

Richard Rosario Rodrigues

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

3,237
citations

471371

17
h-index

642610

23
g-index

27
all docs

27
docs citations

27
times ranked

3714
citing authors

#	ARTICLE	IF	CITATIONS
1	Intestinal microbiota signatures of clinical response and immune-related adverse events in melanoma patients treated with anti-PD-1. <i>Nature Medicine</i> , 2022, 28, 545-556.	15.2	167
2	Microbiota and adipocyte mitochondrial damage in type 2 diabetes are linked by <i>Mmp12</i> + macrophages. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	24
3	Transkingdom interactions between <i>Lactobacilli</i> and hepatic mitochondria attenuate western diet-induced diabetes. <i>Nature Communications</i> , 2021, 12, 101.	5.8	86
4	Fecal microbiota transplant overcomes resistance to anti-PD-1 therapy in melanoma patients. <i>Science</i> , 2021, 371, 595-602.	6.0	746
5	Microbiota triggers STING-type I IFN-dependent monocyte reprogramming of the tumor microenvironment. <i>Cell</i> , 2021, 184, 5338-5356.e21.	13.5	229
6	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response. <i>Science</i> , 2021, 374, 1632-1640.	6.0	369
7	Role of gut microbiota in type 2 diabetes pathophysiology. <i>EBioMedicine</i> , 2020, 51, 102590.	2.7	954
8	Improvements in Metabolic Syndrome by Xanthohumol Derivatives Are Linked to Altered Gut Microbiota and Bile Acid Metabolism. <i>Molecular Nutrition and Food Research</i> , 2020, 64, e1900789.	1.5	32
9	Gut-resident CX3CR1 ^{hi} macrophages induce tertiary lymphoid structures and IgA response in situ. <i>Science Immunology</i> , 2020, 5, .	5.6	63
10	Unprecedented bacterial community richness in soybean nodules vary with cultivar and water status. <i>Microbiome</i> , 2019, 7, 63.	4.9	51
11	Foliar application of Fe resonates to the belowground rhizosphere microbiome in Andean landrace potatoes. <i>Applied Soil Ecology</i> , 2018, 131, 89-98.	2.1	8
12	Transkingdom Networks: A Systems Biology Approach to Identify Causal Members of Host-Microbiota Interactions. <i>Methods in Molecular Biology</i> , 2018, 1849, 227-242.	0.4	23
13	Transcriptomic Analysis of Hepatic Cells in Multicellular Organotypic Liver Models. <i>Scientific Reports</i> , 2018, 8, 11306.	1.6	8
14	COREMIC: a web-tool to search for a niche associated CORE MICRObiome. <i>PeerJ</i> , 2018, 6, e4395.	0.9	23
15	Transkingdom network reveals bacterial players associated with cervical cancer gene expression program. <i>PeerJ</i> , 2018, 6, e5590.	0.9	24
16	Microbial communities and diazotrophic activity differ in the root-zone of Alamo and Dacotah switchgrass feedstocks. <i>GCB Bioenergy</i> , 2017, 9, 1057-1070.	2.5	24
17	Antibiotic-Induced Alterations in Gut Microbiota Are Associated with Changes in Glucose Metabolism in Healthy Mice. <i>Frontiers in Microbiology</i> , 2017, 8, 2306.	1.5	103
18	Honey Bee Gut Microbiome Is Altered by In-Hive Pesticide Exposures. <i>Frontiers in Microbiology</i> , 2016, 7, 1255.	1.5	165

#	ARTICLE	IF	CITATIONS
19	Plant Invasions Associated with Change in Root-Zone Microbial Community Structure and Diversity. PLoS ONE, 2015, 10, e0141424.	1.1	64
20	Reconciling differential gene expression data with molecular interaction networks. Bioinformatics, 2013, 29, 622-629.	1.8	17
21	Designing a Multicellular Organotypic 3D Liver Model with a Detachable, Nanoscale Polymeric Space of Disse. Tissue Engineering - Part C: Methods, 2013, 19, 875-884.	1.1	33
22	Top-Down Network Analysis to Drive Bottom-Up Modeling of Physiological Processes. Journal of Computational Biology, 2013, 20, 409-418.	0.8	14
23	Gene Pathway Analysis of Hepatocellular Carcinoma Genomic Expression Datasets. Journal of Surgical Research, 2011, 170, e85-e92.	0.8	7