

Emmanuel F Mongodin

List of Publications by Year in descending order

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Version: 2024-02-01

114
papers

11,377
citations

50276

46
h-index

30087

103
g-index

121
all docs

121
docs citations

121
times ranked

15350
citing authors

#	ARTICLE	IF	CITATIONS
1	Viable bacteria abundant in cigarettes are aerosolized in mainstream smoke. <i>Environmental Research</i> , 2022, 212, 113462.	7.5	4
2	Comparison of the skin microbiota in acne and rosacea. <i>Experimental Dermatology</i> , 2021, 30, 1375-1380.	2.9	19
3	A novel tick protein supports integrity of gut peritrophic matrix impacting existence of gut microbiome and Lyme disease pathogens. <i>Cellular Microbiology</i> , 2021, 23, e13275.	2.1	12
4	Microbiological Profile and Human Immune Response Associated with Peri-Implantitis: A Systematic Review. <i>Journal of Prosthodontics</i> , 2021, 30, 210-234.	3.7	24
5	Noninflammatory comedones have greater diversity in microbiome and are more prone to biofilm formation than inflammatory lesions of acne vulgaris. <i>International Journal of Dermatology</i> , 2021, 60, 589-596.	1.0	6
6	Potential role of the skin and gut microbiota in premenarchal vulvar lichen sclerosis: A pilot case-control study. <i>PLoS ONE</i> , 2021, 16, e0245243.	2.5	21
7	A roadmap from unknowns to knowns: Advancing our understanding of the microbiomes of commercially available tobacco products. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 2633-2645.	3.6	12
8	Nasal Microbiota and Infectious Complications After Elective Surgical Procedures. <i>JAMA Network Open</i> , 2021, 4, e218386.	5.9	6
9	Nicotine concentration and mentholation affect bacterial community diversity in SPECTRUM research cigarettes. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 4241-4253.	3.6	2
10	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
11	Coupled DNA-labeling and sequencing approach enables the detection of viable-but-non-culturable <i>Vibrio</i> spp. in irrigation water sources in the Chesapeake Bay watershed. <i>Environmental Microbiomes</i> , 2021, 16, 13.	5.0	6
12	Prospective Observational Study of Bisphosphonate-Related Osteonecrosis of the Jaw in Multiple Myeloma: Microbiota Profiling and Cytokine Expression. <i>Frontiers in Oncology</i> , 2021, 11, 704722.	2.8	7
13	Effect of mupirocin for <i>Staphylococcus aureus</i> decolonization on the microbiome of the nose and throat in community and nursing home dwelling adults. <i>PLoS ONE</i> , 2021, 16, e0252004.	2.5	4
14	Low Diversity in Nasal Microbiome Associated With <i>Staphylococcus aureus</i> Colonization and Bloodstream Infections in Hospitalized Neonates. <i>Open Forum Infectious Diseases</i> , 2021, 8, ofab475.	0.9	6
15	Chronic rejection as a persisting phantom menace in organ transplantation: a new hope in the microbiota?. <i>Current Opinion in Organ Transplantation</i> , 2021, 26, 567-581.	1.6	2
16	Unique and specific Proteobacteria diversity in urinary microbiota of tolerant kidney transplanted recipients. <i>American Journal of Transplantation</i> , 2020, 20, 145-158.	4.7	19
17	Characterization and Analysis of the Skin Microbiota in Rosacea: A Case-Control Study. <i>American Journal of Clinical Dermatology</i> , 2020, 21, 139-147.	6.7	37
18	Comparative metagenomic analysis of microbial taxonomic and functional variations in untreated surface and reclaimed waters used in irrigation applications. <i>Water Research</i> , 2020, 169, 115250.	11.3	21

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19	Metagenomic analysis of bacterial and viral assemblages from a freshwater creek and irrigated field reveals temporal and spatial dynamics. <i>Science of the Total Environment</i> , 2020, 706, 135395.	8.0	11
20	Metabolically-active bacteria in reclaimed water and ponds revealed using bromodeoxyuridine DNA labeling coupled with 16S rRNA and shotgun sequencing. <i>Water Research</i> , 2020, 184, 116185.	11.3	11
21	Zero-Valent Iron Sand Filtration Can Reduce Human and Plant Pathogenic Bacteria While Increasing Plant Growth Promoting Bacteria in Reclaimed Water. <i>Frontiers in Environmental Science</i> , 2020, 8, .	3.3	7
22	Seasonal dynamics in taxonomy and function within bacterial and viral metagenomic assemblages recovered from a freshwater agricultural pond. <i>Environmental Microbiomes</i> , 2020, 15, 18.	5.0	16
23	Antibiotic-resistant <i>Escherichia coli</i> and <i>Klebsiella</i> spp. in greywater reuse systems and pond water used for agricultural irrigation in the West Bank, Palestinian Territories. <i>Environmental Research</i> , 2020, 188, 109777.	7.5	13
24	Minocycline and Its Impact on Microbial Dysbiosis in the Skin and Gastrointestinal Tract of Acne Patients. <i>Annals of Dermatology</i> , 2020, 32, 21.	0.9	35
25	Mentholation triggers brand-specific shifts in the bacterial microbiota of commercial cigarette products. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 6287-6297.	3.6	11
26	Perfect timing: circadian rhythms, sleep, and immunity – an NIH workshop summary. <i>JCI Insight</i> , 2020, 5, .	5.0	136
27	It's complicated!. <i>American Journal of Transplantation</i> , 2019, 19, 2673-2674.	4.7	0
28	The Bacterial Communities of Little Cigars and Cigarillos Are Dynamic Over Time and Varying Storage Conditions. <i>Frontiers in Microbiology</i> , 2019, 10, 2371.	3.5	12
29	The bacterial communities of the small intestine and stool in children with short bowel syndrome. <i>PLoS ONE</i> , 2019, 14, e0215351.	2.5	17
30	The Association Between the Developing Nasal Microbiota of Hospitalized Neonates and <i>Staphylococcus aureus</i> Colonization. <i>Open Forum Infectious Diseases</i> , 2019, 6, ofz062.	0.9	12
31	Quenching by sodium thiosulfate does not influence 16S rRNA gene sequencing profiles of reclaimed water from three sites in the Mid-Atlantic, United States. <i>Environmental Research</i> , 2019, 172, 296-300.	7.5	2
32	The respiratory tract microbiome and its relationship to lung cancer and environmental exposures found in rural china. <i>Environmental and Molecular Mutagenesis</i> , 2019, 60, 617-623.	2.2	22
33	Creek to Table: Tracking fecal indicator bacteria, bacterial pathogens, and total bacterial communities from irrigation water to kale and radish crops. <i>Science of the Total Environment</i> , 2019, 666, 461-471.	8.0	28
34	Little cigars and cigarillos harbor diverse bacterial communities that differ between the tobacco and the wrapper. <i>PLoS ONE</i> , 2019, 14, e0211705.	2.5	12
35	Association of Systemic Antibiotic Treatment of Acne With Skin Microbiota Characteristics. <i>JAMA Dermatology</i> , 2019, 155, 425.	4.1	65
36	Current State of and Future Opportunities for Prediction in Microbiome Research: Report from the Mid-Atlantic Microbiome Meet-up in Baltimore on 9 January 2019. <i>MSystems</i> , 2019, 4, .	3.8	6

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37	Direct Diagnostic Tests for Lyme Disease. <i>Clinical Infectious Diseases</i> , 2019, 68, 1052-1057.	5.8	60
38	De-bugging the system: could antibiotics improve liver transplant outcomes?. <i>Journal of Clinical Investigation</i> , 2019, 129, 3054-3057.	8.2	0
39	Advances in Serodiagnostic Testing for Lyme Disease Are at Hand. <i>Clinical Infectious Diseases</i> , 2018, 66, 1133-1139.	5.8	82
40	Primordial origin and diversification of plasmids in Lyme disease agent bacteria. <i>BMC Genomics</i> , 2018, 19, 218.	2.8	46
41	Plasticity in early immune evasion strategies of a bacterial pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3788-E3797.	7.1	29
42	Perinatal HIV Infection and Exposure and Their Association With Dental Caries in Nigerian Children. <i>Pediatric Infectious Disease Journal</i> , 2018, 37, 59-65.	2.0	18
43	Gut Microbiota Determines Graft Survival Outcome Through Regulation of Anti-Inflammatory and Pro-Inflammatory Responses. <i>Transplantation</i> , 2018, 102, S333.	1.0	0
44	Temporal instability of the post-surgical maxillary sinus microbiota. <i>BMC Infectious Diseases</i> , 2018, 18, 441.	2.9	11
45	Conventional wastewater treatment and reuse site practices modify bacterial community structure but do not eliminate some opportunistic pathogens in reclaimed water. <i>Science of the Total Environment</i> , 2018, 639, 1126-1137.	8.0	43
46	Agricultural Freshwater Pond Supports Diverse and Dynamic Bacterial and Viral Populations. <i>Frontiers in Microbiology</i> , 2018, 9, 792.	3.5	27
47	Microbiota and Dose Response: Evolving Paradigm of Health Triangle. <i>Risk Analysis</i> , 2018, 38, 2013-2028.	2.7	7
48	Gut microbiotaâ€‘dependent modulation of innate immunity and lymph node remodeling affects cardiac allograft outcomes. <i>JCI Insight</i> , 2018, 3, .	5.0	53
49	Microbiological effect of mupirocin and chlorhexidine for <i>Staphylococcus aureus</i> decolonization in community and nursing home based adults. <i>Diagnostic Microbiology and Infectious Disease</i> , 2017, 88, 53-57.	1.8	11
50	Smokeless tobacco products harbor diverse bacterial microbiota that differ across products and brands. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 5391-5403.	3.6	40
51	Mentholation affects the cigarette microbiota by selecting for bacteria resistant to harsh environmental conditions and selecting against potential bacterial pathogens. <i>Microbiome</i> , 2017, 5, 22.	11.1	33
52	Plasmid diversity and phylogenetic consistency in the Lyme disease agent <i>Borrelia burgdorferi</i> . <i>BMC Genomics</i> , 2017, 18, 165.	2.8	72
53	Complete Genome Sequence of a Strain of <i>Bifidobacterium pseudolongum</i> Isolated from Mouse Feces and Associated with Improved Organ Transplant Outcome. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
54	Changes in the microbiota cause genetically modified <i>Anopheles</i> to spread in a population. <i>Science</i> , 2017, 357, 1396-1399.	12.6	57

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55	Comparison of the Microbiota of Older Adults Living in Nursing Homes and the Community. <i>MSphere</i> , 2017, 2, .	2.9	33
56	A robust in vitro model for trans-lymphatic endothelial migration. <i>Scientific Reports</i> , 2017, 7, 1633.	3.3	27
57	High-resolution bacterial 16S rRNA gene profile meta-analysis and biofilm status reveal common colorectal cancer consortia. <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 34.	6.4	237
58	Temporal Variations in Cigarette Tobacco Bacterial Community Composition and Tobacco-Specific Nitrosamine Content Are Influenced by Brand and Storage Conditions. <i>Frontiers in Microbiology</i> , 2017, 08, 358.	3.5	45
59	Amino acid metabolic signaling influences <i>Aedes aegypti</i> midgut microbiome variability. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005677.	3.0	67
60	Functional genomic analyses of <i>Enterobacter</i> , <i>Anopheles</i> and <i>Plasmodium</i> reciprocal interactions that impact vector competence. <i>Malaria Journal</i> , 2016, 15, 425.	2.3	57
61	Global Analysis and Comparison of the Transcriptomes and Proteomes of Group A <i>Streptococcus</i> Biofilms. <i>MSystems</i> , 2016, 1, .	3.8	26
62	Type 2 immunity-dependent reduction of segmented filamentous bacteria in mice infected with the helminthic parasite <i>Nippostrongylus brasiliensis</i> . <i>Microbiome</i> , 2015, 3, 40.	11.1	93
63	Potential Influence of <i>Staphylococcus aureus</i> Clonal Complex 30 Genotype and Transcriptome on Hematogenous Infections. <i>Open Forum Infectious Diseases</i> , 2015, 2, ofv093.	0.9	28
64	Microbiotaâ€™ implications for immunity and transplantation. <i>Nature Reviews Nephrology</i> , 2015, 11, 342-353.	9.6	47
65	Phylogenomic Identification of Regulatory Sequences in Bacteria: an Analysis of Statistical Power and an Application to <i>Borrelia burgdorferi</i> Sensu Lato. <i>MBio</i> , 2015, 6, .	4.1	2
66	Complete Genome Sequence of ER2796, a DNA Methyltransferase-Deficient Strain of <i>Escherichia coli</i> K-12. <i>PLoS ONE</i> , 2015, 10, e0127446.	2.5	31
67	The Oral Bacterial Communities of Children with Well-Controlled HIV Infection and without HIV Infection. <i>PLoS ONE</i> , 2015, 10, e0131615.	2.5	32
68	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	2.5	34
69	Association between cigarette smoking and the vaginal microbiota: a pilot study. <i>BMC Infectious Diseases</i> , 2014, 14, 471.	2.9	107
70	The potential role of lung microbiota in lung cancer attributed to household coal burning exposures. <i>Environmental and Molecular Mutagenesis</i> , 2014, 55, 643-651.	2.2	158
71	<i>BorreliaBase</i> : a phylogeny-centered browser of <i>Borrelia</i> genomes. <i>BMC Bioinformatics</i> , 2014, 15, 233.	2.6	40
72	Culture-Independent Evaluation of the Appendix and Rectum Microbiomes in Children with and without Appendicitis. <i>PLoS ONE</i> , 2014, 9, e95414.	2.5	90

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73	Gut microbiota, tight junction protein expression, intestinal resistance, bacterial translocation and mortality following cholestasis depend on the genetic background of the host. <i>Gut Microbes</i> , 2013, 4, 292-305.	9.8	45
74	Inter- and intra-specific pan-genomes of <i>Borrelia burgdorferi</i> sensu lato: genome stability and adaptive radiation. <i>BMC Genomics</i> , 2013, 14, 693.	2.8	74
75	Increased Gut Microbiome Diversity Following a High Fiber Mediterranean Style Diet. <i>FASEB Journal</i> , 2013, 27, 1056.3.	0.5	4
76	Comparative Genomics of Vancomycin-Resistant <i>Staphylococcus aureus</i> Strains and Their Positions within the Clade Most Commonly Associated with Methicillin-Resistant <i>S. aureus</i> Hospital-Acquired Infection in the United States. <i>MBio</i> , 2012, 3, .	4.1	125
77	Whole-Genome Sequences of <i>Borrelia bissettii</i> , <i>Borrelia valaisiana</i> , and <i>Borrelia spielmanii</i> . <i>Journal of Bacteriology</i> , 2012, 194, 545-546.	2.2	56
78	Analysis of the Gut Microbiota in the Old Order Amish and Its Relation to the Metabolic Syndrome. <i>PLoS ONE</i> , 2012, 7, e43052.	2.5	183
79	Integrated Metagenomics/Metaproteomics Reveals Human Host-Microbiota Signatures of Crohn's Disease. <i>PLoS ONE</i> , 2012, 7, e49138.	2.5	374
80	Genome Stability of Lyme Disease Spirochetes: Comparative Genomics of <i>Borrelia burgdorferi</i> Plasmids. <i>PLoS ONE</i> , 2012, 7, e33280.	2.5	146
81	The importance of a multifaceted approach to characterizing the microbial flora of chronic wounds. <i>Wound Repair and Regeneration</i> , 2011, 19, 532-541.	3.0	129
82	Whole Genome Sequence of an Unusual <i>Borrelia burgdorferi</i> Sensu Lato Isolate. <i>Journal of Bacteriology</i> , 2011, 193, 1489-1490.	2.2	102
83	Pervasive Recombination and Sympatric Genome Diversification Driven by Frequency-Dependent Selection in <i>Borrelia burgdorferi</i> , the Lyme Disease Bacterium. <i>Genetics</i> , 2011, 189, 951-966.	2.9	69
84	Whole-Genome Sequences of Thirteen Isolates of <i>Borrelia burgdorferi</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1018-1020.	2.2	108
85	Whole-Genome Sequences of Two <i>Borrelia afzelii</i> and Two <i>Borrelia garinii</i> Lyme Disease Agent Isolates. <i>Journal of Bacteriology</i> , 2011, 193, 6995-6996.	2.2	63
86	Strategies for Metagenomic-Guided Whole-Community Proteomics of Complex Microbial Environments. <i>PLoS ONE</i> , 2011, 6, e27173.	2.5	58
87	Bacterial diversity in the oral cavity of 10 healthy individuals. <i>ISME Journal</i> , 2010, 4, 962-974.	9.8	541
88	Analyzing Endodontic Infections by Deep Coverage Pyrosequencing. <i>Journal of Dental Research</i> , 2010, 89, 980-984.	5.2	104
89	Regulation of the Xylan-degrading Apparatus of <i>Cellvibrio japonicus</i> by a Novel Two-component System. <i>Journal of Biological Chemistry</i> , 2009, 284, 1086-1096.	3.4	19
90	Fast, adaptive evolution at a bacterial host-resistance locus: The PFam54 gene array in <i>Borrelia burgdorferi</i> . <i>Gene</i> , 2009, 445, 26-37.	2.2	46

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91	The Pangenome Structure of <i>Escherichia coli</i> : Comparative Genomic Analysis of <i>E. coli</i> Commensal and Pathogenic Isolates. <i>Journal of Bacteriology</i> , 2008, 190, 6881-6893.	2.2	763
92	Hydrogenomics of the Extremely Thermophilic Bacterium <i>Caldicellulosiruptor saccharolyticus</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 6720-6729.	3.1	142
93	Insights into Plant Cell Wall Degradation from the Genome Sequence of the Soil Bacterium <i>Cellvibrio japonicus</i> . <i>Journal of Bacteriology</i> , 2008, 190, 5455-5463.	2.2	159
94	Extensive Genome Rearrangements and Multiple Horizontal Gene Transfers in a Population of <i>Pyrococcus</i> Isolates from Vulcano Island, Italy. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6447-6451.	3.1	33
95	Serial Analysis of rRNA Genes and the Unexpected Dominance of Rare Members of Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2007, 73, 4532-4542.	3.1	78
96	Evolution of Catabolic Pathways: Genomic Insights into Microbial s-Triazine Metabolism. <i>Journal of Bacteriology</i> , 2007, 189, 674-682.	2.2	98
97	Complete genome sequence of USA300, an epidemic clone of community-acquired methicillin-resistant <i>Staphylococcus aureus</i> . <i>Lancet, The</i> , 2006, 367, 731-739.	13.7	1,440
98	Microbial biochemistry, physiology, and biotechnology of hyperthermophilic Thermotoga species. <i>FEMS Microbiology Reviews</i> , 2006, 30, 872-905.	8.6	108
99	Proteomic profiling of cell envelope-associated proteins from <i>Staphylococcus aureus</i> . <i>Proteomics</i> , 2006, 6, 1530-1549.	2.2	102
100	Comparative proteomic analysis of <i>Staphylococcus aureus</i> strains with differences in resistance to the cell wall-targeting antibiotic vancomycin. <i>Proteomics</i> , 2006, 6, 4246-4258.	2.2	75
101	Galactomannan hydrolysis and mannose metabolism in <i>Cellvibrio mixtus</i> . <i>FEMS Microbiology Letters</i> , 2006, 261, 123-132.	1.8	24
102	Chromosome Evolution in the Thermotogales : Large-Scale Inversions and Strain Diversification of CRISPR Sequences. <i>Journal of Bacteriology</i> , 2006, 188, 2364-2374.	2.2	62
103	Secrets of Soil Survival Revealed by the Genome Sequence of <i>Arthrobacter aurescens</i> TC1. <i>PLoS Genetics</i> , 2006, 2, e214.	3.5	213
104	Outside Forces Helped Shape the <i>Thermotoga</i> Metagenome. <i>Microbe Magazine</i> , 2006, 1, 235-241.	0.4	2
105	Gene Transfer and Genome Plasticity in <i>Thermotoga maritima</i> , a Model Hyperthermophilic Species. <i>Journal of Bacteriology</i> , 2005, 187, 4935-4944.	2.2	43
106	The genome of <i>Salinibacter ruber</i> : Convergence and gene exchange among hyperhalophilic bacteria and archaea. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 18147-18152.	7.1	299
107	Insights on Evolution of Virulence and Resistance from the Complete Genome Analysis of an Early Methicillin-Resistant <i>Staphylococcus aureus</i> Strain and a Biofilm-Producing Methicillin-Resistant <i>Staphylococcus epidermidis</i> Strain. <i>Journal of Bacteriology</i> , 2005, 187, 2426-2438.	2.2	940
108	Major Structural Differences and Novel Potential Virulence Mechanisms from the Genomes of Multiple <i>Campylobacter</i> Species. <i>PLoS Biology</i> , 2005, 3, e15.	5.6	483

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109	A Guild of 45 CRISPR-Associated (Cas) Protein Families and Multiple CRISPR/Cas Subtypes Exist in Prokaryotic Genomes. <i>PLoS Computational Biology</i> , 2005, 1, e60.	3.2	835
110	Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen <i>Listeria monocytogenes</i> reveal new insights into the core genome components of this species. <i>Nucleic Acids Research</i> , 2004, 32, 2386-2395.	14.5	460
111	Microarray Transcription Analysis of Clinical <i>Staphylococcus aureus</i> Isolates Resistant to Vancomycin. <i>Journal of Bacteriology</i> , 2003, 185, 4638-4643.	2.2	115
112	Fibronectin-Binding Proteins of <i>Staphylococcus aureus</i> Are Involved in Adherence to Human Airway Epithelium. <i>Infection and Immunity</i> , 2002, 70, 620-630.	2.2	99
113	Cell Wall-associated Protein A as a Tool for Immunolocalization of <i>Staphylococcus aureus</i> in Infected Human Airway Epithelium. <i>Journal of Histochemistry and Cytochemistry</i> , 2000, 48, 523-533.	2.5	18
114	<i>Campylobacter</i> Pathogenomics: Genomes and Beyond. , 0, , 160-195.		0