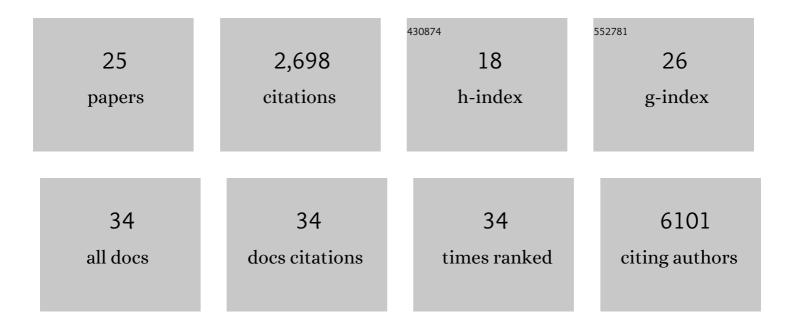
James C Abbott

List of Publications by Year in descending order

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IAMES C ABBOTT

#	Article	IF	CITATIONS
1	Molecular phenomics and metagenomics of hepatic steatosis in non-diabetic obese women. Nature Medicine, 2018, 24, 1070-1080.	30.7	465
2	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
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. Lancet Diabetes and Endocrinology,the, 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. Nature Genetics, 2015, 47, 1282-1293.	21.4	294
5	Structure and evolution of barley powdery mildew effector candidates. BMC Genomics, 2012, 13, 694.	2.8	238
6	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
7	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
8	Iron status influences non-alcoholic fatty liver disease in obesity through the gut microbiome. Microbiome, 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. Plant Physiology, 2002, 128, 844-853.	4.8	68
10	Enabling technologies for manipulating multiple genes on complex pathways. Plant Molecular Biology, 2001, 47, 295-310.	3.9	66
11	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
12	Comparative analysis of the Saccharomyces cerevisiae and Caenorhabditis elegans protein interaction networks. BMC Evolutionary Biology, 2005, 5, 23.	3.2	50
13	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
14	Identifying plant genes shaping microbiota composition in the barley rhizosphere. Nature Communications, 2022, 13, .	12.8	44
15	The South Asian Genome. PLoS ONE, 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. Fungal Genetics and Biology, 2011, 48, 327-334.	2.1	33
17	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
18	Using a periclinal chimera to unravel layerâ€specific gene expression in plants. Plant Journal, 2013, 75, 1039-1049.	5.7	19

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19	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
20	Applications of the indole-alkaloid gramine modulate the assembly of individual members of the barley rhizosphere microbiota. PeerJ, 2021, 9, e12498.	2.0	12
21	Biofilm hydrophobicity in environmental isolates of Bacillus subtilis. Microbiology (United Kingdom), 2021, 167, .	1.8	8
22	Strategies towards sequencing complex crop genomes. Genome Biology, 2012, 13, 322.	9.6	3
23	Genome-Annotated Bacterial Collection of the Barley Rhizosphere Microbiota. Microbiology Resource Announcements, 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. HIV Clinical Trials, 2018, 19, 46-51.	2.0	2
25	Automated Phylogenetic Analysis Using Best Reciprocal BLAST. Methods in Molecular Biology, 2021, 2369, 41-63.	0.9	0