Christopher Bystroff

List of Publications by Year
in descending order

41 papers	1,702 citations	471061 17 h-index	301761 39 g-index
42 all docs	42 docs citations	42 times ranked	1696 citing authors

#	Article	IF	Citations
1	Footprints to singularity: A global population model explains late 20th century slow-down and predicts peak within ten years. PLoS ONE, 2021, 16, e0247214.	1.1	4
2	Complex between a Multicrossover DNA Nanostructure, PX-DNA, and T7 Endonuclease I. Biochemistry, 2019, 58, 1332-1342.	1.2	5
3	Intramembranal disulfide cross-linking elucidates the super-quaternary structure of mammalian CatSpers. Reproductive Biology, 2018, 18, 76-82.	0.9	11
4	Fast design of arbitrary length loops in proteins using InteractiveRosetta. BMC Bioinformatics, 2018, 19, 337.	1.2	4
5	Mispacking and the Fitness Landscape of the Green Fluorescent Protein Chromophore Milieu. Biochemistry, 2017, 56, 736-747.	1.2	11
6	Toward rational thermostabilization of Aspergillus oryzae cutinase: Insights into catalytic and structural stability. Proteins: Structure, Function and Bioinformatics, 2016, 84, 60-72.	1.5	42
7	Influence of surface charge, binding site residues and glycosylation on Thielavia terrestris cutinase biochemical characteristics. Applied Microbiology and Biotechnology, 2016, 100, 4435-4446.	1.7	25
8	Toward Computationally Designed Self-Reporting Biosensors Using Leave-One-Out Green Fluorescent Protein. Biochemistry, 2015, 54, 6263-6273.	1.2	10
9	InteractiveROSETTA: a graphical user interface for the PyRosetta protein modeling suite. Bioinformatics, 2015, 31, 4023-4025.	1.8	21
10	Exploring the folding pathway of green fluorescent protein through disulfide engineering. Protein Science, 2015, 24, 341-353.	3.1	12
11	Greenâ€lighting green fluorescent protein: Faster and more efficient folding by eliminating a cisâ€“trans peptide isomerization event. Protein Science, 2014, 23, 400-410.	3.1	8
12	Improving computational efficiency and tractability of protein design using a piecemeal approach. A strategy for parallel and distributed protein design. Bioinformatics, 2014, 30, 1138-1145.	1.8	5
13	Expanded Explorations into the Optimization of an Energy Function for Protein Design. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1176-1187.	1.9	5
14	Geofold: Topologyâ€based protein unfolding pathways capture the effects of engineered disulfides on kinetic stability. Proteins: Structure, Function and Bioinformatics, 2012, 80, 920-934.	1.5	18
15	Comparative void-volume analysis of psychrophilic and mesophilic enzymes: Structural bioinformatics of psychrophilic enzymes reveals sources of core flexibility. BMC Structural Biology, 2011, 11, 42.	2.3	67
16	Constraining local structure can speed up folding by promoting structural polarization of the folding pathway. Protein Science, 2011, 20, 959-969.	3.1	3
17	Quantitative in vivo solubility and reconstitution of truncated circular permutants of green fluorescent protein. Protein Science, 2011, 20, 1775-1780.	3.1	15
18	A Rewired Green Fluorescent Protein: Folding and Function in a Nonsequential, Noncircular GFP Permutant. Biochemistry, 2010, 49, 10773-10779.	1.2	12

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19	Simulating protein folding initiation sites using an alphaâ€carbonâ€only knowledgeâ€based force field. Proteins: Structure, Function and Bioinformatics, 2009, 76, 331-342.	1.5	4
20	Alpha helical crossovers favor rightâ€handed supersecondary structures by kinetic trapping: The phone cord effect in protein folding. Protein Science, 2009, 18, 1602-1608.	3.1	18
21	Complementation and Reconstitution of Fluorescence from Circularly Permuted and Truncated Green Fluorescent Protein. Biochemistry, 2009, 48, 929-940.	1.2	32
22	Context shapes: Efficient complementary shape matching for proteinâ€“protein docking. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1056-1073.	1.5	27
23	Hidden Markov Models for Prediction of Protein Features. , 2008, 413, 173-198.		17
24	Pairwise covariance adds little to secondary structure prediction but improves the prediction of non-canonical local structure. BMC Bioinformatics, 2008, 9, 429.	1.2	1
25	Modeling Protein Folding Pathways. Nucleic Acids and Molecular Biology, 2008, , 97-122.	0.2	1
26	Identifying the subproteome of kinetically stable proteins via diagonal 2D SDS/PAGE. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 17329-17334.	3.3	73
27	Protein Contact Map Prediction. , 2007, , 255-277.		5
28	Non-sequential structure-based alignments reveal topology-independent core packing arrangements in proteins. Bioinformatics, 2005, 21, 1010-1019.	1.8	45
29	Five Hierarchical Levels of Sequence-Structure Correlation in Proteins. Applied Bioinformatics, 2004, 3, 97-104.	1.7	6
30	Ab Initio Protein Structure Prediction Using Pathway Models. Comparative and Functional Genomics, 2003, 4, 397-401.	2.0	4
31	Helix propensities of short peptides: Molecular dynamics versus bioinformatics. Proteins: Structure, Function and Bioinformatics, 2003, 50, 552-562.	1.5	25
32	Predicting interresidue contacts using templates and pathways. Proteins: Structure, Function and Bioinformatics, 2003, 53, 497-502.	1.5	68
33	MASKER: improved solvent-excluded molecular surface area estimations using Boolean masks. Protein Engineering, Design and Selection, 2002, 15, 959-965.	1.0	21
34	Fully automated ab initio protein structure prediction using I-SITES, HMMSTR and ROSETTA. Bioinformatics, 2002, 18, S54-S61.	1.8	117
35	An alternative derivation of the equations of motion in torsion space for a branched linear chain. Protein Engineering, Design and Selection, 2001, 14, 825-828.	1.0	7
36	HMMSTR: a hidden Markov model for local sequence-structure correlations in proteins 1 1Edited by J. Thornton. Journal of Molecular Biology, 2000, 301, 173-190.	2.0	286

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37	Prediction of local structure in proteins using a library of sequence-structure motifs. Journal of Molecular Biology, 1998, 281, 565-577.	2.0	331
38	Threeâ€dimensional structures and contexts associated with recurrent amino acid sequence patterns. Protein Science, 1997, 6, 1587-1590.	3.1	35
39	Blind predictions of local protein structure in CASP2 targets using the I-sites library. Proteins: Structure, Function and Bioinformatics, 1997, 29, 167-171.	1.5	23
40	Local sequence-structure correlations in proteins. Current Opinion in Biotechnology, 1996, 7, 417-421.	3.3	67
41	Crystal structure of unliganded Escherichia coli dihydrofolate reductase. Ligand-induced conformational changes and cooperativity in binding. Biochemistry, 1991, 30, 2227-2239.	1.2	211