic properties of the structure of the docking and dimerization domain of protein kinase A II \pm . <i>FEBS Journal</i> , 2002, 269, 2040-2051.	0.2	13
116	A novel mechanism of PKA anchoring revealed by solution structures of anchoring complexes. <i>EMBO Journal</i> , 2001, 20, 1651-1662.	7.8	179
117	Binding Kinetics, Structure-Activity Relationship, and Biotransformation of the Complement Inhibitor Compstatin. <i>Journal of Immunology</i> , 2000, 165, 2491-2499.	0.8	105
118	Structure Calculations of Symmetric Dimers using Molecular Dynamics/Simulated Annealing and NMR Restraints: The Case of the RI \pm Subunit of Protein Kinase A. <i>Nonconvex Optimization and Its Applications</i> , 2000, , 141-156.	0.1	1
119	The molecular basis for protein kinase A anchoring revealed by solution NMR. <i>Nature Structural Biology</i> , 1999, 6, 222-227.	9.7	181
120	Solution structure of Compstatin, a potent complement inhibitor. <i>Protein Science</i> , 1998, 7, 619-627.	7.6	87
121	Hydrogen Exchange in the Carbon Monoxide Complex of Soybean Leghemoglobin. <i>FEBS Journal</i> , 1996, 237, 212-220.	0.2	17
122	Hydration of the partially folded peptide RN-24 studied by multidimensional NMR. <i>Journal of Biomolecular NMR</i> , 1995, 5, 353-6.	2.8	14
123	^1H resonance assignments and secondary structure of the carbon monoxide complex of soybean leghemoglobin determined by homonuclear two-dimensional and three-dimensional NMR spectroscopy. <i>FEBS Journal</i> , 1994, 219, 611-626.	0.2	10
124	Determination of local ligand conformations in slowly tumbling proteins by homonuclear 2D and 3D NMR: application to heme propionates in leghemoglobin. <i>Journal of the American Chemical Society</i> , 1993, 115, 6238-6246.	13.7	10
125	NMR evidence for multiple conformations in a highly helical model peptide. <i>Biochemistry</i> , 1993, 32, 13089-13097.	2.5	61
126	Low pH myoglobin photoproducts. <i>Biophysical Journal</i> , 1992, 61, 1041-1044.	0.5	9

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127	Conformational interconversion in protein crystals. <i>Journal of Molecular Biology</i> , 1992, 224, 207-215.	4.2	56
128	Spectroscopic studies of myoglobin at low pH: heme structure and ligation. <i>Biochemistry</i> , 1991, 30, 1227-1237.	2.5	162
129	The iron-histidine mode of myoglobin revisited: resonance Raman studies of isotopically labeled <i>Escherichia coli</i> -expressed myoglobin. <i>Journal of the American Chemical Society</i> , 1991, 113, 9655-9660.	13.7	61
130	Resonance Raman scattering as a probe of electron-nuclear coupling: applications to heme proteins. <i>The Journal of Physical Chemistry</i> , 1991, 95, 3391-3398.	2.9	36
131	Alteration of sperm whale myoglobin heme axial ligation by site-directed mutagenesis. <i>Biochemistry</i> , 1990, 29, 9783-9791.	2.5	121
132	Resonance Raman investigations of site-directed mutants of myoglobin: effects of distal histidine replacement. <i>Biochemistry</i> , 1989, 28, 4791-4800.	2.5	197
133	Resonance Raman studies of oriented chromophores: Metmyoglobin single crystals. <i>Journal of Chemical Physics</i> , 1989, 90, 3015-3032.	3.0	25
134	Resonance Raman studies of myoglobin single crystals. <i>Journal of the American Chemical Society</i> , 1988, 110, 6341-6342.	13.7	21
135	Alteration of heme axial ligands by site-directed mutagenesis: a cytochrome becomes a catalytic demethylase. <i>Journal of the American Chemical Society</i> , 1987, 109, 7896-7897.	13.7	77
136	Complement Inhibitors Targeting C3, C4, and C5. , 0, , 75-112.		10
137	Electrostatic modeling of peptides derived from the V3-loop of HIV-1 gp120: Implications of the interaction with chemokine receptor CCR5. <i>International Journal of Molecular Medicine</i> , 0, , .	4.0	5