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	Prediction of local structure in proteins using a library of sequence-structure motifs. Journal of Molecular Biology, 1998, 281, 565-577.	2.0	331
2	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
3	Crystal structure of unliganded Escherichia coli dihydrofolate reductase. Ligand-induced conformational changes and cooperativity in binding. Biochemistry, 1991, 30, 2227-2239.	1.2	211
4	Fully automated ab initio protein structure prediction using I-SITES, HMMSTR and ROSETTA. Bioinformatics, 2002, 18, S54-S61.	1.8	117
5	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
6	Predicting interresidue contacts using templates and pathways. Proteins: Structure, Function and Bioinformatics, 2003, 53, 497-502.	1.5	68
7	Local sequence-structure correlations in proteins. Current Opinion in Biotechnology, 1996, 7, 417-421.	3.3	67
8	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
9	Non-sequential structure-based alignments reveal topology-independent core packing arrangements in proteins. Bioinformatics, 2005, 21, 1010-1019.	1.8	45
10	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
11	Threeâ€dimensional structures and contexts associated with recurrent amino acid sequence patterns. Protein Science, 1997, 6, 1587-1590.	3.1	35
12	Complementation and Reconstitution of Fluorescence from Circularly Permuted and Truncated Green Fluorescent Protein. Biochemistry, 2009, 48, 929-940.	1.2	32
13	Context shapes: Efficient complementary shape matching for proteinâ€“protein docking. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1056-1073.	1.5	27
14	Helix propensities of short peptides: Molecular dynamics versus bioinformatics. Proteins: Structure, Function and Bioinformatics, 2003, 50, 552-562.	1.5	25
15	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
16	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
17	MASKER: improved solvent-excluded molecular surface area estimations using Boolean masks. Protein Engineering, Design and Selection, 2002, 15, 959-965.	1.0	21
18	InteractiveROSETTA: a graphical user interface for the PyRosetta protein modeling suite. Bioinformatics, 2015, 31, 4023-4025.	1.8	21

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19	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
20	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
21	Hidden Markov Models for Prediction of Protein Features. , 2008, 413, 173-198.		17
22	Quantitative in vivo solubility and reconstitution of truncated circular permutants of green fluorescent protein. Protein Science, 2011, 20, 1775-1780.	3.1	15
23	A Rewired Green Fluorescent Protein: Folding and Function in a Nonsequential, Noncircular GFP Permutant. Biochemistry, 2010, 49, 10773-10779.	1.2	12
24	Exploring the folding pathway of green fluorescent protein through disulfide engineering. Protein Science, 2015, 24, 341-353.	3.1	12
25	Mispacking and the Fitness Landscape of the Green Fluorescent Protein Chromophore Milieu. Biochemistry, 2017, 56, 736-747.	1.2	11
26	Intramembranal disulfide cross-linking elucidates the super-quaternary structure of mammalian CatSpers. Reproductive Biology, 2018, 18, 76-82.	0.9	11
27	Toward Computationally Designed Self-Reporting Biosensors Using Leave-One-Out Green Fluorescent Protein. Biochemistry, 2015, 54, 6263-6273.	1.2	10
28	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
29	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
30	Five Hierarchical Levels of Sequence-Structure Correlation in Proteins. Applied Bioinformatics, 2004, 3, 97-104.	1.7	6
31	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
32	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
33	Complex between a Multicrossover DNA Nanostructure, PX-DNA, and T7 Endonuclease I. Biochemistry, 2019, 58, 1332-1342.	1.2	5
34	Protein Contact Map Prediction. , 2007, , 255-277.		5
35	Ab Initio Protein Structure Prediction Using Pathway Models. Comparative and Functional Genomics, 2003, 4, 397-401.	2.0	4
36	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

#	Article	IF	Citations
37	Fast design of arbitrary length loops in proteins using InteractiveRosetta. BMC Bioinformatics, 2018, 19, 337.	1.2	4
38	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
39	Constraining local structure can speed up folding by promoting structural polarization of the folding pathway. Protein Science, 2011, 20, 959-969.	3.1	3
40	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
41	Modeling Protein Folding Pathways. Nucleic Acids and Molecular Biology, 2008, , 97-122.	0.2	1