

Katherine A Dunn

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

29
papers

1,206
citations

18
h-index

31
g-index

31
ext. papers

1,570
ext. citations

5.3
avg, IF

4.06
L-index

#	Paper	IF	Citations
29	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	1.9	1
28	Gut bacterial gene changes following pegaspargase treatment in pediatric patients with acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2021 , 62, 3244-3255	1.9	1
27	The impact of the host intestinal microbiome on carcinogenesis and the response to chemotherapy. <i>Future Oncology</i> , 2021 , 17, 4371-4387	3.6	1
26	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	4.5	18
25	Investigating Gut Microbial Taxa and Asparaginase Related Genes in Children Showing Different Direction of Change in Serum Asparaginase Activity Levels during Pegasparginase Treatment for Acute Lymphoblastic Leukemia. <i>Blood</i> , 2020 , 136, 40-41	2.2	
24	The relationship between fecal bile acids and microbiome community structure in pediatric Crohn's disease. <i>ISME Journal</i> , 2020 , 14, 702-713	11.9	27
23	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	13.3	194
22	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	6
21	Multi-omics differentially classify disease state and treatment outcome in pediatric Crohn's disease. <i>Microbiome</i> , 2018 , 6, 13	16.6	55
20	Bayesian Inference of Microbial Community Structure from Metagenomic Data Using BioMiCo. <i>Methods in Molecular Biology</i> , 2018 , 1849, 267-289	1.4	
19	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	4.5	23
18	Functional Divergence of the Nuclear Receptor NR2C1 as a Modulator of Pluripotentiality During Hominid Evolution. <i>Genetics</i> , 2016 , 203, 905-22	4	18
17	Novel Strategies for Applied Metagenomics. <i>Inflammatory Bowel Diseases</i> , 2016 , 22, 709-18	4.5	13
16	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	4.5	48
15	BioMiCo: a supervised Bayesian model for inference of microbial community structure. <i>Microbiome</i> , 2015 , 3, 8	16.6	35
14	A Robust ANOVA Approach to Estimating a Phylogeny from Multiple Genes. <i>Molecular Biology and Evolution</i> , 2015 , 32, 2186-94	8.3	1
13	Seasonal assemblages and short-lived blooms in coastal north-west Atlantic Ocean bacterioplankton. <i>Environmental Microbiology</i> , 2015 , 17, 3642-61	5.2	30

12	BiomeNet: a Bayesian model for inference of metabolic divergence among microbial communities. <i>PLoS Computational Biology</i> , 2014 , 10, e1003918	5	23
11	Improving evolutionary models for mitochondrial protein data with site-class specific amino acid exchangeability matrices. <i>PLoS ONE</i> , 2013 , 8, e55816	3.7	9
10	Molecular clocks keep dispersal hypotheses afloat: evidence for trans-Atlantic rafting by rodents. <i>Journal of Biogeography</i> , 2010 , 37, 305-324	4.1	61
9	Reconciling ecological and genomic divergence among lineages of listeria under an "extended mosaic genome concept". <i>Molecular Biology and Evolution</i> , 2009 , 26, 2605-15	8.3	22
8	Multilocus genotyping assays for single nucleotide polymorphism-based subtyping of <i>Listeria monocytogenes</i> isolates. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 7629-42	4.8	128
7	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	8.3	12
6	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 Suppl 1, S5	3	10
5	A new time-scale for ray-finned fish evolution. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007 , 274, 489-98	4.4	248
4	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, 14824-9	11.5	62
3	Molecular phylogenetics of myliobatiform fishes (Chondrichthyes: Myliobatiformes), with comments on the effects of missing data on parsimony and likelihood. <i>Molecular Phylogenetics and Evolution</i> , 2003 , 27, 259-70	4.1	46
2	Substitution rates in <i>Drosophila</i> nuclear genes: implications for translational selection. <i>Genetics</i> , 2001 , 157, 295-305	4	58
1	Rates of nucleotide substitution and mammalian nuclear gene evolution. Approximate and maximum-likelihood methods lead to different conclusions. <i>Genetics</i> , 2000 , 156, 1299-308	4	56