Michael J Cox

List of Publications by Citations

Source: https://exaly.com/author-pdf/4311953/michael-j-cox-publications-by-citations.pdf

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44 4,963 27 53 g-index

53 6,331 6.6 2.32 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
44	Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. <i>BMC Biology</i> , 2014 , 12, 87	7.3	1745
43	Airway microbiota and pathogen abundance in age-stratified cystic fibrosis patients. <i>PLoS ONE</i> , 2010 , 5, e11044	3.7	331
42	The role of bacteria in the pathogenesis and progression of idiopathic pulmonary fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2014 , 190, 906-13	10.2	320
41	Outgrowth of the bacterial airway microbiome after rhinovirus exacerbation of chronic obstructive pulmonary disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013 , 188, 1224-31	10.2	262
40	Mans best friend? The effect of pet ownership on house dust microbial communities. <i>Journal of Allergy and Clinical Immunology</i> , 2010 , 126, 410-2, 412.e1-3	11.5	178
39	A persistent and diverse airway microbiota present during chronic obstructive pulmonary disease exacerbations. <i>OMICS A Journal of Integrative Biology</i> , 2010 , 14, 9-59	3.8	178
38	Stable-isotope probing implicates Methylophaga spp and novel Gammaproteobacteria in marine methanol and methylamine metabolism. <i>ISME Journal</i> , 2007 , 1, 480-91	11.9	145
37	Improved detection of bifidobacteria with optimised 16S rRNA-gene based pyrosequencing. <i>PLoS ONE</i> , 2012 , 7, e32543	3.7	143
36	Isolation of viruses responsible for the demise of an Emiliania huxleyi bloom in the English Channel. <i>Journal of the Marine Biological Association of the United Kingdom</i> , 2002 , 82, 369-377	1.1	129
35	Dysbiosis anticipating necrotizing enterocolitis in very premature infants. <i>Clinical Infectious Diseases</i> , 2015 , 60, 389-97	11.6	118
34	Bacterial microbiota of the upper respiratory tract and childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 139, 826-834.e13	11.5	117
33	Host-Microbial Interactions in Idiopathic Pulmonary Fibrosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017 , 195, 1640-1650	10.2	114
32	Respiratory Disease following Viral Lung Infection Alters the Murine Gut Microbiota. <i>Frontiers in Immunology</i> , 2018 , 9, 182	8.4	114
31	Changes in the respiratory microbiome during acute exacerbations of idiopathic pulmonary fibrosis. <i>Respiratory Research</i> , 2017 , 18, 29	7-3	108
30	Lactobacillus casei abundance is associated with profound shifts in the infant gut microbiome. <i>PLoS ONE</i> , 2010 , 5, e8745	3.7	93
29	Sequencing the human microbiome in health and disease. <i>Human Molecular Genetics</i> , 2013 , 22, R88-94	5.6	89
28	Progression of whole-blood transcriptional signatures from interferon-induced to neutrophil-associated patterns in severe influenza. <i>Nature Immunology</i> , 2018 , 19, 625-635	19.1	82

27	Respiratory Viral Infection Alters the Gut Microbiota by Inducing Inappetence. MBio, 2020, 11,	7.8	79
26	Longitudinal assessment of sputum microbiome by sequencing of the 16S rRNA gene in non-cystic fibrosis bronchiectasis patients. <i>PLoS ONE</i> , 2017 , 12, e0170622	3.7	70
25	Upper airways microbiota in antibiotic-nalle wheezing and healthy infants from the tropics of rural Ecuador. <i>PLoS ONE</i> , 2012 , 7, e46803	3.7	69
24	Identification of carbohydrate metabolism genes in the metagenome of a marine biofilm community shown to be dominated by gammaproteobacteria and bacteroidetes. <i>Genes</i> , 2010 , 1, 371-8	4 ^{4.2}	62
23	Late-Onset Bloodstream Infection and Perturbed Maturation of the Gastrointestinal Microbiota in Premature Infants. <i>PLoS ONE</i> , 2015 , 10, e0132923	3.7	56
22	New opportunities for managing acute and chronic lung infections. <i>Nature Reviews Microbiology</i> , 2018 , 16, 111-120	22.2	46
21	Methods in Lung Microbiome Research. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2020 , 62, 283-299	5.7	36
20	Cellulose degradation by micromonosporas recovered from freshwater lakes and classification of these actinomycetes by DNA gyrase B gene sequencing. <i>Applied and Environmental Microbiology</i> , 2008 , 74, 7080-4	4.8	35
19	Use of DNA-stable isotope probing and functional gene probes to investigate the diversity of methyl chloride-utilizing bacteria in soil. <i>Environmental Microbiology</i> , 2005 , 7, 1318-28	5.2	35
18	Aminobacter ciceronei sp. nov. and Aminobacter lissarensis sp. nov., isolated from various terrestrial environments. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2005 , 55, 1827-1832	2.2	33
17	Detection of novel Fibrobacter populations in landfill sites and determination of their relative abundance via quantitative PCR. <i>Environmental Microbiology</i> , 2008 , 10, 1310-9	5.2	26
16	Multilocus characterization scheme for shiga toxin-encoding bacteriophages. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 8032-40	4.8	26
15	Reagent contamination can critically impact sequence-based microbiome analyses		16
14	The fungal airway microbiome in cystic fibrosis and non-cystic fibrosis bronchiectasis. <i>Journal of Cystic Fibrosis</i> , 2021 , 20, 295-302	4.1	16
13	Gut microbiota and protection from pneumococcal pneumonia. <i>Gut</i> , 2017 , 66, 384	19.2	13
12	Comparison of the upper and lower airway microbiota in children with chronic lung diseases. <i>PLoS ONE</i> , 2018 , 13, e0201156	3.7	13
11	A molecular comparison of microbial communities in bronchiectasis and cystic fibrosis. <i>European Respiratory Journal</i> , 2013 , 41, 991-3	13.6	12
10	Longitudinal development of the airway microbiota in infants with cystic fibrosis. <i>Scientific Reports</i> , 2019 , 9, 5143	4.9	11

9	Diversity of methyl halide-degrading microorganisms in oceanic and coastal waters. <i>FEMS Microbiology Letters</i> , 2012 , 334, 111-8	2.9	8	
8	Nucleic acid extraction efficiency and bacterial recovery from maxillary sinus mucosal samples obtained by brushing or biopsy. <i>American Journal of Rhinology and Allergy</i> , 2010 , 24, 263-5	2.4	8	
7	A Haemophilus sp. dominates the microbiota of sputum from UK adults with non-severe community acquired pneumonia and chronic lung disease. <i>Scientific Reports</i> , 2019 , 9, 2388	4.9	5	
6	Airway microbial communities, smoking and asthma in a general population sample. <i>EBioMedicine</i> , 2021 , 71, 103538	8.8	5	
5	Sampling the lung microbiome 2019 , 1-17		2	
4	Longitudinal assessment of sputum microbiome by sequencing of the 16S rRNA gene in non-CF bronchiectasis patients		2	
3	Haemophilus, Antibiotic Therapy and the Airway Microbiome in Chronic Obstructive Pulmonarydisease		1	
2	Respiratory viral infection alters the gut microbiota by inducing inappetence		1	
1	CTAB extraction of DNA and RNA of respiratory samples for microbial work v1		1	