Christopher Langmead

List of Publications by Year
in descending order

21 papers	1,042 citations	623734 14 h-index	713466 21 g-index
23 all docs	23 docs citations	23 times ranked	1806 citing authors

#	Article	IF	Citations
1	Learning generative models for protein fold families. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1061-1078.	2.6	293
2	Serum Biomarker Panels for the Detection of Pancreatic Cancer. Clinical Cancer Research, 2011, 17, 805-816.	7.0	203
3	Dynamic allostery governs cyclophilin Aâ€"HIV capsid interplay. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 14617-14622.	7.1	76
4	Discovering Conformational Sub-States Relevant to Protein Function. PLoS ONE, 2011, 6, e15827.	2.5	61
5	An expectation/maximization nuclear vector replacement algorithm for automated NMR resonance assignments. Journal of Biomolecular NMR, 2004, 29, 111-138.	2.8	55
6	SYMBOLIC APPROACHES FOR FINDING CONTROL STRATEGIES IN BOOLEAN NETWORKS. Journal of Bioinformatics and Computational Biology, 2009, 07, 323-338.	0.8	49
7	Accounting for conformational entropy in predicting binding free energies of proteinâ€protein interactions. Proteins: Structure, Function and Bioinformatics, 2011, 79, 444-462.	2.6	49
8	HIV-1 Capsid Function Is Regulated by Dynamics: Quantitative Atomic-Resolution Insights by Integrating Magic-Angle-Spinning NMR, QM/MM, and MD. Journal of the American Chemical Society, 2016, 138, 14066-14075.	13.7	48
9	A Polynomial-Time Nuclear Vector Replacement Algorithm for Automated NMR Resonance Assignments. Journal of Computational Biology, 2004, 11, 277-298.	1.6	34
10	Parameter Synthesis in Nonlinear Dynamical Systems: Application to Systems Biology. Journal of Computational Biology, 2010, 17, 325-336.	1.6	33
11	Free Energy Estimates of All-Atom Protein Structures Using Generalized Belief Propagation. Journal of Computational Biology, 2008, 15, 755-766.	1.6	29
12	An Online Approach for Mining Collective Behaviors from Molecular Dynamics Simulations. Journal of Computational Biology, 2010, 17, 309-324.	1.6	27
13	Efficient Modeling and Active Learning Discovery of Biological Responses. PLoS ONE, 2013, 8, e83996.	2.5	26
14	Phase-Independent Rhythmic Analysis of Genome-Wide Expression Patterns. Journal of Computational Biology, 2003, 10, 521-536.	1.6	22
15	On-the-Fly Identification of Conformational Substates from Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2011, 7, 778-789.	5.3	15
16	The Marker State Space (MSS) Method for Classifying Clinical Samples. PLoS ONE, 2013, 8, e65905.	2.5	6
17	Learning Sequence Determinants of Protein:Protein Interaction Specificity with Sparse Graphical Models. Journal of Computational Biology, 2015, 22, 474-486.	1.6	5
18	Systematic Testing of Belief-Propagation Estimates for Absolute Free Energies in Atomistic Peptides and Proteins. Journal of Chemical Theory and Computation, 2018, 14, 426-443.	5.3	3

#	Article	IF	Citations
19	Generative Models of Conformational Dynamics. Advances in Experimental Medicine and Biology, 2014, 805, 87-105.	1.6	3
20	Harvestman: a framework for hierarchical feature learning and selection from whole genome sequencing data. BMC Bioinformatics, 2021, 22, 174.	2.6	1
21	Response to Brisinda et al. and Windsor. American Journal of Gastroenterology, 2010, 105, 1673-1674.	0.4	0