Gabriel A Al-Ghalith

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5723595/publications.pdf

Version: 2024-02-01

28 papers 14,966 citations

361045 20 h-index 454577 30 g-index

36 all docs

36 docs citations

36 times ranked 19296 citing authors

#	Article	IF	CITATIONS
1	SHOGUN: a modular, accurate and scalable framework for microbiome quantification. Bioinformatics, 2020, 36, 4088-4090.	1.8	42
2	Wild primate microbiomes prevent weight gain in germ-free mice. Animal Microbiome, 2020, 2, 16.	1.5	7
3	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
4	Daily Sampling Reveals Personalized Diet-Microbiome Associations in Humans. Cell Host and Microbe, 2019, 25, 789-802.e5.	5.1	441
5	Bacterial community structure and function distinguish gut sites in captive redâ€shanked doucs (Pygathrix nemaeus). American Journal of Primatology, 2019, 81, e22977.	0.8	9
6	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477.	5.8	197
7	An Increased Abundance of Clostridiaceae Characterizes Arthritis in Inflammatory Bowel Disease and Rheumatoid Arthritis: A Cross-sectional Study. Inflammatory Bowel Diseases, 2019, 25, 902-913.	0.9	72
8	Distribution of Bacterial $\hat{l}\pm 1,3$ -Galactosyltransferase Genes in the Human Gut Microbiome. Frontiers in Immunology, 2019, 10, 3000.	2.2	39
9	Pretransplant Gut Colonization with Intrinsically Vancomycin-Resistant Enterococci (E. gallinarum) Tj ETQq1 1 0.7 Blood and Marrow Transplantation, 2018, 24, 1260-1263.	84314 rgE 2.0	BT /Overlo <mark>ck</mark> 15
10	Development of the Human Mycobiome over the First Month of Life and across Body Sites. MSystems, 2018, 3, .	1.7	132
10		1.7	132 293
	2018, 3, .		
11	Evaluating the Information Content of Shallow Shotgun Metagenomics. MSystems, 2018, 3, .	1.7	293
11 12	Evaluating the Information Content of Shallow Shotgun Metagenomics. MSystems, 2018, 3, . SHI7 Is a Self-Learning Pipeline for Multipurpose Short-Read DNA Quality Control. MSystems, 2018, 3, . High-Throughput flaA Short Variable Region Sequencing to Assess Campylobacter Diversity in Fecal	1.7	293
11 12 13	Evaluating the Information Content of Shallow Shotgun Metagenomics. MSystems, 2018, 3, . SHI7 Is a Self-Learning Pipeline for Multipurpose Short-Read DNA Quality Control. MSystems, 2018, 3, . High-Throughput flaA Short Variable Region Sequencing to Assess Campylobacter Diversity in Fecal Samples From Birds. Frontiers in Microbiology, 2018, 9, 2201. Urinary microbiome associated with chronic allograft dysfunction in kidney transplant recipients.	1.7 1.7 1.5	293 66 8
11 12 13	Evaluating the Information Content of Shallow Shotgun Metagenomics. MSystems, 2018, 3, . SHI7 Is a Self-Learning Pipeline for Multipurpose Short-Read DNA Quality Control. MSystems, 2018, 3, . High-Throughput flaA Short Variable Region Sequencing to Assess Campylobacter Diversity in Fecal Samples From Birds. Frontiers in Microbiology, 2018, 9, 2201. Urinary microbiome associated with chronic allograft dysfunction in kidney transplant recipients. Clinical Transplantation, 2018, 32, e13436.	1.7 1.7 1.5 0.8	293 66 8 24
11 12 13 14	Evaluating the Information Content of Shallow Shotgun Metagenomics. MSystems, 2018, 3, . SHI7 Is a Self-Learning Pipeline for Multipurpose Short-Read DNA Quality Control. MSystems, 2018, 3, . High-Throughput flaA Short Variable Region Sequencing to Assess Campylobacter Diversity in Fecal Samples From Birds. Frontiers in Microbiology, 2018, 9, 2201. Urinary microbiome associated with chronic allograft dysfunction in kidney transplant recipients. Clinical Transplantation, 2018, 32, e13436. US Immigration Westernizes the Human Gut Microbiome. Cell, 2018, 175, 962-972.e10. Mo1934 - Gut Microbial Markers of Arthritis Including Inflammatory Bowel Disease Associated	1.7 1.7 1.5 0.8	293 66 8 24 511

#	Article	IF	Citations
19	Antibiotic-induced acceleration of type 1 diabetes alters maturation of innate intestinal immunity. ELife, $2018, 7, .$	2.8	70
20	High-Fat Diet Changes Fungal Microbiomes and Interkingdom Relationships in the Murine Gut. MSphere, 2017, 2, .	1.3	94
21	Patterns of seasonality and group membership characterize the gut microbiota in a longitudinal study of wild Verreaux's sifakas (<i>Propithecus verreauxi</i>). Ecology and Evolution, 2017, 7, 5732-5745.	0.8	90
22	Moving beyond <i>de novo</i> clustering in fungal community ecology. New Phytologist, 2017, 216, 629-634.	3.5	17
23	Captivity humanizes the primate microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10376-10381.	3.3	369
24	Pretreatment gut microbiome predicts chemotherapy-related bloodstream infection. Genome Medicine, 2016, 8, 49.	3.6	136
25	NINJA-OPS: Fast Accurate Marker Gene Alignment Using Concatenated Ribosomes. PLoS Computational Biology, 2016, 12, e1004658.	1.5	66
26	Bygiene: The New Paradigm of Bidirectional Hygiene. Yale Journal of Biology and Medicine, 2015, 88, 359-65.	0.2	12
27	The guts of obesity: progress and challenges in linking gut microbes to obesity. Discovery Medicine, 2015, 19, 81-8.	0.5	8
28	Complex host genetics influence the microbiome in inflammatory bowel disease. Genome Medicine, 2014, 6, 107.	3.6	322