Joseph P Bielawski

List of Publications by Year
in descending order

72	6,828	126708	98622
papers	citations	33	67
		h-index	g-index

73	73	73	8176
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Statistical methods for detecting molecular adaptation. Trends in Ecology and Evolution, 2000, 15, 496-503.	4.2	1,532
2	Accuracy and Power of the Likelihood Ratio Test in Detecting Adaptive Molecular Evolution. Molecular Biology and Evolution, 2001, 18, 1585-1592.	3.5	658
3	Ancestral polymorphism and adaptive evolution in the trichothecene mycotoxin gene cluster of phytopathogenic Fusarium. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9278-9283.	3.3	489
4	Prevalence and Evolution of Core Photosystem II Genes in Marine Cyanobacterial Viruses and Their Hosts. PLoS Biology, 2006, 4, e234.	2.6	394
5	Accuracy and Power of Bayes Prediction of Amino Acid Sites Under Positive Selection. Molecular Biology and Evolution, 2002, 19, 950-958.	3.5	388
6	Crohn's Disease Exclusion Diet Plus Partial Enteral Nutrition Induces Sustained Remission in a Randomized Controlled Trial. Gastroenterology, 2019, 157, 440-450.e8.	0.6	378
7	A Maximum Likelihood Method for Detecting Functional Divergence at Individual Codon Sites, with Application to Gene Family Evolution. Journal of Molecular Evolution, 2004, 59, 121-32.	0.8	267
8	Multilocus Genotyping Assays for Single Nucleotide Polymorphism-Based Subtyping of <i>Listeria monocytogenes</i> Isolates. Applied and Environmental Microbiology, 2008, 74, 7629-7642.	1.4	173
9	Maximum likelihood methods for detecting adaptive evolution after gene duplication. Journal of Structural and Functional Genomics, 2003, 3, 201-212.	1.2	152
10	Potential photosynthesis gene recombination between Prochlorococcus and Synechococcus via viral intermediates. Environmental Microbiology, 2005, 7, 1505-1513.	1.8	149
11	Novel Proteorhodopsin variants from the Mediterranean and Red Seas. Environmental Microbiology, 2003, 5, 842-849.	1.8	109
12	Positive and Negative Selection in the DAZ Gene Family. Molecular Biology and Evolution, 2001, 18, 523-529.	3.5	100
13	Portal protein diversity and phage ecology. Environmental Microbiology, 2008, 10, 2810-2823.	1.8	100
14	Widespread Adaptive Evolution in the Human Immunodeficiency Virus Type 1 Genome. Journal of Molecular Evolution, 2003, 57, 212-221.	0.8	98
15	Darwinian adaptation of proteorhodopsin to different light intensities in the marine environment. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14824-14829.	3.3	96
16	Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. Microbiome, 2018, 6, 13.	4.9	94
17	Adaptive Evolution of Multicolored Fluorescent Proteins in Reef-Building Corals. Journal of Molecular Evolution, 2006, 62, 332-339.	0.8	90
18	Maximum likelihood methods for detecting adaptive evolution after gene duplication. Journal of Structural and Functional Genomics, 2003, 3, 201-12.	1.2	90

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19	Positive Darwinian Selection in the Piston That Powers Proton Pumps in Complex I of the Mitochondria of Pacific Salmon. PLoS ONE, 2011, 6, e24127.	1.1	84
20	Rates of Nucleotide Substitution and Mammalian Nuclear Gene Evolution: Approximate and Maximum-Likelihood Methods Lead to Different Conclusions. Genetics, 2000, 156, 1299-1308.	1.2	75
21	Substitution Rates in Drosophila Nuclear Genes: Implications for Translational Selection. Genetics, 2001, 157, 295-305.	1.2	74
22	Molecular Evolutionary Characterization of a V1R Subfamily Unique to Strepsirrhine Primates. Genome Biology and Evolution, 2014, 6, 213-227.	1.1	71
23	Review and meta-analysis of natural selection in mitochondrial complex I in metazoans. Journal of Zoological Systematics and Evolutionary Research, 2015, 53, 1-17.	0.6	70
24	Early Changes in Microbial Community Structure Are Associated with Sustained Remission After Nutritional Treatment of Pediatric CrohnÊ¼s Disease. Inflammatory Bowel Diseases, 2016, 22, 2853-2862.	0.9	69
25	The origin and evolution of geminivirus-related DNA sequences in Nicotiana. Heredity, 2004, 92, 352-358.	1.2	65
26	The relationship between fecal bile acids and microbiome community structure in pediatric Crohn's disease. ISME Journal, 2020, 14, 702-713.	4.4	59
27	Randomly amplified polymorphic DNA (RAPD) analysis of Atlantic Coast striped bass. Heredity, 1997, 78, 32-40.	1.2	57
28	Adaptive Diversification of Vomeronasal Receptor 1 Genes in Rodents. Journal of Molecular Evolution, 2005, 60, 566-576.	0.8	56
29	Mutation Patterns of Mitochondrial H- and L-Strand DNA in Closely Related Cyprinid Fishes. Genetics, 2002, 161, 1589-1597.	1.2	52
30	Seasonal assemblages and shortâ€lived blooms in coastal northâ€west <scp>A</scp>tlantic <scp>O</scp>cean bacterioplankton. Environmental Microbiology, 2015, 17, 3642-3661.	1.8	51
31	Recombination Detection Under Evolutionary Scenarios Relevant to Functional Divergence. Journal of Molecular Evolution, 2011, 73, 273-286.	0.8	49
32	BioMiCo: a supervised Bayesian model for inference of microbial community structure. Microbiome, 2015, 3, 8.	4.9	43
33	Evolutionary Rates and Expression Level in Chlamydomonas. Genetics, 2006, 172, 1567-1576.	1.2	37
34	Bacterial Taxa and Functions Are Predictive of Sustained Remission Following Exclusive Enteral Nutrition in Pediatric Crohn's Disease. Inflammatory Bowel Diseases, 2020, 26, 1026-1037.	0.9	35
35	Gene Conversion and Functional Divergence in the ?-Globin Gene Family. Journal of Molecular Evolution, 2004, 59, 177-189.	0.8	34
36	The Gut Microbiome of Pediatric CrohnÊ¼s Disease Patients Differs from Healthy Controls in Genes That Can Influence the Balance Between a Healthy and Dysregulated Immune Response. Inflammatory Bowel Diseases, 2016, 22, 2607-2618.	0.9	33

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37	Functional Divergence of the Nuclear Receptor *NR2C1* as a Modulator of Pluripotentiality During Hominid Evolution. Genetics, 2016, 203, 905-922.	1.2	33
38	Maximum Likelihood Methods for Detecting Adaptive Protein Evolution. , 2005, , 103-124.		32
39	BiomeNet: A Bayesian Model for Inference of Metabolic Divergence among Microbial Communities. PLoS Computational Biology, 2014, 10, e1003918.	1.5	30
40	Evolutionary rate variation among vertebrate Î² globin genes: Implications for dating gene family duplication events. Gene, 2006, 380, 21-29.	1.0	29
41	Novel Strategies for Applied Metagenomics. Inflammatory Bowel Diseases, 2016, 22, 709-718.	0.9	25
42	Shifting Balance on a Static Mutationâ€"Selection Landscape: A Novel Scenario of Positive Selection. Molecular Biology and Evolution, 2016, 34, msw237.	3.5	24
43	Reconciling Ecological and Genomic Divergence among Lineages of Listeria under an "Extended Mosaic Genome Concept". Molecular Biology and Evolution, 2009, 26, 2605-2615.	3.5	23
44	Phenomenological Load on Model Parameters Can Lead to False Biological Conclusions. Molecular Biology and Evolution, 2018, 35, 1473-1488.	3.5	23
45	Large-scale analyses of synonymous substitution rates can be sensitive to assumptions about the process of mutation. Gene, 2006, 378, 58-64.	1.0	21
46	Proposed standard nomenclature for the .ALPHA.- and .BETA.-globin gene families. Genes and Genetic Systems, 2006, 81, 367-371.	0.2	20
47	Re-evaluating the relationship between missing heritability and the microbiome. Microbiome, 2020, 8, 87.	4.9	17
48	Methods for selecting fixed-effect models for heterogeneous codon evolution, with comments on their application to gene and genome data. BMC Evolutionary Biology, 2007, 7, S5.	3.2	15
49	Likelihood-Based Clustering (LiBaC) for Codon Models, a Method for Grouping Sites according to Similarities in the Underlying Process of Evolution. Molecular Biology and Evolution, 2008, 25, 1995-2007.	3.5	13
50	Inference of Episodic Changes in Natural Selection Acting on Protein Coding Sequences via CODEML. Current Protocols in Bioinformatics, 2016, 54, 6.15.1-6.15.32.	25.8	13
51	Randomly amplified polymorphic DNA (RAPD) analysis of Atlantic Coast striped bass. Heredity, 1997, 78, 32-40.	1.2	13
52	Detecting the Signatures of Adaptive Evolution in Proteinâ€Coding Genes. Current Protocols in Molecular Biology, 2013, 101, Unit 19.1..	2.9	12
53	A Phenotypeâ€"Genotype Codon Model for Detecting Adaptive Evolution. Systematic Biology, 2020, 69, 722-738.	2.7	12
54	The role of purifying selection in the origin and maintenance of complex function. Studies in History and Philosophy of Science Part A, 2021, 87, 125-135.	0.6	12

#	ARTICLE	IF	CITATIONS
55	Improving Evolutionary Models for Mitochondrial Protein Data with Site-Class Specific Amino Acid Exchangeability Matrices. PLoS ONE, 2013, 8, e55816.	1.1	11
56	Improved inference of site-specific positive selection under a generalized parametric codon model when there are multinucleotide mutations and multiple nonsynonymous rates. BMC Evolutionary Biology, 2019, 19, 22.	3.2	11
57	Trade-Offs Between Efficiency and Robustness in Bacterial Metabolic Networks Are Associated with Niche Breadth. Journal of Molecular Evolution, 2009, 68, 506-515.	0.8	9
58	Introduction to Genome Biology and Diversity. Methods in Molecular Biology, 2019, 1910, 3-31.	0.4	8
59	Inference of Functional Divergence Among Proteins When the Evolutionary Process is Non-stationary. Journal of Molecular Evolution, 2013, 76, 205-215.	0.8	7
60	Consequences of Stability-Induced Epistasis for Substitution Rates. Molecular Biology and Evolution, 2020, 37, 3131-3148.	3.5	7
61	Evolution of amino acid propensities under stability-mediated epistasis. Molecular Biology and Evolution, 2022, , .	3.5	7
62	Phylogenetic relationships within the genus Pimephales as inferred from ND4 and ND4L nucleotide sequences. Journal of Fish Biology, 2002, 61, 293-297.	0.7	6
63	Smoothed Bootstrap Aggregation for Assessing Selection Pressure at Amino Acid Sites. Molecular Biology and Evolution, 2016, 33, 2976-2989.	3.5	6
64	Shifts in amino acid preferences as proteins evolve: A synthesis of experimental and theoretical work. Protein Science, 2021, 30, 2009-2028.	3.1	5
65	Investigating the gut microbial community and genes in children with differing levels of change in serum asparaginase activity during pegaspargase treatment for acute lymphoblastic leukemia. Leukemia and Lymphoma, 2021, 62, 927-936.	0.6	4
66	Looking for Darwin in Genomic Sequences: Validity and Success Depends on the Relationship Between Model and Data. Methods in Molecular Biology, 2019, 1910, 399-426.	0.4	4
67	ModL: exploring and restoring regularity when testing for positive selection. Bioinformatics, 2019, 35, 2545-2554.	1.8	3
68	Gut bacterial gene changes following pegaspargase treatment in pediatric patients with acute lymphoblastic leukemia. Leukemia and Lymphoma, 2021, 62, 1-12.	0.6	2
69	Portal protein diversity and phage ecology. Environmental Microbiology, 2011, 13, 2832-2832.	1.8	0
70	Bayesian Inference of Microbial Community Structure from Metagenomic Data Using BioMiCo. Methods in Molecular Biology, 2018, 1849, 267-289.	0.4	0
71	Likelihood-based clustering (LiBaC) for codon models. , 2012, , 60-72.		0
72	Novel application of survival models for predicting microbial community transitions with variable selection for eDNA. Applied and Environmental Microbiology, 2022, , AEM0214621.	1.4	0