Robert G Beiko

List of Publications by Year
in descending order

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51
papers

13,057
citations

186265
28
h-index

206112
48
g-index

61
all docs

61
docs citations

61
times ranked

20986
citing authors

#	Article	IF	Citations
1	deepSimDEF: deep neural embeddings of gene products and gene ontology terms for functional analysis of genes. Bioinformatics, 2022, 38, 3051-3061.	4.1	4
2	Machine Learning for Antimicrobial Resistance Prediction: Current Practice, Limitations, and Clinical Perspective. Clinical Microbiology Reviews, 2022, 35, .	13.6	33
3	Identifying novel Î²-lactamase substrate activity through in silico prediction of antimicrobial resistance. Microbial Genomics, 2021, 7, .	2.0	8
4	CARD 2020: antibiotic resistome surveillance with the comprehensive antibiotic resistance database. Nucleic Acids Research, 2020, 48, D517-D525.	14.5	1,605
5	PSORTm: a bacterial and archaeal protein subcellular localization prediction tool for metagenomics data. Bioinformatics, 2020, 36, 3043-3048.	4.1	10
6	Metagenome-assembled genome binning methods with short reads disproportionately fail for plasmids and genomic Islands. Microbial Genomics, 2020, 6, .	2.0	67
7	Identification of Primary Antimicrobial Resistance Drivers in Agricultural Nontyphoidal Salmonella enterica Serovars by Using Machine Learning. MSystems, 2019, 4, .	3.8	21
8	Cellulaseâˆ’Hemicellulase Activities and Bacterial Community Composition of Different Soils from Algerian Ecosystems. Microbial Ecology, 2019, 77, 713-725.	2.8	21
9	RADProc: A computationally efficient de novo locus assembler for population studies using RADseq data. Molecular Ecology Resources, 2019, 19, 272-282.	4.8	14
10	Investigating biogeographical patterns using pointâ€•based cartograms. Global Ecology and Biogeography, 2018, 27, 380-388.	5.8	0
11	A climate-associated multispecies cryptic cline in the northwest Atlantic. Science Advances, 2018, 4, eaaq0929.	10.3	91
12	Applications of random forest feature selection for fineâ€•scale genetic population assignment. Evolutionary Applications, 2018, 11, 153-165.	3.1	101
13	Predicting the Functional Potential of the Microbiome from Marker Genes Using PICRUSt. Methods in Molecular Biology, 2018, 1849, 169-177.	0.9	155
14	Environmental extremes drive population structure at the northern range limit of Atlantic salmon in North America. Molecular Ecology, 2018, 27, 4026-4040.	3.9	26
15	Phylogenetic Clustering of Genes Reveals Shared Evolutionary Trajectories and Putative Gene Functions. Genome Biology and Evolution, 2018, 10, 2255-2265.	2.5	19
16	<scp>megasat</scp>: automated inference of microsatellite genotypes from sequence data. Molecular Ecology Resources, 2017, 17, 247-256.	4.8	59
17	Scaling Up the Phylogenetic Detection of Lateral Gene Transfer Events. Methods in Molecular Biology, 2017, 1525, 421-432.	0.9	2
18	<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.	1.9	42

#	ARTICLE	IF	CITATIONS
19	Range-wide parallel climate-associated genomic clines in Atlantic salmon. Royal Society Open Science, 2017, 4, 171394.	2.4	35
20	Inter-personal diversity and temporal dynamics of dental, tongue, and salivary microbiota in the healthy oral cavity. Npj Biofilms and Microbiomes, 2017, 3, 2.	6.4	158
21	Ananke: temporal clustering reveals ecological dynamics of microbial communities. PeerJ, 2017, 5, e3812.	2.0	25
22	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.	3.4	11
23	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.	4.0	67
24	simDEF: definition-based semantic similarity measure of gene ontology terms for functional similarity analysis of genes. Bioinformatics, 2016, 32, 1380-1387.	4.1	24
25	Fixed-Parameter and Approximation Algorithms for Maximum Agreement Forests of Multifurcating Trees. Algorithmica, 2016, 74, 1019-1054.	1.3	8
26	Genomic Comparison of Non-Typhoidal Salmonella enterica Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens. PLoS ONE, 2015, 10, e0128773.	2.5	53
27	Transfer of energy pathway genes in microbial enhanced biological phosphorus removal communities. BMC Genomics, 2015, 16, 526.	2.8	6
28	Microbial Malaise: How Can We Classify the Microbiome?. Trends in Microbiology, 2015, 23, 671-679.	7.7	36
29	Phylogenetic approaches to microbial community classification. Microbiome, 2015, 3, 47.	11.1	39
30	A Phylogenomic View of Ecological Specialization in the Lachnospiraceae, a Family of Digestive Tract-Associated Bacteria. Genome Biology and Evolution, 2014, 6, 703-713.	2.5	601
31	Microbial shifts in the aging mouse gut. Microbiome, 2014, 2, 50.	11.1	354
32	Supertrees Based on the Subtree Prune-and-Regraft Distance. Systematic Biology, 2014, 63, 566-581.	5.6	63
33	Conservation and stewardship of the human microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14312-14313.	7.1	21
34	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology, 2013, 31, 814-821.	17.5	8,049
35	Measures of phylogenetic differentiation provide robust and complementary insights into microbial communities. ISME Journal, 2013, 7, 173-183.	9.8	41
36	Being Aquifex aeolicus: Untangling a Hyperthermophileâ€™s Checkered Past. Genome Biology and Evolution, 2013, 5, 2478-2497.	2.5	22

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37	GenGIS 2: Geospatial Analysis of Traditional and Genetic Biodiversity, with New Gradient Algorithms and an Extensible Plugin Framework. PLoS ONE, 2013, 8, e69885.	2.5	118
38	Rapid identification of high-confidence taxonomic assignments for metagenomic data. Nucleic Acids Research, 2012, 40, e111-e111.	14.5	57
39	Classifying short genomic fragments from novel lineages using composition and homology. BMC Bioinformatics, 2011, 12, 328.	2.6	64
40	Telling the whole story in a 10,000-genome world. Biology Direct, 2011, 6, 34.	4.6	45
41	Gene sharing and genome evolution: networks in trees and trees in networks. Biology and Philosophy, 2010, 25, 659-673.	1.4	8
42	GenGIS: A geospatial information system for genomic data. Genome Research, 2009, 19, 1896-1904.	5.5	119
43	Untangling Hybrid Phylogenetic Signals: Horizontal Gene Transfer and Artifacts of Phylogenetic Reconstruction. Methods in Molecular Biology, 2009, 532, 241-256.	0.9	17
44	Quantitative visualizations of hierarchically organized data in a geographic context. , 2009, , .		5
45	Detecting Lateral Genetic Transfer. Methods in Molecular Biology, 2008, 452, 457-469.	0.9	25
46	Large-scale detection of recombination in nucleotide sequences. AIP Conference Proceedings, 2008, , .	0.4	1
47	The Impact of Reticulate Evolution on Genome Phylogeny. Systematic Biology, 2008, 57, 844-856.	5.6	47
48	A simulation test bed for hypotheses of genome evolution. Bioinformatics, 2007, 23, 825-831.	4.1	45
49	Do different surrogate methods detect lateral genetic transfer events of different relative ages?. Trends in Microbiology, 2006, 14, 4-8.	7.7	79
50	Highways of gene sharing in prokaryotes. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14332-14337.	7.1	467
51	Microbial phylogenomics: Branching out. Nature, 2003, 421, 217-217.	27.8	28