Robert G Beiko

List of Publications by Year
in descending order

51 papers	13,057 citations	185998 28 h-index	205818 48 g-index
61 all docs	61 docs citations	61 times ranked	20986 citing authors

#	Article	IF	Citations
1	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology, 2013, 31, 814-821.	9.4	8,049
2	CARD 2020: antibiotic resistome surveillance with the comprehensive antibiotic resistance database. Nucleic Acids Research, 2020, 48, D517-D525.	6.5	1,605
3	A Phylogenomic View of Ecological Specialization in the Lachnospiraceae, a Family of Digestive Tract-Associated Bacteria. Genome Biology and Evolution, 2014, 6, 703-713.	1.1	601
4	Highways of gene sharing in prokaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14332-14337.	3.3	467
5	Microbial shifts in the aging mouse gut. Microbiome, 2014, 2, 50.	4.9	354
6	Inter-personal diversity and temporal dynamics of dental, tongue, and salivary microbiota in the healthy oral cavity. Npj Biofilms and Microbiomes, 2017, 3, 2.	2.9	158
7	Predicting the Functional Potential of the Microbiome from Marker Genes Using PICRUSt. Methods in Molecular Biology, 2018, 1849, 169-177.	0.4	155
8	GenGIS: A geospatial information system for genomic data. Genome Research, 2009, 19, 1896-1904.	2.4	119
9	GenGIS 2: Geospatial Analysis of Traditional and Genetic Biodiversity, with New Gradient Algorithms and an Extensible Plugin Framework. PLoS ONE, 2013, 8, e69885.	1.1	118
10	Applications of random forest feature selection for fine‐scale genetic population assignment. Evolutionary Applications, 2018, 11, 153-165.	1.5	101
11	A climate-associated multispecies cryptic cline in the northwest Atlantic. Science Advances, 2018, 4, eaaq0929.	4.7	91
12	Do different surrogate methods detect lateral genetic transfer events of different relative ages?. Trends in Microbiology, 2006, 14, 4-8.	3.5	79
13	A new way to contemplate Darwin's tangled bank: how DNA barcodes are reconnecting biodiversity science and biomonitoring. Philosophical Transactions of the Royal Society B: Biological Sciences, 2016, 371, 20150330.	1.8	67
14	Metagenome-assembled genome binning methods with short reads disproportionately fail for plasmids and genomic Islands. Microbial Genomics, 2020, 6, .	1.0	67
15	Classifying short genomic fragments from novel lineages using composition and homology. BMC Bioinformatics, 2011, 12, 328.	1.2	64
16	Supertrees Based on the Subtree Prune-and-Regraft Distance. Systematic Biology, 2014, 63, 566-581.	2.7	63
17	<scp>megasat</scp>: automated inference of microsatellite genotypes from sequence data. Molecular Ecology Resources, 2017, 17, 247-256.	2.2	59
18	Rapid identification of high-confidence taxonomic assignments for metagenomic data. Nucleic Acids Research, 2012, 40, e111-e111.	6.5	57

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19	Genomic Comparison of Non-Typhoidal Salmonella enterica Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens. PLoS ONE, 2015, 10, e0128773.	1.1	53
20	The Impact of Reticulate Evolution on Genome Phylogeny. Systematic Biology, 2008, 57, 844-856.	2.7	47
21	A simulation test bed for hypotheses of genome evolution. Bioinformatics, 2007, 23, 825-831.	1.8	45
22	Telling the whole story in a 10,000-genome world. Biology Direct, 2011, 6, 34.	1.9	45
23	<scp>RAD</scp> sequencing reveals genomewide divergence between independent invasions of the European green crab (<i>Carcinus maenas</i>) in the Northwest Atlantic. Ecology and Evolution, 2017, 7, 2513-2524.	0.8	42
24	Measures of phylogenetic differentiation provide robust and complementary insights into microbial communities. ISME Journal, 2013, 7, 173-183.	4.4	41
25	Phylogenetic approaches to microbial community classification. Microbiome, 2015, 3, 47.	4.9	39
26	Microbial Malaise: How Can We Classify the Microbiome?. Trends in Microbiology, 2015, 23, 671-679.	3.5	36
27	Range-wide parallel climate-associated genomic clines in Atlantic salmon. Royal Society Open Science, 2017, 4, 171394.	1.1	35
28	Machine Learning for Antimicrobial Resistance Prediction: Current Practice, Limitations, and Clinical Perspective. Clinical Microbiology Reviews, 2022, 35, .	5.7	33
29	Microbial phylogenomics: Branching out. Nature, 2003, 421, 217-217.	13.7	28
30	Environmental extremes drive population structure at the northern range limit of Atlantic salmon in North America. Molecular Ecology, 2018, 27, 4026-4040.	2.0	26
31	Detecting Lateral Genetic Transfer. Methods in Molecular Biology, 2008, 452, 457-469.	0.4	25
32	Ananke: temporal clustering reveals ecological dynamics of microbial communities. PeerJ, 2017, 5, e3812.	0.9	25
33	simDEF: definition-based semantic similarity measure of gene ontology terms for functional similarity analysis of genes. Bioinformatics, 2016, 32, 1380-1387.	1.8	24
34	Being Aquifex aeolicus: Untangling a Hyperthermophileâ€™s Checkered Past. Genome Biology and Evolution, 2013, 5, 2478-2497.	1.1	22
35	Conservation and stewardship of the human microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14312-14313.	3.3	21
36	Identification of Primary Antimicrobial Resistance Drivers in Agricultural Nontyphoidal Salmonella enterica Serovars by Using Machine Learning. MSystems, 2019, 4, .	1.7	21

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37	Cellulaseâˆ'Hemicellulase Activities and Bacterial Community Composition of Different Soils from Algerian Ecosystems. Microbial Ecology, 2019, 77, 713-725.	1.4	21
38	Phylogenetic Clustering of Genes Reveals Shared Evolutionary Trajectories and Putative Gene Functions. Genome Biology and Evolution, 2018, 10, 2255-2265.	1.1	19
39	Untangling Hybrid Phylogenetic Signals: Horizontal Gene Transfer and Artifacts of Phylogenetic Reconstruction. Methods in Molecular Biology, 2009, 532, 241-256.	0.4	17
40	RADProc: A computationally efficient de novo locus assembler for population studies using RADseq data. Molecular Ecology Resources, 2019, 19, 272-282.	2.2	14
41	Discovery of an expanded set of avian leukosis subgroup E proviruses in chickens using Vermillion, a novel sequence capture and analysis pipeline. Poultry Science, 2016, 95, 2250-2258.	1.5	11
42	PSORTm: a bacterial and archaeal protein subcellular localization prediction tool for metagenomics data. Bioinformatics, 2020, 36, 3043-3048.	1.8	10
43	Gene sharing and genome evolution: networks in trees and trees in networks. Biology and Philosophy, 2010, 25, 659-673.	0.7	8
44	Fixed-Parameter and Approximation Algorithms for Maximum Agreement Forests of Multifurcating Trees. Algorithmica, 2016, 74, 1019-1054.	1.0	8
45	Identifying novel Î²-lactamase substrate activity through in silico prediction of antimicrobial resistance. Microbial Genomics, 2021, 7, .	1.0	8
46	Transfer of energy pathway genes in microbial enhanced biological phosphorus removal communities. BMC Genomics, 2015, 16, 526.	1.2	6
47	Quantitative visualizations of hierarchically organized data in a geographic context. , 2009, , .		5
48	deepSimDEF: deep neural embeddings of gene products and gene ontology terms for functional analysis of genes. Bioinformatics, 2022, 38, 3051-3061.	1.8	4
49	Scaling Up the Phylogenetic Detection of Lateral Gene Transfer Events. Methods in Molecular Biology, 2017, 1525, 421-432.	0.4	2
50	Large-scale detection of recombination in nucleotide sequences. AIP Conference Proceedings, 2008, , .	0.3	1
51	Investigating biogeographical patterns using pointâ€based cartograms. Global Ecology and Biogeography, 2018, 27, 380-388.	2.7	0