

Emmanuel F Mongodin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9016446/publications.pdf>

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	Complete genome sequence of USA300, an epidemic clone of community-acquired methicillin-resistant <i>Staphylococcus aureus</i> . <i>Lancet</i> , The, 2006, 367, 731-739.	13.7	1,440
2	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
3	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
4	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
5	Bacterial diversity in the oral cavity of 10 healthy individuals. <i>ISME Journal</i> , 2010, 4, 962-974.	9.8	541
6	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
7	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
8	Integrated Metagenomics/Metaproteomics Reveals Human Host-Microbiota Signatures of Crohn's Disease. <i>PLoS ONE</i> , 2012, 7, e49138.	2.5	374
9	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
10	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
11	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
12	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
13	A global metagenomic map of urban microbiomes and antimicrobial resistance. <i>Cell</i> , 2021, 184, 3376-3393.e17.	28.9	164
14	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
15	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
16	Genome Stability of Lyme Disease Spirochetes: Comparative Genomics of <i>Borrelia burgdorferi</i> Plasmids. <i>PLoS ONE</i> , 2012, 7, e33280.	2.5	146
17	Hydrogenomics of the Extremely Thermophilic Bacterium <i>Caldicellulosiruptor saccharolyticus</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 6720-6729.	3.1	142
18	Perfect timing: circadian rhythms, sleep, and immunity – an NIH workshop summary. <i>JCI Insight</i> , 2020, 5, .	5.0	136

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	Microbial biochemistry, physiology, and biotechnology of hyperthermophilic Thermotogaspecies. <i>FEMS Microbiology Reviews</i> , 2006, 30, 872-905.	8.6	108
23	Whole-Genome Sequences of Thirteen Isolates of <i>Borrelia burgdorferi</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1018-1020.	2.2	108
24	Association between cigarette smoking and the vaginal microbiota: a pilot study. <i>BMC Infectious Diseases</i> , 2014, 14, 471.	2.9	107
25	Analyzing Endodontic Infections by Deep Coverage Pyrosequencing. <i>Journal of Dental Research</i> , 2010, 89, 980-984.	5.2	104
26	Proteomic profiling of cell envelope-associated proteins from <i>Staphylococcus aureus</i> . <i>Proteomics</i> , 2006, 6, 1530-1549.	2.2	102
27	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
28	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
29	Evolution of Catabolic Pathways: Genomic Insights into Microbial s-Triazine Metabolism. <i>Journal of Bacteriology</i> , 2007, 189, 674-682.	2.2	98
30	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
31	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
32	Advances in Serodiagnostic Testing for Lyme Disease Are at Hand. <i>Clinical Infectious Diseases</i> , 2018, 66, 1133-1139.	5.8	82
33	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
34	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
35	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
36	Plasmid diversity and phylogenetic consistency in the Lyme disease agent <i>Borrelia burgdorferi</i> . <i>BMC Genomics</i> , 2017, 18, 165.	2.8	72

#	ARTICLE	IF	CITATIONS
37	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
38	Amino acid metabolic signaling influences <i>Aedes aegypti</i> midgut microbiome variability. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005677.	3.0	67
39	Association of Systemic Antibiotic Treatment of Acne With Skin Microbiota Characteristics. <i>JAMA Dermatology</i> , 2019, 155, 425.	4.1	65
40	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
41	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
42	Direct Diagnostic Tests for Lyme Disease. <i>Clinical Infectious Diseases</i> , 2019, 68, 1052-1057.	5.8	60
43	Strategies for Metagenomic-Guided Whole-Community Proteomics of Complex Microbial Environments. <i>PLoS ONE</i> , 2011, 6, e27173.	2.5	58
44	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
45	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
46	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
47	Gut microbiota-dependent modulation of innate immunity and lymph node remodeling affects cardiac allograft outcomes. <i>JCI Insight</i> , 2018, 3, .	5.0	53
48	Microbiota implications for immunity and transplantation. <i>Nature Reviews Nephrology</i> , 2015, 11, 342-353.	9.6	47
49	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
50	Primordial origin and diversification of plasmids in Lyme disease agent bacteria. <i>BMC Genomics</i> , 2018, 19, 218.	2.8	46
51	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
52	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
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	BorreliaBase: a phylogeny-centered browser of Borrelia genomes. BMC Bioinformatics, 2014, 15, 233.	2.6	40
56	Smokeless tobacco products harbor diverse bacterial microbiota that differ across products and brands. Applied Microbiology and Biotechnology, 2017, 101, 5391-5403.	3.6	40
57	Characterization and Analysis of the Skin Microbiota in Rosacea: A Caseâ€“Control Study. American Journal of Clinical Dermatology, 2020, 21, 139-147.	6.7	37
58	Minocycline and Its Impact on Microbial Dysbiosis in the Skin and Gastrointestinal Tract of Acne Patients. Annals of Dermatology, 2020, 32, 21.	0.9	35
59	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. PLoS ONE, 2014, 9, e99979.	2.5	34
60	Extensive Genome Rearrangements and Multiple Horizontal Gene Transfers in a Population of <i>Pyrococcus</i> Isolates from Vulcano Island, Italy. Applied and Environmental Microbiology, 2008, 74, 6447-6451.	3.1	33
61	Mentholation affects the cigarette microbiota by selecting for bacteria resistant to harsh environmental conditions and selecting against potential bacterial pathogens. Microbiome, 2017, 5, 22.	11.1	33
62	Comparison of the Microbiota of Older Adults Living in Nursing Homes and the Community. MSphere, 2017, 2, .	2.9	33
63	The Oral Bacterial Communities of Children with Well-Controlled HIV Infection and without HIV Infection. PLoS ONE, 2015, 10, e0131615.	2.5	32
64	Complete Genome Sequence of ER2796, a DNA Methyltransferase-Deficient Strain of Escherichia coli K-12. PLoS ONE, 2015, 10, e0127446.	2.5	31
65	Plasticity in early immune evasion strategies of a bacterial pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3788-E3797.	7.1	29
66	Potential Influence of Staphylococcus aureus Clonal Complex 30 Genotype and Transcriptome on Hematogenous Infections. Open Forum Infectious Diseases, 2015, 2, ofv093.	0.9	28
67	Creek to Table: Tracking fecal indicator bacteria, bacterial pathogens, and total bacterial communities from irrigation water to kale and radish crops. Science of the Total Environment, 2019, 666, 461-471.	8.0	28
68	A robust in vitro model for trans-lymphatic endothelial migration. Scientific Reports, 2017, 7, 1633.	3.3	27
69	Agricultural Freshwater Pond Supports Diverse and Dynamic Bacterial and Viral Populations. Frontiers in Microbiology, 2018, 9, 792.	3.5	27
70	Global Analysis and Comparison of the Transcriptomes and Proteomes of Group A <i>Streptococcus</i> Biofilms. MSystems, 2016, 1, .	3.8	26
71	Galactomannan hydrolysis and mannose metabolism in <i>Cellvibrio mixtus</i> . FEMS Microbiology Letters, 2006, 261, 123-132.	1.8	24
72	Microbiological Profile and Human Immune Response Associated with Periâ€“implantitis: A Systematic Review. Journal of Prosthodontics, 2021, 30, 210-234.	3.7	24

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	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
76	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
77	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
78	Comparison of the skin microbiota in acne and rosacea. <i>Experimental Dermatology</i> , 2021, 30, 1375-1380.	2.9	19
79	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
80	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
81	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
82	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
83	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
84	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
85	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
86	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
87	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
88	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
89	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
90	Temporal instability of the post-surgical maxillary sinus microbiota. <i>BMC Infectious Diseases</i> , 2018, 18, 441.	2.9	11

#	ARTICLE	IF	CITATIONS
91	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
92	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
93	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
94	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
95	Microbiota and Dose Response: Evolving Paradigm of Health Triangle. <i>Risk Analysis</i> , 2018, 38, 2013-2028.	2.7	7
96	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
97	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
98	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
99	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
100	Nasal Microbiota and Infectious Complications After Elective Surgical Procedures. <i>JAMA Network Open</i> , 2021, 4, e218386.	5.9	6
101	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
102	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
103	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
104	Increased Gut Microbiome Diversity Following a High Fiber Mediterranean Style Diet. <i>FASEB Journal</i> , 2013, 27, 1056.3.	0.5	4
105	Viable bacteria abundant in cigarettes are aerosolized in mainstream smoke. <i>Environmental Research</i> , 2022, 212, 113462.	7.5	4
106	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
107	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
108	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

#	ARTICLE	IF	CITATIONS
109	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
110	Outside Forces Helped Shape the <i>Thermotoga</i> Metagenome. <i>Microbe Magazine</i> , 2006, 1, 235-241.	0.4	2
111	Gut Microbiota Determines Graft Survival Outcome Through Regulation of Anti-Inflammatory and Pro-Inflammatory Responses. <i>Transplantation</i> , 2018, 102, S333.	1.0	0
112	It's complicated!. <i>American Journal of Transplantation</i> , 2019, 19, 2673-2674.	4.7	0
113	<i>Campylobacter</i> Pathogenomics: Genomes and Beyond. , 0, , 160-195.		0
114	De-bugging the system: could antibiotics improve liver transplant outcomes?. <i>Journal of Clinical Investigation</i> , 2019, 129, 3054-3057.	8.2	0