

Abigail L Manson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4215352/publications.pdf>

Version: 2024-02-01

57
papers

5,832
citations

136950

32
h-index

138484

58
g-index

65
all docs

65
docs citations

65
times ranked

8889
citing authors

#	ARTICLE	IF	CITATIONS
1	Individual intestinal symbionts induce a distinct population of ROR γ regulatory T cells. <i>Science</i> , 2015, 349, 993-997.	12.6	707
2	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.	11.0	523
3	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
4	Emergence of Epidemic Multidrug-Resistant <i>Enterococcus faecium</i> from Animal and Commensal Strains. <i>MBio</i> , 2013, 4, .	4.1	336
5	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. Ebricht. <i>Journal of Molecular Biology</i> , 1998, 284, 241-254.	4.2	319
6	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.	21.4	258
7	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.	8.4	236
8	Tracing the Enterococci from Paleozoic Origins to the Hospital. <i>Cell</i> , 2017, 169, 849-861.e13.	28.9	209
9	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.	3.4	199
10	Clinically relevant mutations in core metabolic genes confer antibiotic resistance. <i>Science</i> , 2021, 371, .	12.6	187
11	Conservation of DNA Regulatory Motifs and Discovery of New Motifs in Microbial Genomes. <i>Genome Research</i> , 2000, 10, 744-757.	5.5	180
12	Adaptive evolution of virulence and persistence in carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Nature Medicine</i> , 2020, 26, 705-711.	30.7	148
13	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.	21.4	145
14	Bacterial virulence phenotypes of <i>Escherichia coli</i> and host susceptibility determine risk for urinary tract infections. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	139
15	Cross-kingdom patterns of alternative splicing and splice recognition. <i>Genome Biology</i> , 2008, 9, R50.	9.6	126
16	Evidence of Extensive DNA Transfer between <i>Bacteroidales</i> Species within the Human Gut. <i>MBio</i> , 2014, 5, e01305-14.	4.1	126
17	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.	3.9	117
18	4E Binding Proteins Inhibit the Translation Factor eIF4E without Folded Structure. <i>Biochemistry</i> , 1998, 37, 9-15.	2.5	116

#	ARTICLE	IF	CITATIONS
19	Deciphering drug resistance in <i>Mycobacterium tuberculosis</i> using whole-genome sequencing: progress, promise, and challenges. <i>Genome Medicine</i> , 2019, 11, 45.	8.2	88
20	Evolution of Invasion in a Diverse Set of <i>Fusobacterium</i> Species. <i>MBio</i> , 2014, 5, e01864.	4.1	82
21	Comparative analysis of mycobacterium and related actinomycetes yields insight into the evolution of mycobacterium tuberculosis pathogenesis. <i>BMC Genomics</i> , 2012, 13, 120.	2.8	80
22	<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.	5.8	76
23	Computational Methods for Strain-Level Microbial Detection in Colony and Metagenome Sequencing Data. <i>Frontiers in Microbiology</i> , 2020, 11, 1925.	3.5	66
24	Predicting regulons and their cis-regulatory motifs by comparative genomics. <i>Nucleic Acids Research</i> , 2000, 28, 4523-4530.	14.5	65
25	Spatially distinct physiology of <i>Bacteroides fragilis</i> within the proximal colon of gnotobiotic mice. <i>Nature Microbiology</i> , 2020, 5, 746-756.	13.3	57
26	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.	6.4	56
27	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.	5.5	55
28	Longitudinal multi-omics analyses link gut microbiome dysbiosis with recurrent urinary tract infections in women. <i>Nature Microbiology</i> , 2022, 7, 630-639.	13.3	54
29	Unencapsulated <i>Streptococcus pneumoniae</i> from conjunctivitis encode variant traits and belong to a distinct phylogenetic cluster. <i>Nature Communications</i> , 2014, 5, 5411.	12.8	45
30	ProphET, prophage estimation tool: A stand-alone prophage sequence prediction tool with self-updating reference database. <i>PLoS ONE</i> , 2019, 14, e0223364.	2.5	45
31	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.	3.0	41
32	Relationship of the Third Heart Sound to Transmitral Flow Velocity Deceleration. <i>Circulation</i> , 1995, 92, 388-394.	1.6	39
33	Key Transitions in the Evolution of Rapid and Slow Growing Mycobacteria Identified by Comparative Genomics. <i>Frontiers in Microbiology</i> , 2019, 10, 3019.	3.5	37
34	StrainGE: a toolkit to track and characterize low-abundance strains in complex microbial communities. <i>Genome Biology</i> , 2022, 23, 74.	8.8	35
35	Chicken Meat-Associated Enterococci: Influence of Agricultural Antibiotic Use and Connection to the Clinic. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	34
36	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, .	3.2	32

#	ARTICLE	IF	CITATIONS
37	Impact of antibiotic treatment and host innate immune pressure on enterococcal adaptation in the human bloodstream. <i>Science Translational Medicine</i> , 2019, 11, .	12.4	32
38	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, .	3.2	30
39	QuantTB â€“ a method to classify mixed <i>Mycobacterium tuberculosis</i> infections within whole genome sequencing data. <i>BMC Genomics</i> , 2020, 21, 80.	2.8	30
40	Can Transmitral Doppler E-Waves Differentiate Hypertensive Hearts From Normal?. <i>Hypertension</i> , 1997, 30, 788-795.	2.7	30
41	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.	12.8	27
42	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.	2.5	26
43	Whole Genome Sequencing detects Inter-Facility Transmission of Carbapenem-resistant <i>Klebsiella pneumoniae</i> . <i>Journal of Infection</i> , 2019, 78, 187-199.	3.3	26
44	Comparison of diastolic filling models and their fit to transmitral Doppler contours. <i>Ultrasound in Medicine and Biology</i> , 1995, 21, 989-999.	1.5	24
45	Extensive global movement of multidrug-resistant <i>M. tuberculosis</i> strains revealed by whole-genome analysis. <i>Thorax</i> , 2019, 74, 882-889.	5.6	24
46	Modulating the evolutionary trajectory of tolerance using antibiotics with different metabolic dependencies. <i>Nature Communications</i> , 2022, 13, 2525.	12.8	22
47	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.	2.8	21
48	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.	3.3	21
49	Genes Contributing to the Unique Biology and Intrinsic Antibiotic Resistance of <i>Enterococcus faecalis</i> . <i>MBio</i> , 2020, 11, .	4.1	19
50	SynerClust: a highly scalable, synteny-aware orthologue clustering tool. <i>Microbial Genomics</i> , 2018, 4, .	2.0	18
51	Identification of Highly Specific Diversity-Oriented Synthesis-Derived Inhibitors of <i>Clostridium difficile</i> . <i>ACS Infectious Diseases</i> , 2017, 3, 349-359.	3.8	15
52	Genetic determinants facilitating the evolution of resistance to carbapenem antibiotics. <i>ELife</i> , 2021, 10, .	6.0	15
53	Inter-species geographic signatures for tracing horizontal gene transfer and long-term persistence of carbapenem resistance. <i>Genome Medicine</i> , 2022, 14, 37.	8.2	15
54	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

#	ARTICLE	IF	CITATIONS
55	Evidence for Highly Variable, Region-Specific Patterns of T-Cell Epitope Mutations Accumulating in Mycobacterium tuberculosis Strains. <i>Frontiers in Immunology</i> , 2019, 10, 195.	4.8	6
56	Conserved Secondary Structures in Aspergillus. <i>PLoS ONE</i> , 2008, 3, e2812.	2.5	4
57	Reply to Lee and Howden. <i>Clinical Infectious Diseases</i> , 2018, 66, 160-161.	5.8	1