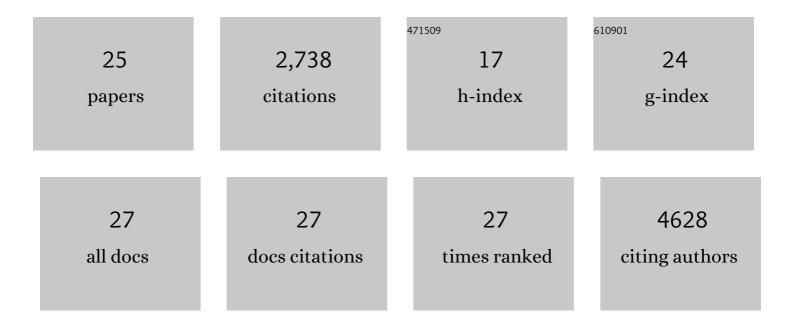
Andrew C Tolonen

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Engineering <i>Clostridium acetobutylicum</i> to utilize cellulose by heterologous expression of a family 5 cellulase. Biofuels, 2022, 13, 431-436.	2.4	3
2	Synthetic glycans control gut microbiome structure and mitigate colitis in mice. Nature Communications, 2022, 13, 1244.	12.8	25
3	Genome-Wide TSS Distribution in Three Related Clostridia with Normalized Capp-Switch Sequencing. Microbiology Spectrum, 2022, , e0228821.	3.0	1
4	Rapid identification of methylase specificity (RIMS-seq) jointly identifies methylated motifs and generates shotgun sequencing of bacterial genomes. Nucleic Acids Research, 2021, 49, e113-e113.	14.5	9
5	Cell Type– and Stimulation-Dependent Transcriptional Programs Regulated by Atg16L1 and Its Crohn's Disease Risk Variant T300A. Journal of Immunology, 2020, 205, 414-424.	0.8	7
6	ABC Transporters Required for Hexose Uptake by Clostridium phytofermentans. Journal of Bacteriology, 2019, 201, .	2.2	10
7	Invertible promoters mediate bacterial phase variation, antibiotic resistance, and host adaptation in the gut. Science, 2019, 363, 181-187.	12.6	85
8	A Targetron-Recombinase System for Large-Scale Genome Engineering of Clostridia. MSphere, 2019, 4, .	2.9	10
9	Evolution of a Biomass-Fermenting Bacterium To Resist Lignin Phenolics. Applied and Environmental Microbiology, 2017, 83, .	3.1	18
10	Human genetic variation and the gut microbiome in disease. Nature Reviews Genetics, 2017, 18, 690-699.	16.3	383
11	Global repositioning of transcription start sites in a plant-fermenting bacterium. Nature Communications, 2016, 7, 13783.	12.8	25
12	Genome and Transcriptome of Clostridium phytofermentans, Catalyst for the Direct Conversion of Plant Feedstocks to Fuels. PLoS ONE, 2015, 10, e0118285.	2.5	28
13	Physiology, Genomics, and Pathway Engineering of an Ethanol-Tolerant Strain of Clostridium phytofermentans. Applied and Environmental Microbiology, 2015, 81, 5440-5448.	3.1	20
14	Fungal lysis by a soil bacterium fermenting cellulose. Environmental Microbiology, 2015, 17, 2618-2627.	3.8	21
15	Functional Diversity of Carbohydrate-Active Enzymes Enabling a Bacterium to Ferment Plant Biomass. PLoS Genetics, 2014, 10, e1004773.	3.5	90
16	Quantitative Proteomics Using Reductive Dimethylation for Stable Isotope Labeling. Journal of Visualized Experiments, 2014, , .	0.3	37
17	CHAPTER 7. Technologies to Study Plant Biomass Fermentation Using the Model Bacterium Clostridium Phytofermentans. RSC Energy and Environment Series, 2013, , 114-139.	0.5	3
18	Precise Manipulation of Chromosomes in Vivo Enables Genome-Wide Codon Replacement. Science, 2011, 333, 348-353.	12.6	512

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19	Proteomeâ€wide systems analysis of a cellulosic biofuelâ€producing microbe. Molecular Systems Biology, 2011, 7, 461.	7.2	81
20	Targeted gene inactivation in <i>Clostridium phytofermentans</i> shows that cellulose degradation requires the family 9 hydrolase Cphy3367. Molecular Microbiology, 2009, 74, 1300-1313.	2.5	76
21	Global gene expression of Prochlorococcus ecotypes in response to changes in nitrogen availability. Molecular Systems Biology, 2006, 2, 53.	7.2	150
22	Genetic Manipulation of Prochlorococcus Strain MIT9313: Green Fluorescent Protein Expression from an RSF1010 Plasmid and Tn5 Transposition. Applied and Environmental Microbiology, 2006, 72, 7607-7613.	3.1	48
23	Transfer of photosynthesis genes to and from <i>Prochlorococcus</i> viruses. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11013-11018.	7.1	477
24	DAF-16 Target Genes That Control C. elegans Life-Span and Metabolism. Science, 2003, 300, 644-647.	12.6	606
25	Optimized in situ construction of oligomers on an array surface. Nucleic Acids Research, 2002, 30, 107e-107.	14.5	13