Gordon D Pusch

List of Publications by Year
in descending order

20 papers	21,665 citations	516561 16 h-index	794469 19 g-index
20 all docs	20 docs citations	20 times ranked	21611 citing authors

#	Article	IF	Citations
1	The RAST Server: Rapid Annotations using Subsystems Technology. BMC Genomics, 2008, 9, 75.	1.2	9,977
2	The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Research, 2014, 42, D206-D214.	6.5	3,832
3	RASTtk: A modular and extensible implementation of the RAST algorithm for building custom annotation pipelines and annotating batches of genomes. Scientific Reports, 2015, 5, 8365.	1.6	2,080
4	The Subsystems Approach to Genome Annotation and its Use in the Project to Annotate 1000 Genomes. Nucleic Acids Research, 2005, 33, 5691-5702.	6.5	1,806
5	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. Nucleic Acids Research, 2017, 45, D535-D542.	6.5	1,445
6	PATRIC, the bacterial bioinformatics database and analysis resource. Nucleic Acids Research, 2014, 42, D581-D591.	6.5	1,222
7	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. Nucleic Acids Research, 2020, 48, D606-D612.	6.5	552
8	SEED Servers: High-Performance Access to the SEED Genomes, Annotations, and Metabolic Models. PLoS ONE, 2012, 7, e48053.	1.1	169
9	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. Frontiers in Microbiology, 2016, 7, 118.	1.5	153
10	PATRIC as a unique resource for studying antimicrobial resistance. Briefings in Bioinformatics, 2019, 20, 1094-1102.	3.2	93
11	The National Microbial Pathogen Database Resource (NMPDR): a genomics platform based on subsystem annotation. Nucleic Acids Research, 2007, 35, D347-D353.	6.5	87
12	Assembly, Annotation, and Comparative Genomics in PATRIC, the All Bacterial Bioinformatics Resource Center. Methods in Molecular Biology, 2018, 1704, 79-101.	0.4	73
13	Phage Genome Annotation Using the RAST Pipeline. Methods in Molecular Biology, 2018, 1681, 231-238.	0.4	64
14	Real Time Metagenomics: Using k-mers to annotate metagenomes. Bioinformatics, 2012, 28, 3316-3317.	1.8	35
15	A machine learning-based service for estimating quality of genomes using PATRIC. BMC Bioinformatics, 2019, 20, 486.	1.2	32
16	Sensitivity analysis of the MM5 weather model using automatic differentiation. Computers in Physics, 1996, 10, 605.	0.6	18
17	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. Briefings in Bioinformatics, 2021, 22, .	3.2	15
18	Supervised extraction of near-complete genomes from metagenomic samples: A new service in PATRIC. PLoS ONE, 2021, 16, e0250092.	1.1	7

#	Article	IF	Citations
19	Enabling comparative modeling of closely related genomes: example genus Brucella. 3 Biotech, 2015, 5, 101-105.	1.1	5
20	Grounding annotations in published literature with an emphasis on the functional roles used in metabolic models. 3 Biotech, 2012, 2, 135-140.	1.1	0