## Joshua L Payne

List of Publications by Year in descending order

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LOSHUA L DAVNE

#	Article	IF	CITATIONS
1	The causes of evolvability and their evolution. Nature Reviews Genetics, 2019, 20, 24-38.	16.3	208
2	The Robustness and Evolvability of Transcription Factor Binding Sites. Science, 2014, 343, 875-877.	12.6	139
3	Cryptic genetic variation accelerates evolution by opening access to diverse adaptive peaks. Science, 2019, 365, 347-353.	12.6	96
4	Mechanisms of mutational robustness in transcriptional regulation. Frontiers in Genetics, 2015, 6, 322.	2.3	89
5	A thousand empirical adaptive landscapes and their navigability. Nature Ecology and Evolution, 2017, 1, 45.	7.8	79
6	The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64
7	Information cascades on degree-correlated random networks. Physical Review E, 2009, 80, 026125.	2.1	53
8	Transition bias influences the evolution of antibiotic resistance in Mycobacterium tuberculosis. PLoS Biology, 2019, 17, e3000265.	5.6	50
9	Analysis of a threshold model of social contagion on degree-correlated networks. Physical Review E, 2009, 79, 066115.	2.1	49
10	From genotypes to organisms: State-of-the-art and perspectives of a cornerstone in evolutionary dynamics. Physics of Life Reviews, 2021, 38, 55-106.	2.8	49
11	Robustness, Evolvability, and the Logic of Genetic Regulation. Artificial Life, 2014, 20, 111-126.	1.3	43
12	Enhancers Facilitate the Birth of De Novo Genes and Gene Integration into Regulatory Networks. Molecular Biology and Evolution, 2020, 37, 1165-1178.	8.9	41
13	Function does not follow form in gene regulatory circuits. Scientific Reports, 2015, 5, 13015.	3.3	40
14	Evolutionary Dynamics on Scale-Free Interaction Networks. IEEE Transactions on Evolutionary Computation, 2009, 13, 895-912.	10.0	37
15	Mutation bias shapes the spectrum of adaptive substitutions. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	34
16	Constraint and Contingency in Multifunctional Gene Regulatory Circuits. PLoS Computational Biology, 2013, 9, e1003071.	3.2	33
17	RNA-mediated gene regulation is less evolvable than transcriptional regulation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3481-E3490.	7.1	31
18	Evolutionary dynamics on multiple scales: a quantitative analysis of the interplay between genotype, phenotype, and fitness in linear genetic programming. Genetic Programming and Evolvable Machines, 2012, 13, 305-337.	2.2	30

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19	The architecture of an empirical genotype-phenotype map. Evolution; International Journal of Organic Evolution, 2018, 72, 1242-1260.	2.3	27
20	Mutation bias interacts with composition bias to influence adaptive evolution. PLoS Computational Biology, 2020, 16, e1008296.	3.2	21
21	Genomic mining for complex disease traits with "random chemistry― Genetic Programming and Evolvable Machines, 2007, 8, 395-411.	2.2	20
22	Exploiting graphics processing units for computational biology and bioinformatics. Interdisciplinary Sciences, Computational Life Sciences, 2010, 2, 213-220.	3.6	20
23	The evolution of conditional dispersal and reproductive isolation along environmental gradients. Journal of Theoretical Biology, 2011, 273, 147-155.	1.7	20
24	Latent phenotypes pervade gene regulatory circuits. BMC Systems Biology, 2014, 8, 64.	3.0	16
25	The influence of assortativity on the robustness of signal-integration logic in gene regulatory networks. Journal of Theoretical Biology, 2012, 296, 21-32.	1.7	15
26	Complex and dynamic population structures: synthesis, open questions, and future directions. Soft Computing, 2013, 17, 1109-1120.	3.6	15
27	Exact solutions for social and biological contagion models on mixed directed and undirected, degree-correlated random networks. Physical Review E, 2011, 84, 016110.	2.1	14
28	Genonets server—a web server for the construction, analysis and visualization of genotype networks. Nucleic Acids Research, 2016, 44, W70-W76.	14.5	12
29	Phenotypic Robustness and the Assortativity Signature of Human Transcription Factor Networks. PLoS Computational Biology, 2014, 10, e1003780.	3.2	11
30	The influence of assortativity on the robustness and evolvability of gene regulatory networks upon gene birth. Journal of Theoretical Biology, 2013, 330, 26-36.	1.7	10
31	Sensible Initialization of a Computational Evolution System Using Expert Knowledge for Epistasis Analysis in Human Genetics. Adaptation, Learning, and Optimization, 2010, , 215-226.	0.6	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. Physical Review E, 2011, 83, 056122.	2.1	8
34	Takeover times on scale-free topologies. , 2007, , .		7
35	Underdominance, Multiscale Interactions, and Self-Organizing Barriers to Gene Flow. Journal of Artificial Evolution and Applications, 2009, 2009, 1-13.	1.8	7
36	Pair Approximations of Takeover Dynamics in Regular Population Structures. Evolutionary Computation, 2009, 17, 203-229.	3.0	7

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#	Article	IF	CITATIONS
37	Little Evidence the Standard Genetic Code Is Optimized for Resource Conservation. Molecular Biology and Evolution, 2021, 38, 5127-5133.	8.9	6
38	Exploiting Expert Knowledge of Protein-Protein Interactions in a Computational Evolution System for Detecting Epistasis. Genetic and Evolutionary Computation, 2011, , 195-210.	1.0	5
39	Sensitivity of Self-Organized Speciation to Long-Disctance Dispersal. , 2007, , .		2
40	No tradeoff between versatility and robustness in gene circuit motifs. Physica A: Statistical Mechanics and Its Applications, 2016, 449, 192-199.	2.6	2
41	Robustness and Evolvability in Transcriptional Regulation. , 2021, , 197-219.		1
42	Sexual Recombination in Self-Organizing Interaction Networks. Lecture Notes in Computer Science, 2010, , 41-50.	1.3	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