

Alice R Wattam

List of Publications by Citations

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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.

35
papers

6,446
citations

20
h-index

35
g-index

35
ext. papers

9,385
ext. citations

6.9
avg, IF

5.03
L-index

#	Paper	IF	Citations
35	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
34	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
33	PATRIC, the bacterial bioinformatics database and analysis resource. <i>Nucleic Acids Research</i> , 2014 , 42, D581-91	20.1	823
32	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. <i>Nucleic Acids Research</i> , 2017 , 45, D535-D542	20.1	809
31	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. <i>Nucleic Acids Research</i> , 2020 , 48, D606-D612	20.1	206
30	PATRIC: the comprehensive bacterial bioinformatics resource with a focus on human pathogenic species. <i>Infection and Immunity</i> , 2011 , 79, 4286-98	3.7	198
29	Antimicrobial Resistance Prediction in PATRIC and RAST. <i>Scientific Reports</i> , 2016 , 6, 27930	4.9	120
28	Analysis of ten Brucella genomes reveals evidence for horizontal gene transfer despite a preferred intracellular lifestyle. <i>Journal of Bacteriology</i> , 2009 , 191, 3569-79	3.5	86
27	Comparative phylogenomics and evolution of the Brucellae reveal a path to virulence. <i>Journal of Bacteriology</i> , 2014 , 196, 920-30	3.5	73
26	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. <i>Frontiers in Microbiology</i> , 2016 , 7, 118	5.7	65
25	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
24	Insight of Genus : Ascertaining the Role of Pathogenic and Non-pathogenic Species. <i>Frontiers in Microbiology</i> , 2017 , 8, 1937	5.7	45
23	PATRIC as a unique resource for studying antimicrobial resistance. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1094-1102	13.4	43
22	Brucella spp. of amphibians comprise genomically diverse motile strains competent for replication in macrophages and survival in mammalian hosts. <i>Scientific Reports</i> , 2017 , 7, 44420	4.9	41
21	Comparative mangrove metagenome reveals global prevalence of heavy metals and antibiotic resistome across different ecosystems. <i>Scientific Reports</i> , 2018 , 8, 11187	4.9	38
20	Curation, integration and visualization of bacterial virulence factors in PATRIC. <i>Bioinformatics</i> , 2015 , 31, 252-8	7.2	37
19	Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. <i>Scientific Reports</i> , 2017 , 7, 8859	4.9	37

18	Comparative genomics of early-diverging Brucella strains reveals a novel lipopolysaccharide biosynthesis pathway. <i>MBio</i> , 2012 , 3, e00246-11	7.8	23
17	Comparative genomics of early-diverging Brucella strains reveals a novel lipopolysaccharide biosynthesis pathway. <i>MBio</i> , 2012 , 3, e00246-12	7.8	23
16	The Complete Genome Sequence of the Emerging Pathogen Mycobacterium haemophilum Explains Its Unique Culture Requirements. <i>MBio</i> , 2015 , 6, e01313-15	7.8	22
15	A synthesis of bacterial and archaeal phenotypic trait data. <i>Scientific Data</i> , 2020 , 7, 170	8.2	20
14	Comparative genomic analysis at the PATRIC, a bioinformatic resource center. <i>Methods in Molecular Biology</i> , 2014 , 1197, 287-308	1.4	15
13	Comparative genomic analysis between <i>Corynebacterium pseudotuberculosis</i> strains isolated from buffalo. <i>PLoS ONE</i> , 2017 , 12, e0176347	3.7	14
12	Identification and molecular epidemiology of methicillin resistant <i>Staphylococcus pseudintermedius</i> strains isolated from canine clinical samples in Argentina. <i>BMC Veterinary Research</i> , 2019 , 15, 264	2.7	13
11	<i>Helicobacter pylori</i> Infections in the Bronx, New York: Surveying Antibiotic Susceptibility and Strain Lineage by Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2020 , 58,	9.7	11
10	RNA-Rocket: an RNA-Seq analysis resource for infectious disease research. <i>Bioinformatics</i> , 2015 , 31, 1496-8	6.8	9
9	Comparative Genomics for Prokaryotes. <i>Methods in Molecular Biology</i> , 2018 , 1704, 55-78	1.4	7
8	Coccidian parasites (Apicomplexa: Eimeriidae) from insectivores. IV. Four new species in <i>Talpa europaea</i> from England. <i>Journal of Protozoology</i> , 1988 , 35, 58-62		7
7	Characterization of the First A-Positive Multidrug-Resistant Isolated from an Argentinian Patient. <i>Microbial Drug Resistance</i> , 2020 , 26, 717-721	2.9	5
6	Coccidian parasites (Apicomplexa: Eimeriidae) from insectivores. V. Ten forms from the moles of Japan (<i>Euroscaptor</i> , <i>Mogera</i> spp.). <i>Journal of Protozoology</i> , 1988 , 35, 55-7		4
5	Enabling comparative modeling of closely related genomes: example genus <i>Brucella</i> . <i>3 Biotech</i> , 2015 , 5, 101-105	2.8	3
4	Panaconda: Application of pan-synteny graph models to genome content analysis		2
3	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	2
2	Cell Division in genus <i>Corynebacterium</i> : protein-protein interaction and molecular docking of SepF and FtsZ in the understanding of cytokinesis in pathogenic species. <i>Anais Da Academia Brasileira De Ciencias</i> , 2018 , 90, 2179-2188	1.4	2
1	Identification and Characterization of Mycobacterial Species Using Whole-Genome Sequences. <i>Methods in Molecular Biology</i> , 2021 , 2314, 399-457	1.4	

