

# David A Liberles

## List of Publications by Year in descending order

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69  
papers

3,606  
citations

218677

26  
h-index

155660

55  
g-index

120  
all docs

120  
docs citations

120  
times ranked

4831  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Atlantic salmon genome provides insights into rediploidization. <i>Nature</i> , 2016, 533, 200-205.	27.8	1,021
2	Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014, 5, 3636.	12.8	371
3	Subfunctionalization of duplicated genes as a transition state to neofunctionalization. <i>BMC Evolutionary Biology</i> , 2005, 5, 28.	3.2	311
4	The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.	7.6	188
5	Evolution after gene duplication: models, mechanisms, sequences, systems, and organisms. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 58-73.	1.3	148
6	Evolution in the light of fitness landscape theory. <i>Trends in Ecology and Evolution</i> , 2019, 34, 69-82.	8.7	124
7	Optimal Gene Trees from Sequences and Species Trees Using a Soft Interpretation of Parsimony. <i>Journal of Molecular Evolution</i> , 2006, 63, 240-250.	1.8	78
8	A systematic search for positive selection in higher plants (Embryophytes). <i>BMC Plant Biology</i> , 2006, 6, 12.	3.6	78
9	The Adaptive Evolution Database (TAED): a phylogeny based tool for comparative genomics. <i>Nucleic Acids Research</i> , 2004, 33, D495-D497.	14.5	73
10	Functional inferences from reconstructed evolutionary biology involving rectified databases – an evolutionarily grounded approach to functional genomics. <i>Research in Microbiology</i> , 2000, 151, 97-106.	2.1	58
11	Toward a General Model for the Evolutionary Dynamics of Gene Duplicates. <i>Genome Biology and Evolution</i> , 2011, 3, 1197-1209.	2.5	57
12	The Pattern of Evolution of Smaller-Scale Gene Duplicates in Mammalian Genomes is More Consistent with Neo- than Subfunctionalisation. <i>Journal of Molecular Evolution</i> , 2007, 65, 574-588.	1.8	52
13	State-of the art methodologies dictate new standards for phylogenetic analysis. <i>BMC Evolutionary Biology</i> , 2013, 13, 161.	3.2	51
14	The Evolution of Protein Structures and Structural Ensembles Under Functional Constraint. <i>Genes</i> , 2011, 2, 748-762.	2.4	50
15	Biophysical and structural considerations for protein sequence evolution. <i>BMC Evolutionary Biology</i> , 2011, 11, 361.	3.2	50
16	Role of architectural elements in combinatorial regulation of initiation of DNA replication in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1997, 26, 261-275.	2.5	47
17	Visualising very large phylogenetic trees in three dimensional hyperbolic space. <i>BMC Bioinformatics</i> , 2004, 5, 48.	2.6	47
18	Selection on protein structure, interaction, and sequence. <i>Protein Science</i> , 2016, 25, 1168-1178.	7.6	47

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19	Extracting functional trends from whole genome duplication events using comparative genomics. <i>Biological Procedures Online</i> , 2016, 18, 11.	2.9	45
20	On the Need for Mechanistic Models in Computational Genomics and Metagenomics. <i>Genome Biology and Evolution</i> , 2013, 5, 2008-2018.	2.5	40
21	Myostatin rapid sequence evolution in ruminants predates domestication. <i>Molecular Phylogenetics and Evolution</i> , 2004, 33, 782-790.	2.7	38
22	The adaptive evolution database (TAED). <i>Genome Biology</i> , 2001, 2, research0028.1.	9.6	35
23	Models for gene duplication when dosage balance works as a transition state to subsequent neo- or sub-functionalization. <i>BMC Evolutionary Biology</i> , 2016, 16, 45.	3.2	35
24	Triple-Helix Formation by Pyrimidine Oligonucleotides Containing Nonnatural Nucleosides with Extended Aromatic Nucleobases: Intercalation from the major groove as a method for recognizing CÂ·G and T Â· A base pairs. <i>Helvetica Chimica Acta</i> , 1997, 80, 2002-2022.	1.6	32
25	Finding the balance between the mathematical and biological optima in multiple sequence alignment. <i>Trends in Evolutionary Biology</i> , 2010, 2, 7.	0.4	30
26	ProtASR: An Evolutionary Framework for Ancestral Protein Reconstruction with Selection on Folding Stability. <i>Systematic Biology</i> , 2017, 66, syw121.	5.6	29
27	Keeping the blood flowingâ€”plasminogen activator genes and feeding behavior in vampire bats. <i>Die Naturwissenschaften</i> , 2009, 96, 39-47.	1.6	27
28	Binding constraints on the evolution of enzymes and signalling proteins: the important role of negative pleiotropy. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2011, 278, 1930-1935.	2.6	27
29	Detecting and understanding natural selection. , 2012, , 73-96.		26
30	Ancestral Sequence Reconstruction: From Chemical Paleogenetics to Maximum Likelihood Algorithms and Beyond. <i>Journal of Molecular Evolution</i> , 2021, 89, 157-164.	1.8	25
31	Using Evolutionary Information and Ancestral Sequences to Understand the Sequenceâ€“Function Relationship in GLP-1 Agonists. <i>Journal of Molecular Biology</i> , 2006, 363, 977-988.	4.2	23
32	A Phylogenetic Analysis of Normal Modes Evolution in Enzymes and Its Relationship to Enzyme Function. <i>Journal of Molecular Biology</i> , 2012, 422, 442-459.	4.2	22
33	Genetic Simulation Tools for Postâ€“Genome Wide Association Studies of Complex Diseases. <i>Genetic Epidemiology</i> , 2015, 39, 11-19.	1.3	22
34	Analysis of a mechanistic Markov model for gene duplicates evolving under subfunctionalization. <i>BMC Evolutionary Biology</i> , 2017, 17, 38.	3.2	17
35	Protocols for the Molecular Evolutionary Analysis of Membrane Protein Gene Duplicates. <i>Methods in Molecular Biology</i> , 2019, 1851, 49-62.	0.9	16
36	Flux Control in Glycolysis Varies Across the Tree of Life. <i>Journal of Molecular Evolution</i> , 2016, 82, 146-161.	1.8	15

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37	Selection on metabolic pathway function in the presence of mutation-selection-drift balance leads to rate-limiting steps that are not evolutionarily stable. <i>Biology Direct</i> , 2016, 11, 31.	4.6	15
38	Characterizing selective pressures on the pathway for de novo biosynthesis of pyrimidines in yeast. <i>BMC Evolutionary Biology</i> , 2015, 15, 232.	3.2	14
39	A generalized birth and death process for modeling the fates of gene duplication. <i>BMC Evolutionary Biology</i> , 2015, 15, 275.	3.2	12
40	Using the Mutation-Selection Framework to Characterize Selection on Protein Sequences. <i>Genes</i> , 2018, 9, 409.	2.4	12
41	Protein evolution depends on multiple distinct population size parameters. <i>BMC Evolutionary Biology</i> , 2018, 18, 17.	3.2	11
42	On Mechanistic Modeling of Gene Content Evolution: Birth-Death Models and Mechanisms of Gene Birth and Gene Retention. <i>Computation</i> , 2014, 2, 112-130.	2.0	10
43	Characterizing the roles of changing population size and selection on the evolution of flux control in metabolic pathways. <i>BMC Evolutionary Biology</i> , 2017, 17, 117.	3.2	9
44	A new parameter-rich structure-aware mechanistic model for amino acid substitution during evolution. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 218-228.	2.6	8
45	Emerging Frontiers in the Study of Molecular Evolution. <i>Journal of Molecular Evolution</i> , 2020, 88, 211-226.	1.8	8
46	CASS: Protein sequence simulation with explicit genotype-phenotype mapping. <i>Trends in Evolutionary Biology</i> , 2012, 4, 9.	0.4	7
47	Level-dependent QBD models for the evolution of a family of gene duplicates. <i>Stochastic Models</i> , 2020, 36, 285-311.	0.5	6
48	Probabilistic models and their impact on the accuracy of reconstructed ancestral protein sequences. <i>Journal of Molecular Evolution</i> , 2007, 65, 43-57.		6
49	A systematic analysis of lineage-specific evolution in metabolic pathways. <i>Gene</i> , 2007, 387, 67-74.	2.2	5
50	Fast Side Chain Replacement in Proteins Using a Coarse-Grained Approach for Evaluating the Effects of Mutation During Evolution. <i>Journal of Molecular Evolution</i> , 2011, 73, 23-33.	1.8	5
51	What Fraction of Duplicates Observed in Recently Sequenced Genomes Is Segregating and Destined to Fail to Fix?. <i>Genome Biology and Evolution</i> , 2015, 7, 2258-2264.	2.5	5
52	The Adaptive Evolution Database (TAED): A New Release of a Database of Phylogenetically Indexed Gene Families from Chordates. <i>Journal of Molecular Evolution</i> , 2017, 85, 46-56.	1.8	5
53	Evolutionary Processes and Biophysical Mechanisms: Revisiting Why Evolved Proteins Are Marginally Stable. <i>Journal of Molecular Evolution</i> , 2020, 88, 415-417.	1.8	5
54	Modeling Proteins at the Interface of Structure, Evolution, and Population Genetics. <i>Biological and Medical Physics Series</i> , 2012, 1, 347-361.	0.4	4

#	ARTICLE	IF	CITATIONS
55	Linking sequence to function in drug design with ancestral sequence reconstruction. , 2007, , 34-40.		3
56	Evolution and Structure of Proteins and Proteomes. Genes, 2018, 9, 583.	2.4	3
57	A New Editorial Beginning at Journal of Molecular Evolution. Journal of Molecular Evolution, 2019, 87, 69-71.	1.8	2
58	Detecting Signatures of Positive Selection against a Backdrop of Compensatory Processes. Molecular Biology and Evolution, 2020, 37, 3353-3362.	8.9	2
59	The Journal of Molecular Evolution Turns 50. Journal of Molecular Evolution, 2021, 89, 119-121.	1.8	2
60	Inferring the number and position of changes in selective regime in a non-equilibrium mutation-selection framework. BMC Ecology and Evolution, 2021, 21, 39.	1.6	2
61	Detecting Selection on Segregating Gene Duplicates in a Population. Journal of Molecular Evolution, 2021, 89, 554-564.	1.8	2
62	Genomics and Bioinformatics of the PVC Superphylum. , 2013, , 165-193.		2
63	Reading the Story in DNA: A Beginner's Guide to Molecular Evolution. Systematic Biology, 2009, 58, 161-162.	5.6	0
64	Evolutionary Models. , 2019, , 712-718.		0
65	2019 Zuckerkandl Prize. Journal of Molecular Evolution, 2020, 88, 121-121.	1.8	0
66	Characterizing lineage-specific evolution and the processes driving genomic diversification in chordates. BMC Evolutionary Biology, 2020, 20, 24.	3.2	0
67	Characterizing amino acid substitution with complete linkage of sites on a lineage. Genome Biology and Evolution, 2021, 13, .	2.5	0
68	2020 Zuckerkandl Prize. Journal of Molecular Evolution, 2021, 89, 1-1.	1.8	0
69	2021 Zuckerkandl Prize. Journal of Molecular Evolution, 2022, 90, 1-1.	1.8	0