James C Abbott

List of Publications by Year
in descending order

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25
papers

2,698
citations

430874
18
h-index

552781
26
g-index

34
all docs

34
docs citations

34
times ranked

6101
citing authors

#	Article	IF	Citations
1	Genome-Annotated Bacterial Collection of the Barley Rhizosphere Microbiota. Microbiology Resource Announcements, 2022, 11, e0106421.	0.6	3
2	Identifying plant genes shaping microbiota composition in the barley rhizosphere. Nature Communications, 2022, 13, .	12.8	44
3	Automated Phylogenetic Analysis Using Best Reciprocal BLAST. Methods in Molecular Biology, 2021, 2369, 41-63.	0.9	0
4	Iron status influences non-alcoholic fatty liver disease in obesity through the gut microbiome. Microbiome, 2021, 9, 104.	11.1	70
5	Biofilm hydrophobicity in environmental isolates of Bacillus subtilis. Microbiology (United Kingdom), 2021, 167, .	1.8	8
6	Applications of the indole-alkaloid gramine modulate the assembly of individual members of the barley rhizosphere microbiota. PeerJ, 2021, 9, e12498.	2.0	12
7	Genomic Differences between Listeria monocytogenes EGDe Isolates Reveal Crucial Roles for SigB and Wall Rhamnosylation in Biofilm Formation. Journal of Bacteriology, 2020, 202, .	2.2	16
8	Pulcherrimin formation controls growth arrest of the <i>Bacillus subtilis</i> biofilm. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 13553-13562.	7.1	46
9	EMSY expression affects multiple components of the skin barrier with relevance to atopic dermatitis. Journal of Allergy and Clinical Immunology, 2019, 144, 470-481.	2.9	23
10	Use of next-generation sequencing in the CHAT study (acute HCV in HIV): effect of baseline resistance-associated NS3 variants on treatment failure. HIV Clinical Trials, 2018, 19, 46-51.	2.0	2
11	Molecular phenomics and metagenomics of hepatic steatosis in non-diabetic obese women. Nature Medicine, 2018, 24, 1070-1080.	30.7	465
12	Genome sequence and plasmid transformation of the model high-yield bacterial cellulose producer Gluconacetobacter hansenii ATCC 53582. Scientific Reports, 2016, 6, 23635.	3.3	61
13	Engineering control of bacterial cellulose production using a genetic toolkit and a new cellulose-producing strain. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E3431-40.	7.1	173
14	Epigenome-wide association of DNA methylation markers in peripheral blood from Indian Asians and Europeans with incident type 2 diabetes: a nested case-control study. Lancet Diabetes and Endocrinology,the, 2015, 3, 526-534.	11.4	396
15	Emergence of a New Highly Successful Acapsular Group A <i>Streptococcus</i> Clade of Genotype <i>emm</i> 89 in the United Kingdom. MBio, 2015, 6, e00622.	4.1	126
16	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	21.4	294
17	The South Asian Genome. PLoS ONE, 2014, 9, e102645.	2.5	43
18	Using a periclinal chimera to unravel layerâ€specific gene expression in plants. Plant Journal, 2013, 75, 1039-1049.	5.7	19

#	ARTICLE	IF	CITATIONS
19	Structure and evolution of barley powdery mildew effector candidates. BMC Genomics, 2012, 13, 694.	2.8	238
20	Strategies towards sequencing complex crop genomes. Genome Biology, 2012, 13, 322.	9.6	3
21	Comparative sequence analysis of wheat and barley powdery mildew fungi reveals gene colinearity, dates divergence and indicates host-pathogen co-evolution. Fungal Genetics and Biology, 2011, 48, 327-334.	2.1	33
22	c-di-AMP Is a New Second Messenger in Staphylococcus aureus with a Role in Controlling Cell Size and Envelope Stress. PLoS Pathogens, 2011, 7, e1002217.	4.7	398
23	Comparative analysis of the Saccharomyces cerevisiae and Caenorhabditis elegans protein interaction networks. BMC Evolutionary Biology, 2005, 5, 23.	3.2	50
24	Simultaneous Suppression of Multiple Genes by Single Transgenes. Down-Regulation of Three Unrelated Lignin Biosynthetic Genes in Tobacco. Plant Physiology, 2002, 128, 844-853.	4.8	68
25	Enabling technologies for manipulating multiple genes on complex pathways. Plant Molecular Biology, 2001, 47, 295-310.	3.9	66