Alice R Wattam

List of Publications by Year
in descending order

34	10,795	279487	395343
papers	citations	23	33
		h-index	g-index

35	35	35	13267
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The SEED and the Rapid Annotation of microbial genomes using Subsystems Technology (RAST). Nucleic Acids Research, 2014, 42, D206-D214.	6.5	3,832
2	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
3	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. Nucleic Acids Research, 2017, 45, D535-D542.	6.5	1,445
4	PATRIC, the bacterial bioinformatics database and analysis resource. Nucleic Acids Research, 2014, 42, D581-D591.	6.5	1,222
5	The PATRIC Bioinformatics Resource Center: expanding data and analysis capabilities. Nucleic Acids Research, 2020, 48, D606-D612.	6.5	552
6	PATRIC: the Comprehensive Bacterial Bioinformatics Resource with a Focus on Human Pathogenic Species. Infection and Immunity, 2011, 79, 4286-4298.	1.0	252
7	Antimicrobial Resistance Prediction in PATRIC and RAST. Scientific Reports, 2016, 6, 27930.	1.6	179
8	PATtyFams: Protein Families for the Microbial Genomes in the PATRIC Database. Frontiers in Microbiology, 2016, 7, 118.	1.5	153
9	Comparative Phylogenomics and Evolution of the Brucellae Reveal a Path to Virulence. Journal of Bacteriology, 2014, 196, 920-930.	1.0	122
10	Analysis of Ten *Brucella* Genomes Reveals Evidence for Horizontal Gene Transfer Despite a Preferred Intracellular Lifestyle. Journal of Bacteriology, 2009, 191, 3569-3579.	1.0	103
11	Brucella spp. of amphibians comprise genomically diverse motile strains competent for replication in macrophages and survival in mammalian hosts. Scientific Reports, 2017, 7, 44420.	1.6	96
12	PATRIC as a unique resource for studying antimicrobial resistance. Briefings in Bioinformatics, 2019, 20, 1094-1102.	3.2	93
13	Insight of Genus Corynebacterium: Ascertaining the Role of Pathogenic and Non-pathogenic Species. Frontiers in Microbiology, 2017, 8, 1937.	1.5	80
14	Assembly, Annotation, and Comparative Genomics in PATRIC, the All Bacterial Bioinformatics Resource Center. Methods in Molecular Biology, 2018, 1704, 79-101.	0.4	73
15	Comparative mangrove metagenome reveals global prevalence of heavy metals and antibiotic resistome across different ecosystems. Scientific Reports, 2018, 8, 11187.	1.6	63
16	A synthesis of bacterial and archaeal phenotypic trait data. Scientific Data, 2020, 7, 170.	2.4	59
17	Curation, integration and visualization of bacterial virulence factors in PATRIC. Bioinformatics, 2015, 31, 252-258.	1.8	58
18	Searching for signatures across microbial communities: Metagenomic analysis of soil samples from mangrove and other ecosystems. Scientific Reports, 2017, 7, 8859.	1.6	50

#	Article	IF	Citations
19	Comparative Genomics of Early-Diverging Brucella Strains Reveals a Novel Lipopolysaccharide Biosynthesis Pathway. MBio, 2012, 3, e00246-12.	1.8	37
20	Comparative Genomics of Early-Diverging <i>Brucella</i> Strains Reveals a Novel Lipopolysaccharide Biosynthesis Pathway. MBio, 2012, 3, e00246-11.	1.8	33
21	The Complete Genome Sequence of the Emerging Pathogen Mycobacterium haemophilum Explains Its Unique Culture Requirements. MBio, 2015, 6, e01313-15.	1.8	30
22	Comparative genomic analysis between Corynebacterium pseudotuberculosis strains isolated from buffalo. PLoS ONE, 2017, 12, e0176347.	1.1	30
23	Comparative Genomic Analysis at the PATRIC, A Bioinformatic Resource Center. Methods in Molecular Biology, 2014, 1197, 287-308.	0.4	29
24	Identification and molecular epidemiology of methicillin resistant Staphylococcus pseudintermedius strains isolated from canine clinical samples in Argentina. BMC Veterinary Research, 2019, 15, 264.	0.7	25
25	Helicobacter pylori Infections in the Bronx, New York: Surveying Antibiotic Susceptibility and Strain Lineage by Whole-Genome Sequencing. Journal of Clinical Microbiology, 2020, 58, .	1.8	20
26	Comparative Genomics for Prokaryotes. Methods in Molecular Biology, 2018, 1704, 55-78.	0.4	15
27	A genomic data resource for predicting antimicrobial resistance from laboratory-derived antimicrobial susceptibility phenotypes. Briefings in Bioinformatics, 2021, 22, .	3.2	15
28	Coccidian Parasites (Apicomplexa: Eimeriidae) from Insectivores. IV. Four New Species inTalpa europaeafrom England1. Journal of Protozoology, 1988, 35, 58-62.	0.9	11
29	RNA-Rocket: an RNA-Seq analysis resource for infectious disease research. Bioinformatics, 2015, 31, 1496-1498.	1.8	11
30	Characterization of the First<i>mec</i>A-Positive Multidrug-Resistant<i>Staphylococcus pseudintermedius</i>Isolated from an Argentinian Patient. Microbial Drug Resistance, 2020, 26, 717-721.	0.9	9
31	Coccidian Parasites (Apicomplexa: Eimeriidae) from Insectivores. V. Ten Forms from the Moles of Japan (Euroscaptor, Mogeraspp.)1. Journal of Protozoology, 1988, 35, 55-57.	0.9	7
32	Enabling comparative modeling of closely related genomes: example genus Brucella. 3 Biotech, 2015, 5, 101-105.	1.1	5
33	Cell Division in genus Corynebacterium: protein-protein interaction and molecular docking of SepF and FtsZ in the understanding of cytokinesis in pathogenic species. Anais Da Academia Brasileira De Ciencias, 2018, 90, 2179-2188.	0.3	3
34	Identification and Characterization of Mycobacterial Species Using Whole-Genome Sequences. Methods in Molecular Biology, 2021, 2314, 399-457.	0.4	0