

# Robert G Beiko

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4820689/publications.pdf>

Version: 2024-02-01

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	deepSimDEF: deep neural embeddings of gene products and gene ontology terms for functional analysis of genes. <i>Bioinformatics</i> , 2022, 38, 3051-3061.	1.8	4
2	Machine Learning for Antimicrobial Resistance Prediction: Current Practice, Limitations, and Clinical Perspective. <i>Clinical Microbiology Reviews</i> , 2022, 35, .	5.7	33
3	Identifying novel $\beta$ -lactamase substrate activity through in silico prediction of antimicrobial resistance. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
4	CARD 2020: antibiotic resistance surveillance with the comprehensive antibiotic resistance database. <i>Nucleic Acids Research</i> , 2020, 48, D517-D525.	6.5	1,605
5	PSORTm: a bacterial and archaeal protein subcellular localization prediction tool for metagenomics data. <i>Bioinformatics</i> , 2020, 36, 3043-3048.	1.8	10
6	Metagenome-assembled genome binning methods with short reads disproportionately fail for plasmids and genomic islands. <i>Microbial Genomics</i> , 2020, 6, .	1.0	67
7	Identification of Primary Antimicrobial Resistance Drivers in Agricultural Nontyphoidal <i>Salmonella enterica</i> Serovars by Using Machine Learning. <i>MSystems</i> , 2019, 4, .	1.7	21
8	Cellulase and Hemicellulase Activities and Bacterial Community Composition of Different Soils from Algerian Ecosystems. <i>Microbial Ecology</i> , 2019, 77, 713-725.	1.4	21
9	RADProc: A computationally efficient de novo locus assembler for population studies using RADseq data. <i>Molecular Ecology Resources</i> , 2019, 19, 272-282.	2.2	14
10	Investigating biogeographical patterns using point-based cartograms. <i>Global Ecology and Biogeography</i> , 2018, 27, 380-388.	2.7	0
11	A climate-associated multispecies cryptic cline in the northwest Atlantic. <i>Science Advances</i> , 2018, 4, eaaq0929.	4.7	91
12	Applications of random forest feature selection for fine-scale genetic population assignment. <i>Evolutionary Applications</i> , 2018, 11, 153-165.	1.5	101
13	Predicting the Functional Potential of the Microbiome from Marker Genes Using PICRUSt. <i>Methods in Molecular Biology</i> , 2018, 1849, 169-177.	0.4	155
14	Environmental extremes drive population structure at the northern range limit of Atlantic salmon in North America. <i>Molecular Ecology</i> , 2018, 27, 4026-4040.	2.0	26
15	Phylogenetic Clustering of Genes Reveals Shared Evolutionary Trajectories and Putative Gene Functions. <i>Genome Biology and Evolution</i> , 2018, 10, 2255-2265.	1.1	19
16	<sc>megasat</sc>: automated inference of microsatellite genotypes from sequence data. <i>Molecular Ecology Resources</i> , 2017, 17, 247-256.	2.2	59
17	Scaling Up the Phylogenetic Detection of Lateral Gene Transfer Events. <i>Methods in Molecular Biology</i> , 2017, 1525, 421-432.	0.4	2
18	<sc>RAD</sc> sequencing reveals genomewide divergence between independent invasions of the European green crab (<i>Carcinus maenas</i>) in the Northwest Atlantic. <i>Ecology and Evolution</i> , 2017, 7, 2513-2524.	0.8	42

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19	Range-wide parallel climate-associated genomic clines in Atlantic salmon. <i>Royal Society Open Science</i> , 2017, 4, 171394.	1.1	35
20	Inter-personal diversity and temporal dynamics of dental, tongue, and salivary microbiota in the healthy oral cavity. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 2.	2.9	158
21	Ananke: temporal clustering reveals ecological dynamics of microbial communities. <i>PeerJ</i> , 2017, 5, e3812.	0.9	25
22	Discovery of an expanded set of avian leukosis subgroup E proviruses in chickens using Vermillion, a novel sequence capture and analysis pipeline. <i>Poultry Science</i> , 2016, 95, 2250-2258.	1.5	11
23	A new way to contemplate Darwin's tangled bank: how DNA barcodes are reconnecting biodiversity science and biomonitoring. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2016, 371, 20150330.	1.8	67
24	simDEF: definition-based semantic similarity measure of gene ontology terms for functional similarity analysis of genes. <i>Bioinformatics</i> , 2016, 32, 1380-1387.	1.8	24
25	Fixed-Parameter and Approximation Algorithms for Maximum Agreement Forests of Multifurcating Trees. <i>Algorithmica</i> , 2016, 74, 1019-1054.	1.0	8
26	Genomic Comparison of Non-Typhoidal <i>Salmonella enterica</i> Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler Chickens. <i>PLoS ONE</i> , 2015, 10, e0128773.	1.1	53
27	Transfer of energy pathway genes in microbial enhanced biological phosphorus removal communities. <i>BMC Genomics</i> , 2015, 16, 526.	1.2	6
28	Microbial Malaise: How Can We Classify the Microbiome?. <i>Trends in Microbiology</i> , 2015, 23, 671-679.	3.5	36
29	Phylogenetic approaches to microbial community classification. <i>Microbiome</i> , 2015, 3, 47.	4.9	39
30	A Phylogenomic View of Ecological Specialization in the Lachnospiraceae, a Family of Digestive Tract-Associated Bacteria. <i>Genome Biology and Evolution</i> , 2014, 6, 703-713.	1.1	601
31	Microbial shifts in the aging mouse gut. <i>Microbiome</i> , 2014, 2, 50.	4.9	354
32	Supertrees Based on the Subtree Prune-and-Regraft Distance. <i>Systematic Biology</i> , 2014, 63, 566-581.	2.7	63
33	Conservation and stewardship of the human microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 14312-14313.	3.3	21
34	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	9.4	8,049
35	Measures of phylogenetic differentiation provide robust and complementary insights into microbial communities. <i>ISME Journal</i> , 2013, 7, 173-183.	4.4	41
36	Being <i>Aquifex aeolicus</i> : Untangling a Hyperthermophile's Checkered Past. <i>Genome Biology and Evolution</i> , 2013, 5, 2478-2497.	1.1	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.	1.1	118
38	Rapid identification of high-confidence taxonomic assignments for metagenomic data. Nucleic Acids Research, 2012, 40, e111-e111.	6.5	57
39	Classifying short genomic fragments from novel lineages using composition and homology. BMC Bioinformatics, 2011, 12, 328.	1.2	64
40	Telling the whole story in a 10,000-genome world. Biology Direct, 2011, 6, 34.	1.9	45
41	Gene sharing and genome evolution: networks in trees and trees in networks. Biology and Philosophy, 2010, 25, 659-673.	0.7	8
42	GenGIS: A geospatial information system for genomic data. Genome Research, 2009, 19, 1896-1904.	2.4	119
43	Untangling Hybrid Phylogenetic Signals: Horizontal Gene Transfer and Artifacts of Phylogenetic Reconstruction. Methods in Molecular Biology, 2009, 532, 241-256.	0.4	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.	0.4	25
46	Large-scale detection of recombination in nucleotide sequences. AIP Conference Proceedings, 2008, , .	0.3	1
47	The Impact of Reticulate Evolution on Genome Phylogeny. Systematic Biology, 2008, 57, 844-856.	2.7	47
48	A simulation test bed for hypotheses of genome evolution. Bioinformatics, 2007, 23, 825-831.	1.8	45
49	Do different surrogate methods detect lateral genetic transfer events of different relative ages?. Trends in Microbiology, 2006, 14, 4-8.	3.5	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.	3.3	467
51	Microbial phylogenomics: Branching out. Nature, 2003, 421, 217-217.	13.7	28