

Joshua L Payne

List of Publications by Year in descending order

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46
papers

1,431
citations

394286

19
h-index

377752

34
g-index

51
all docs

51
docs citations

51
times ranked

1723
citing authors

#	ARTICLE	IF	CITATIONS
1	The causes of evolvability and their evolution. <i>Nature Reviews Genetics</i> , 2019, 20, 24-38.	7.7	208
2	The Robustness and Evolvability of Transcription Factor Binding Sites. <i>Science</i> , 2014, 343, 875-877.	6.0	139
3	Cryptic genetic variation accelerates evolution by opening access to diverse adaptive peaks. <i>Science</i> , 2019, 365, 347-353.	6.0	96
4	Mechanisms of mutational robustness in transcriptional regulation. <i>Frontiers in Genetics</i> , 2015, 6, 322.	1.1	89
5	A thousand empirical adaptive landscapes and their navigability. <i>Nature Ecology and Evolution</i> , 2017, 1, 45.	3.4	79
6	The SIB Swiss Institute of Bioinformatics's™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
7	Information cascades on degree-correlated random networks. <i>Physical Review E</i> , 2009, 80, 026125.	0.8	53
8	Transition bias influences the evolution of antibiotic resistance in <i>Mycobacterium tuberculosis</i> . <i>PLoS Biology</i> , 2019, 17, e3000265.	2.6	50
9	Analysis of a threshold model of social contagion on degree-correlated networks. <i>Physical Review E</i> , 2009, 79, 066115.	0.8	49
10	From genotypes to organisms: State-of-the-art and perspectives of a cornerstone in evolutionary dynamics. <i>Physics of Life Reviews</i> , 2021, 38, 55-106.	1.5	49
11	Robustness, Evolvability, and the Logic of Genetic Regulation. <i>Artificial Life</i> , 2014, 20, 111-126.	1.0	43
12	Enhancers Facilitate the Birth of De Novo Genes and Gene Integration into Regulatory Networks. <i>Molecular Biology and Evolution</i> , 2020, 37, 1165-1178.	3.5	41
13	Function does not follow form in gene regulatory circuits. <i>Scientific Reports</i> , 2015, 5, 13015.	1.6	40
14	Evolutionary Dynamics on Scale-Free Interaction Networks. <i>IEEE Transactions on Evolutionary Computation</i> , 2009, 13, 895-912.	7.5	37
15	Mutation bias shapes the spectrum of adaptive substitutions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	34
16	Constraint and Contingency in Multifunctional Gene Regulatory Circuits. <i>PLoS Computational Biology</i> , 2013, 9, e1003071.	1.5	33
17	RNA-mediated gene regulation is less evolvable than transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3481-E3490.	3.3	31
18	Evolutionary dynamics on multiple scales: a quantitative analysis of the interplay between genotype, phenotype, and fitness in linear genetic programming. <i>Genetic Programming and Evolvable Machines</i> , 2012, 13, 305-337.	1.5	30

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19	The architecture of an empirical genotype-phenotype map. <i>Evolution; International Journal of Organic Evolution</i> , 2018, 72, 1242-1260.	1.1	27
20	Mutation bias interacts with composition bias to influence adaptive evolution. <i>PLoS Computational Biology</i> , 2020, 16, e1008296.	1.5	21
21	Genomic mining for complex disease traits with “random chemistry”. <i>Genetic Programming and Evolvable Machines</i> , 2007, 8, 395-411.	1.5	20
22	Exploiting graphics processing units for computational biology and bioinformatics. <i>Interdisciplinary Sciences, Computational Life Sciences</i> , 2010, 2, 213-220.	2.2	20
23	The evolution of conditional dispersal and reproductive isolation along environmental gradients. <i>Journal of Theoretical Biology</i> , 2011, 273, 147-155.	0.8	20
24	Latent phenotypes pervade gene regulatory circuits. <i>BMC Systems Biology</i> , 2014, 8, 64.	3.0	16
25	The influence of assortativity on the robustness of signal-integration logic in gene regulatory networks. <i>Journal of Theoretical Biology</i> , 2012, 296, 21-32.	0.8	15
26	Complex and dynamic population structures: synthesis, open questions, and future directions. <i>Soft Computing</i> , 2013, 17, 1109-1120.	2.1	15
27	Exact solutions for social and biological contagion models on mixed directed and undirected, degree-correlated random networks. <i>Physical Review E</i> , 2011, 84, 016110.	0.8	14
28	Genonets server—a web server for the construction, analysis and visualization of genotype networks. <i>Nucleic Acids Research</i> , 2016, 44, W70-W76.	6.5	12
29	Phenotypic Robustness and the Assortativity Signature of Human Transcription Factor Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003780.	1.5	11
30	The influence of assortativity on the robustness and evolvability of gene regulatory networks upon gene birth. <i>Journal of Theoretical Biology</i> , 2013, 330, 26-36.	0.8	10
31	Sensible Initialization of a Computational Evolution System Using Expert Knowledge for Epistasis Analysis in Human Genetics. <i>Adaptation, Learning, and Optimization</i> , 2010, , 215-226.	0.5	9
32	The influence of scaling and assortativity on takeover times in scale-free topologies. , 2008, , .		8
33	Direct, physically motivated derivation of the contagion condition for spreading processes on generalized random networks. <i>Physical Review E</i> , 2011, 83, 056122.	0.8	8
34	Takeover times on scale-free topologies. , 2007, , .		7
35	Underdominance, Multiscale Interactions, and Self-Organizing Barriers to Gene Flow. <i>Journal of Artificial Evolution and Applications</i> , 2009, 2009, 1-13.	1.8	7
36	Pair Approximations of Takeover Dynamics in Regular Population Structures. <i>Evolutionary Computation</i> , 2009, 17, 203-229.	2.3	7

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37	Little Evidence the Standard Genetic Code Is Optimized for Resource Conservation. <i>Molecular Biology and Evolution</i> , 2021, 38, 5127-5133.	3.5	6
38	Exploiting Expert Knowledge of Protein-Protein Interactions in a Computational Evolution System for Detecting Epistasis. <i>Genetic and Evolutionary Computation</i> , 2011, , 195-210.	1.0	5
39	Sensitivity of Self-Organized Speciation to Long-Distance Dispersal. , 2007, , .		2
40	No tradeoff between versatility and robustness in gene circuit motifs. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2016, 449, 192-199.	1.2	2
41	Robustness and Evolvability in Transcriptional Regulation. , 2021, , 197-219.		1
42	Sexual Recombination in Self-Organizing Interaction Networks. <i>Lecture Notes in Computer Science</i> , 2010, , 41-50.	1.0	0
43	Mutation bias interacts with composition bias to influence adaptive evolution. , 2020, 16, e1008296.		0
44	Mutation bias interacts with composition bias to influence adaptive evolution. , 2020, 16, e1008296.		0
45	Mutation bias interacts with composition bias to influence adaptive evolution. , 2020, 16, e1008296.		0
46	Mutation bias interacts with composition bias to influence adaptive evolution. , 2020, 16, e1008296.		0