

James C Abbott

List of Publications by Year in descending order

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Version: 2024-02-01

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	Molecular phenomics and metagenomics of hepatic steatosis in non-diabetic obese women. <i>Nature Medicine</i> , 2018, 24, 1070-1080.	30.7	465
2	c-di-AMP Is a New Second Messenger in <i>Staphylococcus aureus</i> with a Role in Controlling Cell Size and Envelope Stress. <i>PLoS Pathogens</i> , 2011, 7, e1002217.	4.7	398
3	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. <i>Lancet Diabetes and Endocrinology</i> , 2015, 3, 526-534.	11.4	396
4	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015, 47, 1282-1293.	21.4	294
5	Structure and evolution of barley powdery mildew effector candidates. <i>BMC Genomics</i> , 2012, 13, 694.	2.8	238
6	Engineering control of bacterial cellulose production using a genetic toolkit and a new cellulose-producing strain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E3431-40.	7.1	173
7	Emergence of a New Highly Successful Acapsular Group A <i>Streptococcus</i> Clade of Genotype <i>emm</i> 89 in the United Kingdom. <i>MBio</i> , 2015, 6, e00622.	4.1	126
8	Iron status influences non-alcoholic fatty liver disease in obesity through the gut microbiome. <i>Microbiome</i> , 2021, 9, 104.	11.1	70
9	Simultaneous Suppression of Multiple Genes by Single Transgenes. Down-Regulation of Three Unrelated Lignin Biosynthetic Genes in Tobacco. <i>Plant Physiology</i> , 2002, 128, 844-853.	4.8	68
10	Enabling technologies for manipulating multiple genes on complex pathways. <i>Plant Molecular Biology</i> , 2001, 47, 295-310.	3.9	66
11	Genome sequence and plasmid transformation of the model high-yield bacterial cellulose producer <i>Gluconacetobacter hansenii</i> ATCC 53582. <i>Scientific Reports</i> , 2016, 6, 23635.	3.3	61
12	Comparative analysis of the <i>Saccharomyces cerevisiae</i> and <i>Caenorhabditis elegans</i> protein interaction networks. <i>BMC Evolutionary Biology</i> , 2005, 5, 23.	3.2	50
13	Pulcherrimin formation controls growth arrest of the <i>Bacillus subtilis</i> biofilm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 13553-13562.	7.1	46
14	Identifying plant genes shaping microbiota composition in the barley rhizosphere. <i>Nature Communications</i> , 2022, 13, .	12.8	44
15	The South Asian Genome. <i>PLoS ONE</i> , 2014, 9, e102645.	2.5	43
16	Comparative sequence analysis of wheat and barley powdery mildew fungi reveals gene colinearity, dates divergence and indicates host-pathogen co-evolution. <i>Fungal Genetics and Biology</i> , 2011, 48, 327-334.	2.1	33
17	EMSY expression affects multiple components of the skin barrier with relevance to atopic dermatitis. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 144, 470-481.	2.9	23
18	Using a periclinal chimera to unravel layer-specific gene expression in plants. <i>Plant Journal</i> , 2013, 75, 1039-1049.	5.7	19

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19	Genomic Differences between <i>Listeria monocytogenes</i> EGDe Isolates Reveal Crucial Roles for SigB and Wall Rhamnosylation in Biofilm Formation. <i>Journal of Bacteriology</i> , 2020, 202, .	2.2	16
20	Applications of the indole-alkaloid gramine modulate the assembly of individual members of the barley rhizosphere microbiota. <i>PeerJ</i> , 2021, 9, e12498.	2.0	12
21	Biofilm hydrophobicity in environmental isolates of <i>Bacillus subtilis</i> . <i>Microbiology (United Kingdom)</i> , 2021, 167, .	1.8	8
22	Strategies towards sequencing complex crop genomes. <i>Genome Biology</i> , 2012, 13, 322.	9.6	3
23	Genome-Annotated Bacterial Collection of the Barley Rhizosphere Microbiota. <i>Microbiology Resource Announcements</i> , 2022, 11, e0106421.	0.6	3
24	Use of next-generation sequencing in the CHAT study (acute HCV in HIV): effect of baseline resistance-associated NS3 variants on treatment failure. <i>HIV Clinical Trials</i> , 2018, 19, 46-51.	2.0	2
25	Automated Phylogenetic Analysis Using Best Reciprocal BLAST. <i>Methods in Molecular Biology</i> , 2021, 2369, 41-63.	0.9	0