

Joseph P Bielawski

List of Publications by Year in descending order

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72
papers

6,828
citations

126907

33
h-index

98798

67
g-index

73
all docs

73
docs citations

73
times ranked

8176
citing authors

#	ARTICLE	IF	CITATIONS
1	Statistical methods for detecting molecular adaptation. <i>Trends in Ecology and Evolution</i> , 2000, 15, 496-503.	8.7	1,532
2	Accuracy and Power of the Likelihood Ratio Test in Detecting Adaptive Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2001, 18, 1585-1592.	8.9	658
3	Ancestral polymorphism and adaptive evolution in the trichothecene mycotoxin gene cluster of phytopathogenic <i>Fusarium</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9278-9283.	7.1	489
4	Prevalence and Evolution of Core Photosystem II Genes in Marine Cyanobacterial Viruses and Their Hosts. <i>PLoS Biology</i> , 2006, 4, e234.	5.6	394
5	Accuracy and Power of Bayes Prediction of Amino Acid Sites Under Positive Selection. <i>Molecular Biology and Evolution</i> , 2002, 19, 950-958.	8.9	388
6	Crohn's Disease Exclusion Diet Plus Partial Enteral Nutrition Induces Sustained Remission in a Randomized Controlled Trial. <i>Gastroenterology</i> , 2019, 157, 440-450.e8.	1.3	378
7	A Maximum Likelihood Method for Detecting Functional Divergence at Individual Codon Sites, with Application to Gene Family Evolution. <i>Journal of Molecular Evolution</i> , 2004, 59, 121-32.	1.8	267
8	Multilocus Genotyping Assays for Single Nucleotide Polymorphism-Based Subtyping of <i>Listeria monocytogenes</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2008, 74, 7629-7642.	3.1	173
9	Maximum likelihood methods for detecting adaptive evolution after gene duplication. <i>Journal of Structural and Functional Genomics</i> , 2003, 3, 201-212.	1.2	152
10	Potential photosynthesis gene recombination between <i>Prochlorococcus</i> and <i>Synechococcus</i> via viral intermediates. <i>Environmental Microbiology</i> , 2005, 7, 1505-1513.	3.8	149
11	Novel Proteorhodopsin variants from the Mediterranean and Red Seas. <i>Environmental Microbiology</i> , 2003, 5, 842-849.	3.8	109
12	Positive and Negative Selection in the DAZ Gene Family. <i>Molecular Biology and Evolution</i> , 2001, 18, 523-529.	8.9	100
13	Portal protein diversity and phage ecology. <i>Environmental Microbiology</i> , 2008, 10, 2810-2823.	3.8	100
14	Widespread Adaptive Evolution in the Human Immunodeficiency Virus Type 1 Genome. <i>Journal of Molecular Evolution</i> , 2003, 57, 212-221.	1.8	98
15	Darwinian adaptation of proteorhodopsin to different light intensities in the marine environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14824-14829.	7.1	96
16	Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. <i>Microbiome</i> , 2018, 6, 13.	11.1	94
17	Adaptive Evolution of Multicolored Fluorescent Proteins in Reef-Building Corals. <i>Journal of Molecular Evolution</i> , 2006, 62, 332-339.	1.8	90
18	Maximum likelihood methods for detecting adaptive evolution after gene duplication. <i>Journal of Structural and Functional Genomics</i> , 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. <i>PLoS ONE</i> , 2011, 6, e24127.	2.5	84
20	Rates of Nucleotide Substitution and Mammalian Nuclear Gene Evolution: Approximate and Maximum-Likelihood Methods Lead to Different Conclusions. <i>Genetics</i> , 2000, 156, 1299-1308.	2.9	75
21	Substitution Rates in <i>Drosophila</i> Nuclear Genes: Implications for Translational Selection. <i>Genetics</i> , 2001, 157, 295-305.	2.9	74
22	Molecular Evolutionary Characterization of a V1R Subfamily Unique to Strepsirrhine Primates. <i>Genome Biology and Evolution</i> , 2014, 6, 213-227.	2.5	71
23	Review and meta-analysis of natural selection in mitochondrial complex I in metazoans. <i>Journal of Zoological Systematics and Evolutionary Research</i> , 2015, 53, 1-17.	1.4	70
24	Early Changes in Microbial Community Structure Are Associated with Sustained Remission After Nutritional Treatment of Pediatric Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 2853-2862.	1.9	69
25	The origin and evolution of geminivirus-related DNA sequences in <i>Nicotiana</i> . <i>Heredity</i> , 2004, 92, 352-358.	2.6	65
26	The relationship between fecal bile acids and microbiome community structure in pediatric Crohn's disease. <i>ISME Journal</i> , 2020, 14, 702-713.	9.8	59
27	Randomly amplified polymorphic DNA (RAPD) analysis of Atlantic Coast striped bass. <i>Heredity</i> , 1997, 78, 32-40.	2.6	57
28	Adaptive Diversification of Vomeronasal Receptor 1 Genes in Rodents. <i>Journal of Molecular Evolution</i> , 2005, 60, 566-576.	1.8	56
29	Mutation Patterns of Mitochondrial H- and L-Strand DNA in Closely Related Cyprinid Fishes. <i>Genetics</i> , 2002, 161, 1589-1597.	2.9	52
30	Seasonal assemblages and short-lived blooms in coastal north-west Atlantic ocean bacterioplankton. <i>Environmental Microbiology</i> , 2015, 17, 3642-3661.	3.8	51
31	Recombination Detection Under Evolutionary Scenarios Relevant to Functional Divergence. <i>Journal of Molecular Evolution</i> , 2011, 73, 273-286.	1.8	49
32	BioMiCo: a supervised Bayesian model for inference of microbial community structure. <i>Microbiome</i> , 2015, 3, 8.	11.1	43
33	Evolutionary Rates and Expression Level in <i>Chlamydomonas</i> . <i>Genetics</i> , 2006, 172, 1567-1576.	2.9	37
34	Bacterial Taxa and Functions Are Predictive of Sustained Remission Following Exclusive Enteral Nutrition in Pediatric Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 1026-1037.	1.9	35
35	Gene Conversion and Functional Divergence in the γ -Globin Gene Family. <i>Journal of Molecular Evolution</i> , 2004, 59, 177-189.	1.8	34
36	The Gut Microbiome of Pediatric Crohn's Disease Patients Differs from Healthy Controls in Genes That Can Influence the Balance Between a Healthy and Dysregulated Immune Response. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 2607-2618.	1.9	33

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37	Functional Divergence of the Nuclear Receptor <i>NR2C1</i> as a Modulator of Pluripotentiality During Hominid Evolution. <i>Genetics</i> , 2016, 203, 905-922.	2.9	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. <i>PLoS Computational Biology</i> , 2014, 10, e1003918.	3.2	30
40	Evolutionary rate variation among vertebrate β globin genes: Implications for dating gene family duplication events. <i>Gene</i> , 2006, 380, 21-29.	2.2	29
41	Novel Strategies for Applied Metagenomics. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 709-718.	1.9	25
42	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
43	Reconciling Ecological and Genomic Divergence among Lineages of <i>Listeria</i> under an "Extended Mosaic Genome Concept". <i>Molecular Biology and Evolution</i> , 2009, 26, 2605-2615.	8.9	23
44	Phenomenological Load on Model Parameters Can Lead to False Biological Conclusions. <i>Molecular Biology and Evolution</i> , 2018, 35, 1473-1488.	8.9	23
45	Large-scale analyses of synonymous substitution rates can be sensitive to assumptions about the process of mutation. <i>Gene</i> , 2006, 378, 58-64.	2.2	21
46	Proposed standard nomenclature for the .ALPHA.- and .BETA.-globin gene families. <i>Genes and Genetic Systems</i> , 2006, 81, 367-371.	0.7	20
47	Re-evaluating the relationship between missing heritability and the microbiome. <i>Microbiome</i> , 2020, 8, 87.	11.1	17
48	Methods for selecting fixed-effect models for heterogeneous codon evolution, with comments on their application to gene and genome data. <i>BMC Evolutionary Biology</i> , 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. <i>Molecular Biology and Evolution</i> , 2008, 25, 1995-2007.	8.9	13
50	Inference of Episodic Changes in Natural Selection Acting on Protein Coding Sequences via CODEML. <i>Current Protocols in Bioinformatics</i> , 2016, 54, 6.15.1-6.15.32.	25.8	13
51	Randomly amplified polymorphic DNA (RAPD) analysis of Atlantic Coast striped bass. <i>Heredity</i> , 1997, 78, 32-40.	2.6	13
52	Detecting the Signatures of Adaptive Evolution in Protein-Coding Genes. <i>Current Protocols in Molecular Biology</i> , 2013, 101, Unit 19.1..	2.9	12
53	A Phenotype "Genotype Codon Model for Detecting Adaptive Evolution. <i>Systematic Biology</i> , 2020, 69, 722-738.	5.6	12
54	The role of purifying selection in the origin and maintenance of complex function. <i>Studies in History and Philosophy of Science Part A</i> , 2021, 87, 125-135.	1.2	12

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55	Improving Evolutionary Models for Mitochondrial Protein Data with Site-Class Specific Amino Acid Exchangeability Matrices. <i>PLoS ONE</i> , 2013, 8, e55816.	2.5	11
56	Improved inference of site-specific positive selection under a generalized parametric codon model when there are multinucleotide mutations and multiple nonsynonymous rates. <i>BMC Evolutionary Biology</i> , 2019, 19, 22.	3.2	11
57	Trade-Offs Between Efficiency and Robustness in Bacterial Metabolic Networks Are Associated with Niche Breadth. <i>Journal of Molecular Evolution</i> , 2009, 68, 506-515.	1.8	9
58	Introduction to Genome Biology and Diversity. <i>Methods in Molecular Biology</i> , 2019, 1910, 3-31.	0.9	8
59	Inference of Functional Divergence Among Proteins When the Evolutionary Process is Non-stationary. <i>Journal of Molecular Evolution</i> , 2013, 76, 205-215.	1.8	7
60	Consequences of Stability-Induced Epistasis for Substitution Rates. <i>Molecular Biology and Evolution</i> , 2020, 37, 3131-3148.	8.9	7
61	Evolution of amino acid propensities under stability-mediated epistasis. <i>Molecular Biology and Evolution</i> , 2022, , .	8.9	7
62	Phylogenetic relationships within the genus <i>Pimephales</i> as inferred from ND4 and ND4L nucleotide sequences. <i>Journal of Fish Biology</i> , 2002, 61, 293-297.	1.6	6
63	Smoothed Bootstrap Aggregation for Assessing Selection Pressure at Amino Acid Sites. <i>Molecular Biology and Evolution</i> , 2016, 33, 2976-2989.	8.9	6
64	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
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 and Lymphoma, 2021, 62, 927-936.	1.3	4
66	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
67	ModL: exploring and restoring regularity when testing for positive selection. <i>Bioinformatics</i> , 2019, 35, 2545-2554.	4.1	3
68	Gut bacterial gene changes following pegaspargase treatment in pediatric patients with acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2021, 62, 1-12.	1.3	2
69	Portal protein diversity and phage ecology. <i>Environmental Microbiology</i> , 2011, 13, 2832-2832.	3.8	0
70	Bayesian Inference of Microbial Community Structure from Metagenomic Data Using BioMiCo. <i>Methods in Molecular Biology</i> , 2018, 1849, 267-289.	0.9	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. <i>Applied and Environmental Microbiology</i> , 2022, , AEM0214621.	3.1	0