

# Edward Susko

## List of Publications by Year in descending order

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46  
papers

1,282  
citations

430874

18  
h-index

414414

32  
g-index

48  
all docs

48  
docs citations

48  
times ranked

1414  
citing authors

#	ARTICLE	IF	CITATIONS
1	On Reduced Amino Acid Alphabets for Phylogenetic Inference. <i>Molecular Biology and Evolution</i> , 2007, 24, 2139-2150.	8.9	157
2	A class frequency mixture model that adjusts for site-specific amino acid frequencies and improves inference of protein phylogeny. <i>BMC Evolutionary Biology</i> , 2008, 8, 331.	3.2	94
3	A SLUF Fe-S Cluster Biogenesis System in the Mitochondrion-Related Organelles of the Anaerobic Protist <i>Pygsuia</i> . <i>Current Biology</i> , 2014, 24, 1176-1186.	3.9	94
4	Covariation Shifts Cause a Long-Branch Attraction Artifact That Unites Microsporidia and Archaeobacteria in EF-1 $\alpha$ Phylogenies. <i>Molecular Biology and Evolution</i> , 2004, 21, 1340-1349.	8.9	93
5	Bootstrap Support Is Not First-Order Correct. <i>Systematic Biology</i> , 2009, 58, 211-223.	5.6	59
6	On the Distributions of Bootstrap Support and Posterior Distributions for a Star Tree. <i>Systematic Biology</i> , 2008, 57, 602-612.	5.6	57
7	Estimation of Rates-Across-Sites Distributions in Phylogenetic Substitution Models. <i>Systematic Biology</i> , 2003, 52, 594-603.	5.6	55
8	Testing for Differences in Rates-Across-Sites Distributions in Phylogenetic Subtrees. <i>Molecular Biology and Evolution</i> , 2002, 19, 1514-1523.	8.9	51
9	Site-and-branch-heterogeneous analyses of an expanded dataset favour mitochondria as sister to known Alphaproteobacteria. <i>Nature Ecology and Evolution</i> , 2022, 6, 253-262.	7.8	48
10	The Relative Importance of Modeling Site Pattern Heterogeneity Versus Partition-Wise Heterotachy in Phylogenomic Inference. <i>Systematic Biology</i> , 2019, 68, 1003-1019.	5.6	45
11	On Inconsistency of the Neighbor-Joining, Least Squares, and Minimum Evolution Estimation When Substitution Processes Are Incorrectly Modeled. <i>Molecular Biology and Evolution</i> , 2004, 21, 1629-1642.	8.9	43
12	First-Order Correct Bootstrap Support Adjustments for Splits that Allow Hypothesis Testing When Using Maximum Likelihood Estimation. <i>Molecular Biology and Evolution</i> , 2010, 27, 1621-1629.	8.9	31
13	A phylogenetic mixture model for the identification of functionally divergent protein residues. <i>Bioinformatics</i> , 2011, 27, 2655-2663.	4.1	27
14	Long Branch Attraction Biases in Phylogenetics. <i>Systematic Biology</i> , 2021, 70, 838-843.	5.6	26
15	Biases in Phylogenetic Estimation Can Be Caused by Random Sequence Segments. <i>Journal of Molecular Evolution</i> , 2005, 61, 351-359.	1.8	25
16	Nuclear genetic codes with a different meaning of the UAG and the UAA codon. <i>BMC Biology</i> , 2017, 15, 8.	3.8	25
17	Shifting Balance on a Static Mutation "Selection Landscape: A Novel Scenario of Positive Selection. <i>Molecular Biology and Evolution</i> , 2016, 34, msw237.	8.9	24
18	Ribosomal RNA Genes Contribute to the Formation of Pseudogenes and Junk DNA in the Human Genome. <i>Genome Biology and Evolution</i> , 2017, 9, 380-397.	2.5	24

#	ARTICLE	IF	CITATIONS
19	Alignment Errors Strongly Impact Likelihood-Based Tests for Comparing Topologies. <i>Molecular Biology and Evolution</i> , 2014, 31, 3057-3067.	8.9	23
20	Phenomenological Load on Model Parameters Can Lead to False Biological Conclusions. <i>Molecular Biology and Evolution</i> , 2018, 35, 1473-1488.	8.9	23
21	Confidence Regions and Hypothesis Tests for Topologies Using Generalized Least Squares. <i>Molecular Biology and Evolution</i> , 2003, 20, 862-868.	8.9	22
22	An Amino Acid Substitution-Selection Model Adjusts Residue Fitness to Improve Phylogenetic Estimation. <i>Molecular Biology and Evolution</i> , 2014, 31, 779-792.	8.9	22
23	Bayesian Long Branch Attraction Bias and Corrections. <i>Systematic Biology</i> , 2015, 64, 243-255.	5.6	22
24	Accelerated Estimation of Frequency Classes in Site-Heterogeneous Profile Mixture Models. <i>Molecular Biology and Evolution</i> , 2018, 35, 1266-1283.	8.9	22
25	On the Use of Information Criteria for Model Selection in Phylogenetics. <i>Molecular Biology and Evolution</i> , 2020, 37, 549-562.	8.9	22
26	CONTINUOUS-TIME MARKOV MODELS FOR SPECIES INTERACTIONS. <i>Ecology</i> , 2005, 86, 3272-3278.	3.2	17
27	Cellular costs underpin micronutrient limitation in phytoplankton. <i>Science Advances</i> , 2021, 7, .	10.3	17
28	Tests for Two Trees Using Likelihood Methods. <i>Molecular Biology and Evolution</i> , 2014, 31, 1029-1039.	8.9	16
29	The Probability of Correctly Resolving a Split as an Experimental Design Criterion in Phylogenetics. <i>Systematic Biology</i> , 2012, 61, 811-821.	5.6	15
30	A Phenotype-Genotype Codon Model for Detecting Adaptive Evolution. <i>Systematic Biology</i> , 2020, 69, 722-738.	5.6	12
31	Evolution: Reconstructing the Timeline of Eukaryogenesis. <i>Current Biology</i> , 2021, 31, R193-R196.	3.9	12
32	Modelling Prokaryote Gene Content. <i>Evolutionary Bioinformatics</i> , 2006, 2, 117693430600200.	1.2	10
33	Evolution of amino acid propensities under stability-mediated epistasis. <i>Molecular Biology and Evolution</i> , 2022, , .	8.9	7
34	Smoothed Bootstrap Aggregation for Assessing Selection Pressure at Amino Acid Sites. <i>Molecular Biology and Evolution</i> , 2016, 33, 2976-2989.	8.9	6
35	Conditions under which distributions of edge length ratios on phylogenetic trees can be used to order evolutionary events. <i>Journal of Theoretical Biology</i> , 2021, 526, 110788.	1.7	6
36	Shifts in amino acid preferences as proteins evolve: A synthesis of experimental and theoretical work. <i>Protein Science</i> , 2021, 30, 2009-2028.	7.6	5

#	ARTICLE	IF	CITATIONS
37	Improved Least Squares Topology Testing and Estimation. <i>Systematic Biology</i> , 2011, 60, 668-675.	5.6	4
38	Looking for Darwin in Genomic Sequences: Validity and Success Depends on the Relationship Between Model and Data. <i>Methods in Molecular Biology</i> , 2019, 1910, 399-426.	0.9	4
39	Estimation of a residual distribution with small numbers of repeated measurements. <i>Canadian Journal of Statistics</i> , 2002, 30, 383-400.	0.9	3
40	ModL: exploring and restoring regularity when testing for positive selection. <i>Bioinformatics</i> , 2019, 35, 2545-2554.	4.1	3
41	Bayes factor biases for non-nested models and corrections. <i>Canadian Journal of Statistics</i> , 2017, 45, 290-309.	0.9	2
42	Ancestral state reconstruction with large numbers of sequences and edge-length estimation. <i>Journal of Mathematical Biology</i> , 2022, 84, 21.	1.9	2
43	Split-specific bootstrap measures for quantifying phylogenetic stability and the influence of taxon selection. <i>Molecular Phylogenetics and Evolution</i> , 2016, 105, 114-125.	2.7	1
44	Using minimum bootstrap support for splits to construct confidence regions for trees. <i>Evolutionary Bioinformatics</i> , 2007, 2, 129-43.	1.2	1
45	Estimation of relaxation time distributions in magnetic resonance imaging. <i>Canadian Journal of Statistics</i> , 2001, 29, 379-394.	0.9	0
46	Statistical Analysis of Expressed Sequence Tags. <i>Methods in Molecular Biology</i> , 2009, 533, 277-287.	0.9	0