

Eric J Deeds

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

1,780
citations

331670

21
h-index

315739

38
g-index

47
all docs

47
docs citations

47
times ranked

2444
citing authors

#	ARTICLE	IF	CITATIONS
1	Curvature in metabolic scaling. <i>Nature</i> , 2010, 464, 753-756.	27.8	293
2	Sizing Up Allometric Scaling Theory. <i>PLoS Computational Biology</i> , 2008, 4, e1000171.	3.2	198
3	From The Cover: A simple physical model for scaling in protein-protein interaction networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 311-316.	7.1	117
4	Machine learning classification can reduce false positives in structure-based virtual screening. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18477-18488.	7.1	111
5	Fundamental trade-offs between information flow in single cells and cellular populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5755-5760.	7.1	106
6	Crosstalk and the evolution of specificity in two-component signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5550-5555.	7.1	95
7	Protein structure and evolutionary history determine sequence space topology. <i>Genome Research</i> , 2005, 15, 385-392.	5.5	82
8	Robust protein protein interactions in crowded cellular environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14952-14957.	7.1	70
9	Understanding ensemble protein folding at atomic detail. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17747-17752.	7.1	64
10	Crosstalk and Competition in Signaling Networks. <i>Biophysical Journal</i> , 2012, 103, 2389-2398.	0.5	57
11	Machines vs. Ensembles: Effective MAPK Signaling through Heterogeneous Sets of Protein Complexes. <i>PLoS Computational Biology</i> , 2013, 9, e1003278.	3.2	46
12	High-resolution protein folding with a transferable potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18914-18919.	7.1	44
13	Combinatorial Complexity and Compositional Drift in Protein Interaction Networks. <i>PLoS ONE</i> , 2012, 7, e32032.	2.5	42
14	Optimizing ring assembly reveals the strength of weak interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 2348-2353.	7.1	41
15	Maturation of the proteasome core particle induces an affinity switch that controls regulatory particle association. <i>Nature Communications</i> , 2015, 6, 6384.	12.8	39
16	Protein Evolution within a Structural Space. <i>Biophysical Journal</i> , 2003, 85, 2962-2972.	0.5	37
17	Prokaryotic phylogenies inferred from protein structural domains. <i>Genome Research</i> , 2005, 15, 393-402.	5.5	34
18	Crosstalk and the evolvability of intracellular communication. <i>Nature Communications</i> , 2017, 8, 16009.	12.8	29

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19	Structural Properties of Non-Traditional Drug Targets Present New Challenges for Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 2073-2081.	5.4	28
20	Phosphatase Specificity and Pathway Insulation in Signaling Networks. <i>Biophysical Journal</i> , 2015, 108, 986-996.	0.5	25
21	Equilibrium Distribution of Mutators in the Single Fitness Peak Model. <i>Physical Review Letters</i> , 2003, 91, 138105.	7.8	23
22	Proteomic Traces of Speciation. <i>Journal of Molecular Biology</i> , 2004, 336, 695-706.	4.2	19
23	Quantifying information accumulation encoded in the dynamics of biochemical signaling. <i>Nature Communications</i> , 2021, 12, 1272.	12.8	18
24	The Botanical Drug Substance Crofelemer as a Model System for Comparative Characterization of Complex Mixture Drugs. <i>Journal of Pharmaceutical Sciences</i> , 2017, 106, 3242-3256.	3.3	14
25	Mathematical Model for Length Control by the Timing of Substrate Switching in the Type III Secretion System. <i>PLoS Computational Biology</i> , 2016, 12, e1004851.	3.2	14
26	Differential Contributions of Actin and Myosin to the Physical Phenotypes and Invasion of Pancreatic Cancer Cells. <i>Cellular and Molecular Bioengineering</i> , 2020, 13, 27-44.	2.1	13
27	Computational approaches to macromolecular interactions in the cell. <i>Current Opinion in Structural Biology</i> , 2019, 55, 59-65.	5.7	12
28	Signal integration and information transfer in an allosterically regulated network. <i>Npj Systems Biology and Applications</i> , 2019, 5, 23.	3.0	11
29	The Emergence of Scaling in Sequence-Based Physical Models of Protein Evolution. <i>Biophysical Journal</i> , 2005, 88, 3905-3911.	0.5	9
30	Quantifying fitness distributions and phenotypic relationships in recombinant yeast populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 10553-10558.	7.1	9
31	Intrinsic limits of information transmission in biochemical signalling motifs. <i>Interface Focus</i> , 2018, 8, 20180039.	3.0	9
32	Chemical Stability of the Botanical Drug Substance Crofelemer: A Model System for Comparative Characterization of Complex Mixture Drugs. <i>Journal of Pharmaceutical Sciences</i> , 2017, 106, 3257-3269.	3.3	6
33	Curvature in metabolic scaling: A reply to MacKay. <i>Journal of Theoretical Biology</i> , 2011, 280, 197-198.	1.7	5
34	Comparative Characterization of Crofelemer Samples Using Data Mining and Machine Learning Approaches With Analytical Stability Data Sets. <i>Journal of Pharmaceutical Sciences</i> , 2017, 106, 3270-3279.	3.3	5
35	Cooperativity in Proteasome Core Particle Maturation. <i>IScience</i> , 2020, 23, 101090.	4.1	5
36	Crosstalk and ultrasensitivity in protein degradation pathways. <i>PLoS Computational Biology</i> , 2020, 16, e1008492.	3.2	5

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37	Robustness and the evolution of length control strategies in the T3SS and flagellar hook. Biophysical Journal, 2021, 120, 3820-3830.	0.5	1
38	Teaching Dynamics to Biology Undergraduates: the UCLA Experience. Bulletin of Mathematical Biology, 2022, 84, 43.	1.9	1
39	Optimizing the Assembly of Stacked Rings. Biophysical Journal, 2015, 108, 220a-221a.	0.5	0
40	Modeling Proteasome Assembly Pathways in Bacteria. Biophysical Journal, 2019, 116, 63a.	0.5	0