

Gordon D Pusch

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.

20
papers

14,597
citations

15
h-index

20
g-index

20
ext. papers

19,603
ext. citations

9.6
avg, IF

5.27
L-index

#	Paper	IF	Citations
20	Supervised extraction of near-complete genomes from metagenomic samples: A new service in PATRIC. <i>PLoS ONE</i> , 2021 , 16, e0250092	3.7	0
19	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
18	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020 , 48, D606-D612	20.1	206
17	PATRIC as a unique resource for studying antimicrobial resistance. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1094-1102	13.4	43
16	A machine learning-based service for estimating quality of genomes using PATRIC. <i>BMC Bioinformatics</i> , 2019 , 20, 486	3.6	11
15	Assembly, Annotation, and Comparative Genomics in PATRIC, the All Bacterial Bioinformatics Resource Center. <i>Methods in Molecular Biology</i> , 2018 , 1704, 79-101	1.4	48
14	Phage Genome Annotation Using the RAST Pipeline. <i>Methods in Molecular Biology</i> , 2018 , 1681, 231-238	1.4	38
13	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. <i>Nucleic Acids Research</i> , 2017 , 45, D535-D542	20.1	809
12	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. <i>Frontiers in Microbiology</i> , 2016 , 7, 118	5.7	65
11	Enabling comparative modeling of closely related genomes: example genus <i>Brucella</i> . <i>3 Biotech</i> , 2015 , 5, 101-105	2.8	3
10	RASTtk: a modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. <i>Scientific Reports</i> , 2015 , 5, 8365	4.9	1061
9	The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). <i>Nucleic Acids Research</i> , 2014 , 42, D206-14	20.1	2534
8	PATRIC, the bacterial bioinformatics database and analysis resource. <i>Nucleic Acids Research</i> , 2014 , 42, D581-91	20.1	823
7	SEED servers: high-performance access to the SEED genomes, annotations, and metabolic models. <i>PLoS ONE</i> , 2012 , 7, e48053	3.7	121
6	Grounding annotations in published literature with an emphasis on the functional roles used in metabolic models. <i>3 Biotech</i> , 2012 , 2, 135-140	2.8	78
5	Real time metagenomics: using k-mers to annotate metagenomes. <i>Bioinformatics</i> , 2012 , 28, 3316-7	7.2	29
4	The RAST Server: rapid annotations using subsystems technology. <i>BMC Genomics</i> , 2008 , 9, 75	4.5	7153

3	The National Microbial Pathogen Database Resource (NMPDR): a genomics platform based on subsystem annotation. <i>Nucleic Acids Research</i> , 2007 , 35, D347-53	20.1	77
2	The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. <i>Nucleic Acids Research</i> , 2005 , 33, 5691-702	20.1	1485
1	Sensitivity analysis of the MM5 weather model using automatic differentiation. <i>Computers in Physics</i> , 1996 , 10, 605		11