

Joseph P Bielawski

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3171601/publications.pdf>

Version: 2024-02-01

72
papers

6,828
citations

126708

33
h-index

98622

67
g-index

73
all docs

73
docs citations

73
times ranked

8176
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Evolution of amino acid propensities under stability-mediated epistasis. <i>Molecular Biology and Evolution</i> , 2022, , . | 3.5 | 7 |
| 2 | Novel application of survival models for predicting microbial community transitions with variable selection for eDNA. <i>Applied and Environmental Microbiology</i> , 2022, , AEM0214621. | 1.4 | 0 |
| 3 | 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. <i>Leukemia and Lymphoma</i> , 2021, 62, 927-936. | 0.6 | 4 |
| 4 | 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. | 0.6 | 12 |
| 5 | Gut bacterial gene changes following pegaspargase treatment in pediatric patients with acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2021, 62, 1-12. | 0.6 | 2 |
| 6 | Shifts in amino acid preferences as proteins evolve: A synthesis of experimental and theoretical work. <i>Protein Science</i> , 2021, 30, 2009-2028. | 3.1 | 5 |
| 7 | A Phenotypeâ€“Genotype Codon Model for Detecting Adaptive Evolution. <i>Systematic Biology</i> , 2020, 69, 722-738. | 2.7 | 12 |
| 8 | The relationship between fecal bile acids and microbiome community structure in pediatric Crohnâ€™s disease. <i>ISME Journal</i> , 2020, 14, 702-713. | 4.4 | 59 |
| 9 | Re-evaluating the relationship between missing heritability and the microbiome. <i>Microbiome</i> , 2020, 8, 87. | 4.9 | 17 |
| 10 | Consequences of Stability-Induced Epistasis for Substitution Rates. <i>Molecular Biology and Evolution</i> , 2020, 37, 3131-3148. | 3.5 | 7 |
| 11 | Bacterial Taxa and Functions Are Predictive of Sustained Remission Following Exclusive Enteral Nutrition in Pediatric Crohnâ€™s Disease. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 1026-1037. | 0.9 | 35 |
| 12 | Crohnâ€™s Disease Exclusion Diet Plus Partial Enteral Nutrition Induces Sustained Remission in a Randomized Controlled Trial. <i>Gastroenterology</i> , 2019, 157, 440-450.e8. | 0.6 | 378 |
| 13 | Introduction to Genome Biology and Diversity. <i>Methods in Molecular Biology</i> , 2019, 1910, 3-31. | 0.4 | 8 |
| 14 | ModL: exploring and restoring regularity when testing for positive selection. <i>Bioinformatics</i> , 2019, 35, 2545-2554. | 1.8 | 3 |
| 15 | 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 |
| 16 | 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. | 0.4 | 4 |
| 17 | Multi-omics differentially classify disease state and treatment outcome in pediatric Crohnâ€™s disease. <i>Microbiome</i> , 2018, 6, 13. | 4.9 | 94 |
| 18 | Phenomenological Load on Model Parameters Can Lead to False Biological Conclusions. <i>Molecular Biology and Evolution</i> , 2018, 35, 1473-1488. | 3.5 | 23 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Bayesian Inference of Microbial Community Structure from Metagenomic Data Using BioMiCo. <i>Methods in Molecular Biology</i> , 2018, 1849, 267-289. | 0.4 | 0 |
| 20 | Novel Strategies for Applied Metagenomics. <i>Inflammatory Bowel Diseases</i> , 2016, 22, 709-718. | 0.9 | 25 |
| 21 | 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 |
| 22 | 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. | 0.9 | 69 |
| 23 | Smoothed Bootstrap Aggregation for Assessing Selection Pressure at Amino Acid Sites. <i>Molecular Biology and Evolution</i> , 2016, 33, 2976-2989. | 3.5 | 6 |
| 24 | Shifting Balance on a Static Mutation Selection Landscape: A Novel Scenario of Positive Selection. <i>Molecular Biology and Evolution</i> , 2016, 34, msw237. | 3.5 | 24 |
| 25 | 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. | 0.9 | 33 |
| 26 | Functional Divergence of the Nuclear Receptor <i>NR2C1</i> as a Modulator of Pluripotentiality During Hominid Evolution. <i>Genetics</i> , 2016, 203, 905-922. | 1.2 | 33 |
| 27 | Seasonal assemblages and short-lived blooms in coastal north-west Atlantic ocean bacterioplankton. <i>Environmental Microbiology</i> , 2015, 17, 3642-3661. | 1.8 | 51 |
| 28 | BioMiCo: a supervised Bayesian model for inference of microbial community structure. <i>Microbiome</i> , 2015, 3, 8. | 4.9 | 43 |
| 29 | 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. | 0.6 | 70 |
| 30 | BiomeNet: A Bayesian Model for Inference of Metabolic Divergence among Microbial Communities. <i>PLoS Computational Biology</i> , 2014, 10, e1003918. | 1.5 | 30 |
| 31 | Molecular Evolutionary Characterization of a V1R Subfamily Unique to Strepsirrhine Primates. <i>Genome Biology and Evolution</i> , 2014, 6, 213-227. | 1.1 | 71 |
| 32 | 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 |
| 33 | Inference of Functional Divergence Among Proteins When the Evolutionary Process is Non-stationary. <i>Journal of Molecular Evolution</i> , 2013, 76, 205-215. | 0.8 | 7 |
| 34 | Improving Evolutionary Models for Mitochondrial Protein Data with Site-Class Specific Amino Acid Exchangeability Matrices. <i>PLoS ONE</i> , 2013, 8, e55816. | 1.1 | 11 |
| 35 | Likelihood-based clustering (LiBaC) for codon models. , 2012, , 60-72. | | 0 |
| 36 | Portal protein diversity and phage ecology. <i>Environmental Microbiology</i> , 2011, 13, 2832-2832. | 1.8 | 0 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | Recombination Detection Under Evolutionary Scenarios Relevant to Functional Divergence. <i>Journal of Molecular Evolution</i> , 2011, 73, 273-286. | 0.8 | 49 |
| 38 | 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. | 1.1 | 84 |
| 39 | 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. | 3.5 | 23 |
| 40 | 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. | 0.8 | 9 |
| 41 | Portal protein diversity and phage ecology. <i>Environmental Microbiology</i> , 2008, 10, 2810-2823. | 1.8 | 100 |
| 42 | 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. | 1.4 | 173 |
| 43 | 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. | 3.5 | 13 |
| 44 | 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 |
| 45 | Evolutionary rate variation among vertebrate $\hat{\nu}^2$ globin genes: Implications for dating gene family duplication events. <i>Gene</i> , 2006, 380, 21-29. | 1.0 | 29 |
| 46 | Large-scale analyses of synonymous substitution rates can be sensitive to assumptions about the process of mutation. <i>Gene</i> , 2006, 378, 58-64. | 1.0 | 21 |
| 47 | Proposed standard nomenclature for the .ALPHA.- and .BETA.-globin gene families. <i>Genes and Genetic Systems</i> , 2006, 81, 367-371. | 0.2 | 20 |
| 48 | Adaptive Evolution of Multicolored Fluorescent Proteins in Reef-Building Corals. <i>Journal of Molecular Evolution</i> , 2006, 62, 332-339. | 0.8 | 90 |
| 49 | Evolutionary Rates and Expression Level in <i>Chlamydomonas</i> . <i>Genetics</i> , 2006, 172, 1567-1576. | 1.2 | 37 |
| 50 | Prevalence and Evolution of Core Photosystem II Genes in Marine Cyanobacterial Viruses and Their Hosts. <i>PLoS Biology</i> , 2006, 4, e234. | 2.6 | 394 |
| 51 | Potential photosynthesis gene recombination between <i>Prochlorococcus</i> and <i>Synechococcus</i> via viral intermediates. <i>Environmental Microbiology</i> , 2005, 7, 1505-1513. | 1.8 | 149 |
| 52 | Adaptive Diversification of Vomeronasal Receptor 1 Genes in Rodents. <i>Journal of Molecular Evolution</i> , 2005, 60, 566-576. | 0.8 | 56 |
| 53 | Maximum Likelihood Methods for Detecting Adaptive Protein Evolution. , 2005, , 103-124. | | 32 |
| 54 | 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. | 3.3 | 96 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 55 | The origin and evolution of geminivirus-related DNA sequences in <i>Nicotiana</i> . <i>Heredity</i> , 2004, 92, 352-358. | 1.2 | 65 |
| 56 | 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. | 0.8 | 267 |
| 57 | Gene Conversion and Functional Divergence in the β -Globin Gene Family. <i>Journal of Molecular Evolution</i> , 2004, 59, 177-189. | 0.8 | 34 |
| 58 | 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 |
| 59 | Widespread Adaptive Evolution in the Human Immunodeficiency Virus Type 1 Genome. <i>Journal of Molecular Evolution</i> , 2003, 57, 212-221. | 0.8 | 98 |
| 60 | Novel Proteorhodopsin variants from the Mediterranean and Red Seas. <i>Environmental Microbiology</i> , 2003, 5, 842-849. | 1.8 | 109 |
| 61 | 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 |
| 62 | 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. | 3.3 | 489 |
| 63 | Accuracy and Power of Bayes Prediction of Amino Acid Sites Under Positive Selection. <i>Molecular Biology and Evolution</i> , 2002, 19, 950-958. | 3.5 | 388 |
| 64 | 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. | 0.7 | 6 |
| 65 | Mutation Patterns of Mitochondrial H- and L-Strand DNA in Closely Related Cyprinid Fishes. <i>Genetics</i> , 2002, 161, 1589-1597. | 1.2 | 52 |
| 66 | Accuracy and Power of the Likelihood Ratio Test in Detecting Adaptive Molecular Evolution. <i>Molecular Biology and Evolution</i> , 2001, 18, 1585-1592. | 3.5 | 658 |
| 67 | Positive and Negative Selection in the DAZ Gene Family. <i>Molecular Biology and Evolution</i> , 2001, 18, 523-529. | 3.5 | 100 |
| 68 | Substitution Rates in <i>Drosophila</i> Nuclear Genes: Implications for Translational Selection. <i>Genetics</i> , 2001, 157, 295-305. | 1.2 | 74 |
| 69 | Statistical methods for detecting molecular adaptation. <i>Trends in Ecology and Evolution</i> , 2000, 15, 496-503. | 4.2 | 1,532 |
| 70 | 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. | 1.2 | 75 |
| 71 | Randomly amplified polymorphic DNA (RAPD) analysis of Atlantic Coast striped bass. <i>Heredity</i> , 1997, 78, 32-40. | 1.2 | 57 |
| 72 | Randomly amplified polymorphic DNA (RAPD) analysis of Atlantic Coast striped bass. <i>Heredity</i> , 1997, 78, 32-40. | 1.2 | 13 |