

Gordon D Pusch

List of Publications by Citations

Source: <https://exaly.com/author-pdf/10581815/gordon-d-pusch-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	The RAST Server: rapid annotations using subsystems technology. <i>BMC Genomics</i> , 2008 , 9, 75	4.5	7153
19	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
18	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
17	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
16	PATRIC, the bacterial bioinformatics database and analysis resource. <i>Nucleic Acids Research</i> , 2014 , 42, D581-91	20.1	823
15	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. <i>Nucleic Acids Research</i> , 2017 , 45, D535-D542	20.1	809
14	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020 , 48, D606-D612	20.1	206
13	SEED servers: high-performance access to the SEED genomes, annotations, and metabolic models. <i>PLoS ONE</i> , 2012 , 7, e48053	3.7	121
12	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
11	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
10	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. <i>Frontiers in Microbiology</i> , 2016 , 7, 118	5.7	65
9	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
8	PATRIC as a unique resource for studying antimicrobial resistance. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1094-1102	13.4	43
7	Phage Genome Annotation Using the RAST Pipeline. <i>Methods in Molecular Biology</i> , 2018 , 1681, 231-238	1.4	38
6	Real time metagenomics: using k-mers to annotate metagenomes. <i>Bioinformatics</i> , 2012 , 28, 3316-7	7.2	29
5	A machine learning-based service for estimating quality of genomes using PATRIC. <i>BMC Bioinformatics</i> , 2019 , 20, 486	3.6	11
4	Sensitivity analysis of the MM5 weather model using automatic differentiation. <i>Computers in Physics</i> , 1996 , 10, 605		11

3	Enabling comparative modeling of closely related genomes: example genus <i>Brucella</i> . <i>3 Biotech</i> , 2015 , 5, 101-105	2.8	3
2	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
1	Supervised extraction of near-complete genomes from metagenomic samples: A new service in PATRIC. <i>PLoS ONE</i> , 2021 , 16, e0250092	3.7	0