

Suparna Mitra

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6882678/publications.pdf>

Version: 2024-02-01

28
papers

4,377
citations

535685

17
h-index

563245

28
g-index

30
all docs

30
docs citations

30
times ranked

9509
citing authors

#	ARTICLE	IF	CITATIONS
1	The <sc>COLOâ€œCOHORT</sc> (Colorectal Cancer Cohort) study: Protocol for a multiâ€œcentre, observational research study and development of a consentâ€œforâ€œcontact research platform. <i>Colorectal Disease</i> , 2022, 24, 1216-1226.	0.7	2
2	Perturbations of the gut microbiome in anti-CCP positive individuals at risk of developing rheumatoid arthritis. <i>Rheumatology</i> , 2021, 60, 3380-3387.	0.9	16
3	Luminal Bioavailability of Orally Administered Î‰-3 PUFAs in the Distal Small Intestine, and Associated Changes to the Ileal Microbiome, in Humans with a Temporary Ileostomy. <i>Journal of Nutrition</i> , 2021, 151, 2142-2152.	1.3	4
4	Trehalose-Induced Remodelling of the Human Microbiota Affects <i>Clostridioides difficile</i> Infection Outcome in an In Vitro Colonic Model: A Pilot Study. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 670935.	1.8	18
5	Microbiota Supplementation with <i>Bifidobacterium</i> and <i>Lactobacillus</i> Modifies the Preterm Infant Gut Microbiota and Metabolome: An Observational Study. <i>Cell Reports Medicine</i> , 2020, 1, 100077.	3.3	119
6	Molecular and culture-based surveys of metabolically active hydrocarbon-degrading archaeal communities in Sundarban mangrove sediments. <i>Ecotoxicology and Environmental Safety</i> , 2020, 195, 110481.	2.9	13
7	Multiple Data Analyses and Statistical Approaches for Analyzing Data from Metagenomic Studies and Clinical Trials. <i>Methods in Molecular Biology</i> , 2019, 1910, 605-634.	0.4	8
8	A randomised trial of the effect of omega-3 polyunsaturated fatty acid supplements on the human intestinal microbiota. <i>Gut</i> , 2018, 67, 1974-1983.	6.1	332
9	Metagenomics Reveals the Influence of Land Use and Rain on the Benthic Microbial Communities in a Tropical Urban Waterway. <i>MSystems</i> , 2018, 3, .	1.7	63
10	A simple statistical test of taxonomic or functional homogeneity using replicated microbiome sequencing samples. <i>Journal of Biotechnology</i> , 2017, 250, 45-50.	1.9	1
11	Optimisation of 16S rRNA gut microbiota profiling of extremely low birth weight infants. <i>BMC Genomics</i> , 2017, 18, 841.	1.2	47
12	Safety and Cost Considerations during the Introduction Period of Laparoscopic Radical Hysterectomy. <i>Obstetrics and Gynecology International</i> , 2017, 2017, 1-6.	0.5	4
13	MEGAN Community Edition - Interactive Exploration and Analysis of Large-Scale Microbiome Sequencing Data. <i>PLoS Computational Biology</i> , 2016, 12, e1004957.	1.5	1,500
14	In silico analyses of metagenomes from human atherosclerotic plaque samples. <i>Microbiome</i> , 2015, 3, 38.	4.9	87
15	Effects of Surgical and Dietary Weight Loss Therapy for Obesity on Gut Microbiota Composition and Nutrient Absorption. <i>BioMed Research International</i> , 2015, 2015, 1-12.	0.9	252
16	Diversity and Distribution of Archaea in the Mangrove Sediment of Sundarbans. <i>Archaea</i> , 2015, 2015, 1-14.	2.3	47
17	Ecogenomics Reveals Metals and Land-Use Pressures on Microbial Communities in the Waterways of a Megacity. <i>Environmental Science & Technology</i> , 2015, 49, 1462-1471.	4.6	53
18	Mining and assessment of catabolic pathways in the metagenome of a common effluent treatment plant to induce the degradative capacity of biomass. <i>Bioresource Technology</i> , 2014, 153, 137-146.	4.8	36

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19	Analysis of the intestinal microbiota using SOLiD 16S rRNA gene sequencing and SOLiD shotgun sequencing. BMC Genomics, 2013, 14, S16.	1.2	40
20	Introduction to the Analysis of Environmental Sequences: Metagenomics with MEGAN. Methods in Molecular Biology, 2012, 856, 415-429.	0.4	74
21	Detection and diversity of pathogenic <i>Vibrio</i> from Fiji. Environmental Microbiology Reports, 2012, 4, 403-411.	1.0	2
22	Integrative analysis of environmental sequences using MEGAN4. Genome Research, 2011, 21, 1552-1560.	2.4	1,245
23	Functional analysis of metagenomes and metatranscriptomes using SEED and KEGG. BMC Bioinformatics, 2011, 12, S21.	1.2	116
24	Analysis of 16S rRNA environmental sequences using MEGAN. BMC Genomics, 2011, 12, S17.	1.2	71
25	Short clones or long clones? A simulation study on the use of paired reads in metagenomics. BMC Bioinformatics, 2010, 11, S12.	1.2	11
26	Comparison of multiple metagenomes using phylogenetic networks based on ecological indices. ISME Journal, 2010, 4, 1236-1242.	4.4	43
27	Visual and statistical comparison of metagenomes. Bioinformatics, 2009, 25, 1849-1855.	1.8	74
28	Methods for comparative metagenomics. BMC Bioinformatics, 2009, 10, S12.	1.2	96