

Christopher Langmead

List of Publications by Year in descending order

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Version: 2024-02-01

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	Harvestman: a framework for hierarchical feature learning and selection from whole genome sequencing data. <i>BMC Bioinformatics</i> , 2021, 22, 174.	2.6	1
2	Systematic Testing of Belief-Propagation Estimates for Absolute Free Energies in Atomistic Peptides and Proteins. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 426-443.	5.3	3
3	HIV-1 Capsid Function Is Regulated by Dynamics: Quantitative Atomic-Resolution Insights by Integrating Magic-Angle-Spinning NMR, QM/MM, and MD. <i>Journal of the American Chemical Society</i> , 2016, 138, 14066-14075.	13.7	48
4	Learning Sequence Determinants of Protein:Protein Interaction Specificity with Sparse Graphical Models. <i>Journal of Computational Biology</i> , 2015, 22, 474-486.	1.6	5
5	Dynamic allostery governs cyclophilin Aâ€™HIV capsid interplay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14617-14622.	7.1	76
6	Generative Models of Conformational Dynamics. <i>Advances in Experimental Medicine and Biology</i> , 2014, 805, 87-105.	1.6	3
7	The Marker State Space (MSS) Method for Classifying Clinical Samples. <i>PLoS ONE</i> , 2013, 8, e65905.	2.5	6
8	Efficient Modeling and Active Learning Discovery of Biological Responses. <i>PLoS ONE</i> , 2013, 8, e83996.	2.5	26
9	On-the-Fly Identification of Conformational Substates from Molecular Dynamics Simulations. <i>Journal of Chemical Theory and Computation</i> , 2011, 7, 778-789.	5.3	15
10	Discovering Conformational Sub-States Relevant to Protein Function. <i>PLoS ONE</i> , 2011, 6, e15827.	2.5	61
11	Accounting for conformational entropy in predicting binding free energies of proteinâ€™protein interactions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 444-462.	2.6	49
12	Learning generative models for protein fold families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1061-1078.	2.6	293
13	Serum Biomarker Panels for the Detection of Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2011, 17, 805-816.	7.0	203
14	Response to Brisinda et al. and Windsor. <i>American Journal of Gastroenterology</i> , 2010, 105, 1673-1674.	0.4	0
15	An Online Approach for Mining Collective Behaviors from Molecular Dynamics Simulations. <i>Journal of Computational Biology</i> , 2010, 17, 309-324.	1.6	27
16	Parameter Synthesis in Nonlinear Dynamical Systems: Application to Systems Biology. <i>Journal of Computational Biology</i> , 2010, 17, 325-336.	1.6	33
17	SYMBOLIC APPROACHES FOR FINDING CONTROL STRATEGIES IN BOOLEAN NETWORKS. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 323-338.	0.8	49
18	Free Energy Estimates of All-Atom Protein Structures Using Generalized Belief Propagation. <i>Journal of Computational Biology</i> , 2008, 15, 755-766.	1.6	29

#	ARTICLE	IF	CITATIONS
19	A Polynomial-Time Nuclear Vector Replacement Algorithm for Automated NMR Resonance Assignments. Journal of Computational Biology, 2004, 11, 277-298.	1.6	34
20	An expectation/maximization nuclear vector replacement algorithm for automated NMR resonance assignments. Journal of Biomolecular NMR, 2004, 29, 111-138.	2.8	55
21	Phase-Independent Rhythmic Analysis of Genome-Wide Expression Patterns. Journal of Computational Biology, 2003, 10, 521-536.	1.6	22