

# David A Liberles

## List of Publications by Year in descending order

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Version: 2024-02-01

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  | 2021 Zuckerkandl Prize. <i>Journal of Molecular Evolution</i> , 2022, 90, 1-1.   | 1.8 | 0         |
| 2  | 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        |
| 3  | The <i>Journal of Molecular Evolution</i> Turns 50. <i>Journal of Molecular Evolution</i> , 2021, 89, 119-121.   | 1.8 | 2         |
| 4  | Inferring the number and position of changes in selective regime in a non-equilibrium mutation-selection framework. <i>Bmc Ecology and Evolution</i> , 2021, 21, 39.   | 1.6 | 2         |
| 5  | Detecting Selection on Segregating Gene Duplicates in a Population. <i>Journal of Molecular Evolution</i> , 2021, 89, 554-564.   | 1.8 | 2         |
| 6  | Characterizing amino acid substitution with complete linkage of sites on a lineage. <i>Genome Biology and Evolution</i> , 2021, 13, .                                  | 2.5 | 0         |
| 7  | 2020 Zuckerkandl Prize. <i>Journal of Molecular Evolution</i> , 2021, 89, 1-1.   | 1.8 | 0         |
| 8  | 2019 Zuckerkandl Prize. <i>Journal of Molecular Evolution</i> , 2020, 88, 121-121.   | 1.8 | 0         |
| 9  | Level-dependent QBD models for the evolution of a family of gene duplicates. <i>Stochastic Models</i> , 2020, 36, 285-311.   | 0.5 | 6         |
| 10 | 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         |
| 11 | Detecting Signatures of Positive Selection against a Backdrop of Compensatory Processes. <i>Molecular Biology and Evolution</i> , 2020, 37, 3353-3362.                 | 8.9 | 2         |
| 12 | Characterizing lineage-specific evolution and the processes driving genomic diversification in chordates. <i>BMC Evolutionary Biology</i> , 2020, 20, 24.              | 3.2 | 0         |
| 13 | Emerging Frontiers in the Study of Molecular Evolution. <i>Journal of Molecular Evolution</i> , 2020, 88, 211-226.   | 1.8 | 8         |
| 14 | <i>Evolutionary Models</i> . , 2019, , 712-718.  |     | 0         |
| 15 | A New Editorial Beginning at <i>Journal of Molecular Evolution</i> . <i>Journal of Molecular Evolution</i> , 2019, 87, 69-71.  | 1.8 | 2         |
| 16 | Evolution in the light of fitness landscape theory. <i>Trends in Ecology and Evolution</i> , 2019, 34, 69-82.  | 8.7 | 124       |
| 17 | Protocols for the Molecular Evolutionary Analysis of Membrane Protein Gene Duplicates. <i>Methods in Molecular Biology</i> , 2019, 1851, 49-62.                        | 0.9 | 16        |
| 18 | Protein evolution depends on multiple distinct population size parameters. <i>BMC Evolutionary Biology</i> , 2018, 18, 17.   | 3.2 | 11        |

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|----|--|------|-----------|
| 19 | 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         |
| 20 | Evolution and Structure of Proteins and Proteomes. <i>Genes</i> , 2018, 9, 583.  | 2.4  | 3         |
| 21 | Using the Mutation-Selection Framework to Characterize Selection on Protein Sequences. <i>Genes</i> , 2018, 9, 409.  | 2.4  | 12        |
| 22 | ProtASR: An Evolutionary Framework for Ancestral Protein Reconstruction with Selection on Folding Stability. <i>Systematic Biology</i> , 2017, 66, syw121.   | 5.6  | 29        |
| 23 | 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         |
| 24 | Analysis of a mechanistic Markov model for gene duplicates evolving under subfunctionalization. <i>BMC Evolutionary Biology</i> , 2017, 17, 38.  | 3.2  | 17        |
| 25 | 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         |
| 26 | Selection on protein structure, interaction, and sequence. <i>Protein Science</i> , 2016, 25, 1168-1178.   | 7.6  | 47        |
| 27 | Flux Control in Glycolysis Varies Across the Tree of Life. <i>Journal of Molecular Evolution</i> , 2016, 82, 146-161.  | 1.8  | 15        |
| 28 | The Atlantic salmon genome provides insights into rediploidization. <i>Nature</i> , 2016, 533, 200-205.  | 27.8 | 1,021     |
| 29 | Extracting functional trends from whole genome duplication events using comparative genomics. <i>Biological Procedures Online</i> , 2016, 18, 11.  | 2.9  | 45        |
| 30 | 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        |
| 31 | 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        |
| 32 | A generalized birth and death process for modeling the fates of gene duplication. <i>BMC Evolutionary Biology</i> , 2015, 15, 275.   | 3.2  | 12        |
| 33 | 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        |
| 34 | 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         |
| 35 | Genetic Simulation Tools for Post-Genome Wide Association Studies of Complex Diseases. <i>Genetic Epidemiology</i> , 2015, 39, 11-19.  | 1.3  | 22        |
| 36 | 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        |

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|----|--|------|-----------|
| 37 | Molecular traces of alternative social organization in a termite genome. <i>Nature Communications</i> , 2014, 5, 3636.   | 12.8 | 371       |
| 38 | State-of the art methodologies dictate new standards for phylogenetic analysis. <i>BMC Evolutionary Biology</i> , 2013, 13, 161.   | 3.2  | 51        |
| 39 | On the Need for Mechanistic Models in Computational Genomics and Metagenomics. <i>Genome Biology and Evolution</i> , 2013, 5, 2008-2018.   | 2.5  | 40        |
| 40 | Genomics and Bioinformatics of the PVC Superphylum. , 2013, , 165-193.   |      | 2         |
| 41 | CASS: Protein sequence simulation with explicit genotype-phenotype mapping. <i>Trends in Evolutionary Biology</i> , 2012, 4, 9.  | 0.4  | 7         |
| 42 | 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        |
| 43 | The interface of protein structure, protein biophysics, and molecular evolution. <i>Protein Science</i> , 2012, 21, 769-785.   | 7.6  | 188       |
| 44 | Modeling Proteins at the Interface of Structure, Evolution, and Population Genetics. <i>Biological and Medical Physics Series</i> , 2012, , 347-361.   | 0.4  | 4         |
| 45 | Detecting and understanding natural selection. , 2012, , 73-96.  |      | 26        |
| 46 | The Evolution of Protein Structures and Structural Ensembles Under Functional Constraint. <i>Genes</i> , 2011, 2, 748-762.   | 2.4  | 50        |
| 47 | Toward a General Model for the Evolutionary Dynamics of Gene Duplicates. <i>Genome Biology and Evolution</i> , 2011, 3, 1197-1209.   | 2.5  | 57        |
| 48 | Biophysical and structural considerations for protein sequence evolution. <i>BMC Evolutionary Biology</i> , 2011, 11, 361.   | 3.2  | 50        |
| 49 | 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         |
| 50 | 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        |
| 51 | 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        |
| 52 | Reading the Story in DNA: A Beginner's Guide to Molecular Evolution. <i>Systematic Biology</i> , 2009, 58, 161-162.  | 5.6  | 0         |
| 53 | Keeping the blood flowingâ€”plasminogen activator genes and feeding behavior in vampire bats. <i>Die Naturwissenschaften</i> , 2009, 96, 39-47.  | 1.6  | 27        |
| 54 | Linking sequence to function in drug design with ancestral sequence reconstruction. , 2007, , 34-40.   |      | 3         |

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|----|--|------|-----------|
| 55 | A systematic analysis of lineage-specific evolution in metabolic pathways. <i>Gene</i> , 2007, 387, 67-74.   | 2.2  | 5         |
| 56 | 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       |
| 57 | 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        |
| 58 | Probabilistic models and their impact on the accuracy of reconstructed ancestral protein sequences. , 2007, , 43-57.   |      | 6         |
| 59 | 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        |
| 60 | 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        |
| 61 | A systematic search for positive selection in higher plants (Embryophytes). <i>BMC Plant Biology</i> , 2006, 6, 12.  | 3.6  | 78        |
| 62 | Subfunctionalization of duplicated genes as a transition state to neofunctionalization. <i>BMC Evolutionary Biology</i> , 2005, 5, 28.   | 3.2  | 311       |
| 63 | The Adaptive Evolution Database (TAED): a phylogeny based tool for comparative genomics. <i>Nucleic Acids Research</i> , 2004, 33, D495-D497.  | 14.5 | 73        |
| 64 | Visualising very large phylogenetic trees in three dimensional hyperbolic space. <i>BMC Bioinformatics</i> , 2004, 5, 48.  | 2.6  | 47        |
| 65 | Myostatin rapid sequence evolution in ruminants predates domestication. <i>Molecular Phylogenetics and Evolution</i> , 2004, 33, 782-790.  | 2.7  | 38        |
| 66 | The adaptive evolution database (TAED). <i>Genome Biology</i> , 2001, 2, research0028.1.   | 9.6  | 35        |
| 67 | Functional inferences from reconstructed evolutionary biology involving rectified databases â€“ an evolutionarily grounded approach to functional genomics. <i>Research in Microbiology</i> , 2000, 151, 97-106.   | 2.1  | 58        |
| 68 | 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        |
| 69 | Triple-Helix Formation by Pyrimidine Oligonucleotides Containing Nonnatural Nucleosides with Extended Aromatic Nucleobases: Intercalation from the major groove as a method for recognizing CÂˆG and T Âˆ A base pairs. <i>Helvetica Chimica Acta</i> , 1997, 80, 2002-2022. | 1.6  | 32        |