

# Abigail L Manson

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

5,832  
citations

136740

32  
h-index

138251

58  
g-index

65  
all docs

65  
docs citations

65  
times ranked

8889  
citing authors

#	ARTICLE	IF	CITATIONS
1	StrainGE: a toolkit to track and characterize low-abundance strains in complex microbial communities. <i>Genome Biology</i> , 2022, 23, 74.	3.8	35
2	Inter-species geographic signatures for tracing horizontal gene transfer and long-term persistence of carbapenem resistance. <i>Genome Medicine</i> , 2022, 14, 37.	3.6	15
3	Modulating the evolutionary trajectory of tolerance using antibiotics with different metabolic dependencies. <i>Nature Communications</i> , 2022, 13, 2525.	5.8	22
4	Longitudinal multi-omics analyses link gut microbiome dysbiosis with recurrent urinary tract infections in women. <i>Nature Microbiology</i> , 2022, 7, 630-639.	5.9	54
5	Clinically relevant mutations in core metabolic genes confer antibiotic resistance. <i>Science</i> , 2021, 371, .	6.0	187
6	Limited effects of long-term daily cranberry consumption on the gut microbiome in a placebo-controlled study of women with recurrent urinary tract infections. <i>BMC Microbiology</i> , 2021, 21, 53.	1.3	21
7	Genetic determinants facilitating the evolution of resistance to carbapenem antibiotics. <i>ELife</i> , 2021, 10, .	2.8	15
8	Global phylogenomic analyses of <i>Mycobacterium abscessus</i> provide context for non cystic fibrosis infections and the evolution of antibiotic resistance. <i>Nature Communications</i> , 2021, 12, 5145.	5.8	27
9	Genes Contributing to the Unique Biology and Intrinsic Antibiotic Resistance of <i>Enterococcus faecalis</i> . <i>MBio</i> , 2020, 11, .	1.8	19
10	Colon Cancer-Associated <i>Fusobacterium nucleatum</i> May Originate From the Oral Cavity and Reach Colon Tumors via the Circulatory System. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 400.	1.8	117
11	Computational Methods for Strain-Level Microbial Detection in Colony and Metagenome Sequencing Data. <i>Frontiers in Microbiology</i> , 2020, 11, 1925.	1.5	66
12	Evidence for Expanding the Role of Streptomycin in the Management of Drug-Resistant <i>Mycobacterium tuberculosis</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	30
13	Spatially distinct physiology of <i>Bacteroides fragilis</i> within the proximal colon of gnotobiotic mice. <i>Nature Microbiology</i> , 2020, 5, 746-756.	5.9	57
14	QuantTB – a method to classify mixed <i>Mycobacterium tuberculosis</i> infections within whole genome sequencing data. <i>BMC Genomics</i> , 2020, 21, 80.	1.2	30
15	Adaptive evolution of virulence and persistence in carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Nature Medicine</i> , 2020, 26, 705-711.	15.2	148
16	Deciphering drug resistance in <i>Mycobacterium tuberculosis</i> using whole-genome sequencing: progress, promise, and challenges. <i>Genome Medicine</i> , 2019, 11, 45.	3.6	88
17	ProphET, prophage estimation tool: A stand-alone prophage sequence prediction tool with self-updating reference database. <i>PLoS ONE</i> , 2019, 14, e0223364.	1.1	45
18	Chicken Meat-Associated Enterococci: Influence of Agricultural Antibiotic Use and Connection to the Clinic. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	34

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19	Extensive global movement of multidrug-resistant <i>M. tuberculosis</i> strains revealed by whole-genome analysis. <i>Thorax</i> , 2019, 74, 882-889.	2.7	24
20	Evidence for Highly Variable, Region-Specific Patterns of T-Cell Epitope Mutations Accumulating in <i>Mycobacterium tuberculosis</i> Strains. <i>Frontiers in Immunology</i> , 2019, 10, 195.	2.2	6
21	Impact of antibiotic treatment and host innate immune pressure on enterococcal adaptation in the human bloodstream. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	32
22	Whole Genome Sequencing detects Inter-Facility Transmission of Carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Journal of Infection</i> , 2019, 78, 187-199.	1.7	26
23	Key Transitions in the Evolution of Rapid and Slow Growing <i>Mycobacteria</i> Identified by Comparative Genomics. <i>Frontiers in Microbiology</i> , 2019, 10, 3019.	1.5	37
24	Identification of Novel Coumestan Derivatives as Polyketide Synthase 13 Inhibitors against <i>Mycobacterium tuberculosis</i> . <i>Journal of Medicinal Chemistry</i> , 2018, 61, 791-803.	2.9	56
25	Reply to Lee and Howden. <i>Clinical Infectious Diseases</i> , 2018, 66, 160-161.	2.9	1
26	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. <i>Microbial Genomics</i> , 2018, 4, .	1.0	18
27	Genomic analysis of globally diverse <i>Mycobacterium tuberculosis</i> strains provides insights into the emergence and spread of multidrug resistance. <i>Nature Genetics</i> , 2017, 49, 395-402.	9.4	258
28	Identification of Highly Specific Diversity-Oriented Synthesis-Derived Inhibitors of <i>Clostridium difficile</i> . <i>ACS Infectious Diseases</i> , 2017, 3, 349-359.	1.8	15
29	<i>Mycobacterium tuberculosis</i> Whole Genome Sequences From Southern India Suggest Novel Resistance Mechanisms and the Need for Region-Specific Diagnostics. <i>Clinical Infectious Diseases</i> , 2017, 64, 1494-1501.	2.9	76
30	Tracing the Enterococci from Paleozoic Origins to the Hospital. <i>Cell</i> , 2017, 169, 849-861.e13.	13.5	209
31	Bacterial virulence phenotypes of <i>Escherichia coli</i> and host susceptibility determine risk for urinary tract infections. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	139
32	Whole-Transcriptome and -Genome Analysis of Extensively Drug-Resistant <i>Mycobacterium tuberculosis</i> Clinical Isolates Identifies Downregulation of <i>ethA</i> as a Mechanism of Ethionamide Resistance. <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	32
33	Genomic and functional analyses of <i>Mycobacterium tuberculosis</i> strains implicate <i>ald</i> in D-cycloserine resistance. <i>Nature Genetics</i> , 2016, 48, 544-551.	9.4	145
34	Fap2 Mediates <i>Fusobacterium nucleatum</i> Colorectal Adenocarcinoma Enrichment by Binding to Tumor-Expressed Gal-GalNAc. <i>Cell Host and Microbe</i> , 2016, 20, 215-225.	5.1	523
35	Whole Genome Sequencing of <i>Mycobacterium africanum</i> Strains from Mali Provides Insights into the Mechanisms of Geographic Restriction. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004332.	1.3	41
36	Individual intestinal symbionts induce a distinct population of ROR $\gamma$ <sup>3</sup> regulatory T cells. <i>Science</i> , 2015, 349, 993-997.	6.0	707

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37	Evolution of Extensively Drug-Resistant Tuberculosis over Four Decades: Whole Genome Sequencing and Dating Analysis of <i>Mycobacterium tuberculosis</i> Isolates from KwaZulu-Natal. <i>PLoS Medicine</i> , 2015, 12, e1001880.	3.9	236
38	Evolution of Invasion in a Diverse Set of <i>Fusobacterium</i> Species. <i>MBio</i> , 2014, 5, e01864.	1.8	82
39	Evidence of Extensive DNA Transfer between <i>Bacteroidales</i> Species within the Human Gut. <i>MBio</i> , 2014, 5, e01305-14.	1.8	126
40	Unencapsulated <i>Streptococcus pneumoniae</i> from conjunctivitis encode variant traits and belong to a distinct phylogenetic cluster. <i>Nature Communications</i> , 2014, 5, 5411.	5.8	45
41	High-Quality Draft Genome Sequence of <i>Vagococcus lutrae</i> Strain LBD1, Isolated from the Largemouth Bass <i>Micropterus salmoides</i> . <i>Genome Announcements</i> , 2013, 1, .	0.8	8
42	Emergence of Epidemic Multidrug-Resistant <i>Enterococcus faecium</i> from Animal and Commensal Strains. <i>MBio</i> , 2013, 4, .	1.8	336
43	Comparative analysis of mycobacterium and related actinomycetes yields insight into the evolution of mycobacterium tuberculosis pathogenesis. <i>BMC Genomics</i> , 2012, 13, 120.	1.2	80
44	Cross-kingdom patterns of alternative splicing and splice recognition. <i>Genome Biology</i> , 2008, 9, R50.	13.9	126
45	Conserved Secondary Structures in <i>Aspergillus</i> . <i>PLoS ONE</i> , 2008, 3, e2812.	1.1	4
46	A Motif Co-Occurrence Approach for Genome-Wide Prediction of Transcription-Factor-Binding Sites in <i>Escherichia coli</i> . <i>Genome Research</i> , 2004, 14, 201-208.	2.4	55
47	Genome-wide Profiling of Promoter Recognition by the Two-component Response Regulator CpxR-P in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2002, 277, 26652-26661.	1.6	199
48	Conservation of DNA Regulatory Motifs and Discovery of New Motifs in Microbial Genomes. <i>Genome Research</i> , 2000, 10, 744-757.	2.4	180
49	Predicting regulons and their cis-regulatory motifs by comparative genomics. <i>Nucleic Acids Research</i> , 2000, 28, 4523-4530.	6.5	65
50	A weight matrix for binding recognition by the redox-response regulator ArcA-P of <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1999, 32, 219-221.	1.2	26
51	Internal and overall motions of the translation factor eIF4E: cap binding and insertion in a CHAPS detergent micelle. <i>Journal of Biomolecular NMR</i> , 1998, 12, 73-88.	1.6	21
52	4E Binding Proteins Inhibit the Translation Factor eIF4E without Folded Structure. <i>Biochemistry</i> , 1998, 37, 9-15.	1.2	116
53	A comprehensive library of DNA-binding site matrices for 55 proteins applied to the complete <i>Escherichia coli</i> K-12 genome 1. Edited by R. Ebright. <i>Journal of Molecular Biology</i> , 1998, 284, 241-254.	2.0	319
54	Structure of translation factor eIF4E bound to m7GDP and interaction with 4E-binding protein. <i>Nature Structural Biology</i> , 1997, 4, 717-724.	9.7	347

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55	Can Transmitral Doppler E-Waves Differentiate Hypertensive Hearts From Normal?. Hypertension, 1997, 30, 788-795.	1.3	30
56	Comparison of diastolic filling models and their fit to transmitral Doppler contours. Ultrasound in Medicine and Biology, 1995, 21, 989-999.	0.7	24
57	Relationship of the Third Heart Sound to Transmitral Flow Velocity Deceleration. Circulation, 1995, 92, 388-394.	1.6	39