

Victoria A Feher

List of Publications by Year in descending order

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21
papers

2,449
citations

411340

20
h-index

759306

22
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docs citations

22
times ranked

3412
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanisms for Benzene Dissociation through the Excited State of T4 Lysozyme L99A Mutant. <i>Biophysical Journal</i> , 2019, 116, 205-214.	0.2	20
2	Emerging Computational Methods for the Rational Discovery of Allosteric Drugs. <i>Chemical Reviews</i> , 2016, 116, 6370-6390.	23.0	176
3	Capturing Invisible Motions in the Transition from Ground to Rare Excited States of T4 Lysozyme L99A. <i>Biophysical Journal</i> , 2016, 111, 1631-1640.	0.2	18
4	Gaussian Accelerated Molecular Dynamics: Unconstrained Enhanced Sampling and Free Energy Calculation. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 3584-3595.	2.3	544
5	Computational approaches to mapping allosteric pathways. <i>Current Opinion in Structural Biology</i> , 2014, 25, 98-103.	2.6	122
6	Computation-Guided Discovery of Influenza Endonuclease Inhibitors. <i>ACS Medicinal Chemistry Letters</i> , 2014, 5, 61-64.	1.3	26
7	A 3-Dimensional Trimeric $\hat{\beta}$ -Barrel Model for Chlamydia MOMP Contains Conserved and Novel Elements of Gram-Negative Bacterial Porins. <i>PLoS ONE</i> , 2013, 8, e68934.	1.1	30
8	Structure-based design, synthesis, and antimicrobial activity of purine derived SAH/MTA nucleosidase inhibitors. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2004, 14, 3165-3168.	1.0	27
9	Structure-Based Design, Synthesis, and Antimicrobial Activity of Indazole-Derived SAH/MTA Nucleosidase Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2003, 46, 5663-5673.	2.9	146
10	The DNA-binding domain in the <i>Bacillus subtilis</i> transition-state regulator AbrB employs significant motion for promiscuous DNA recognition. <i>Journal of Molecular Biology</i> , 2001, 305, 429-439.	2.0	24
11	Alanine mutants of the SpoOF response regulator modifying specificity for sensor kinases in sporulation initiation. <i>Molecular Microbiology</i> , 1999, 33, 389-395.	1.2	38
12	Millisecond-timescale motions contribute to the function of the bacterial response regulator protein SpoOF. <i>Nature</i> , 1999, 400, 289-293.	13.7	212
13	Two-Component Signal Transduction in <i>Bacillus subtilis</i> : How One Organism Sees Its World. <i>Journal of Bacteriology</i> , 1999, 181, 1975-1983.	1.0	331
14	Sequence requirements for stabilization of a peptide reverse turn in water solution. Proline is not essential for stability. <i>FEBS Journal</i> , 1998, 255, 462-471.	0.2	25
15	Identification of communication networks in SpoOF: a model for phosphorylation-induced conformational change and implications for activation of multiple domain bacterial response regulators. <i>FEBS Letters</i> , 1998, 425, 1-6.	1.3	24
16	Characterization of Interactions between a Two-Component Response Regulator, SpoOF, and Its Phosphatase, RapB. <i>Biochemistry</i> , 1998, 37, 16538-16545.	1.2	54
17	High-Resolution NMR Structure and Backbone Dynamics of the <i>Bacillus subtilis</i> Response Regulator, SpoOF: Implications for Phosphorylation and Molecular Recognition. <i>Biochemistry</i> , 1997, 36, 10015-10025.	1.2	67
18	Access of ligands to cavities within the core of a protein is rapid. <i>Nature Structural and Molecular Biology</i> , 1996, 3, 516-521.	3.6	104

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19	^1H , ^{15}N , and ^{13}C backbone chemical shift assignments, secondary structure, and magnesium-binding characteristics of the bacillus subtilis response regulator, SpoOF, determined by heteronuclear high-resolution NMR. <i>Protein Science</i> , 1995, 4, 1801-1814.	3.1	39
20	Stabilization of a type VI turn in a family of linear peptides in water solution. <i>Journal of Molecular Biology</i> , 1994, 243, 736-753.	2.0	152
21	Peptide models of protein folding initiation sites. 1. Secondary structure formation by peptides corresponding to the G- and H-helices of myoglobin. <i>Biochemistry</i> , 1993, 32, 6337-6347.	1.2	209