

Gabriel da Rocha Fernandes

List of Publications by Year in descending order

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Version: 2024-02-01

48
papers

8,023
citations

257450

24
h-index

182427

51
g-index

54
all docs

54
docs citations

54
times ranked

13666
citing authors

#	ARTICLE	IF	CITATIONS
1	Enterotypes of the human gut microbiome. <i>Nature</i> , 2011, 473, 174-180.	27.8	5,800
2	Exercise induction of gut microbiota modifications in obese, non-obese and hypertensive rats. <i>BMC Genomics</i> , 2014, 15, 511.	2.8	244
3	<i>Akkermansia muciniphila</i> mediates negative effects of IFN γ on glucose metabolism. <i>Nature Communications</i> , 2016, 7, 13329.	12.8	232
4	Combination of Mass Cytometry and Imaging Analysis Reveals Origin, Location, and Functional Repopulation of Liver Myeloid Cells in Mice. <i>Gastroenterology</i> , 2016, 151, 1176-1191.	1.3	173
5	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	10.3	142
6	Gut microbiota interactions with the immunomodulatory role of vitamin D in normal individuals. <i>Metabolism: Clinical and Experimental</i> , 2017, 69, 76-86.	3.4	132
7	Subgingival microbiota dysbiosis in systemic lupus erythematosus: association with periodontal status. <i>Microbiome</i> , 2017, 5, 34.	11.1	132
8	Genomic signatures and co-occurrence patterns of the ultra-small <i>Saccharimonadia</i> (phylum) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50 4	3.9	101
9	Oral microbial dysbiosis linked to worsened periodontal condition in rheumatoid arthritis patients. <i>Scientific Reports</i> , 2019, 9, 8379.	3.3	94
10	Worse inflammatory profile in omnivores than in vegetarians associates with the gut microbiota composition. <i>Diabetology and Metabolic Syndrome</i> , 2017, 9, 62.	2.7	78
11	Enterotype May Drive the Dietary-Associated Cardiometabolic Risk Factors. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 47.	3.9	68
12	Transcriptional and Proteomic Responses to Carbon Starvation in <i>Paracoccidioides</i> . <i>PLoS Neglected Tropical Diseases</i> , 2014, 8, e2855.	3.0	65
13	<i>Paracoccidioides brasiliensis</i> presents metabolic reprogramming and secretes a serine proteinase during murine infection. <i>Virulence</i> , 2017, 8, 1417-1434.	4.4	58
14	MicrobiomeDB: a systems biology platform for integrating, mining and analyzing microbiome experiments. <i>Nucleic Acids Research</i> , 2018, 46, D684-D691.	14.5	47
15	Exploring the resistome, virulome and microbiome of drinking water in environmental and clinical settings. <i>Water Research</i> , 2020, 174, 115630.	11.3	44
16	Amino acids biosynthesis and nitrogen assimilation pathways: a great genomic deletion during eukaryotes evolution. <i>BMC Genomics</i> , 2011, 12, S2.	2.8	42
17	Immune and metabolic shifts during neonatal development reprogram liver identity and function. <i>Journal of Hepatology</i> , 2018, 69, 1294-1307.	3.7	42
18	Gut microbiome modulation during treatment of mucositis with the dairy bacterium <i>Lactococcus lactis</i> and recombinant strain secreting human antimicrobial PAP. <i>Scientific Reports</i> , 2018, 8, 15072.	3.3	36

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19	Comparative transcriptomic analysis indicates genes associated with local and systemic resistance to <i>Colletotrichum graminicola</i> in maize. <i>Scientific Reports</i> , 2017, 7, 2483.	3.3	33
20	Insights into novel antimicrobial compounds and antibiotic resistance genes from soil metagenomes. <i>Frontiers in Microbiology</i> , 2014, 5, 489.	3.5	30
21	<i>Staphylococcus epidermidis</i> role in the skin microenvironment. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 5949-5955.	3.6	29
22	ZIKV "CDB: A Collaborative Database to Guide Research Linking SncRNAs and ZIKA Virus Disease Symptoms. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004817.	3.0	28
23	Venom gland transcriptome analyses of two freshwater stingrays (Myliobatiformes): <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 58</i>	3.3	24
24	<i>Paracoccidioides</i> spp. ferrous and ferric iron assimilation pathways. <i>Frontiers in Microbiology</i> , 2015, 6, 821.	3.5	23
25	Prophylactic <i>Faecalibacterium prausnitzii</i> treatment prevents the acute breakdown of colonic epithelial barrier in a preclinical model of pelvic radiation disease. <i>Gut Microbes</i> , 2020, 12, 1812867.	9.8	22
26	Effects of Argentilactone on the Transcriptional Profile, Cell Wall and Oxidative Stress of <i>Paracoccidioides</i> spp.. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0004309.	3.0	19
27	Shedding Some Light over the Floral Metabolism by Arum Lily (<i>Zantedeschia aethiopica</i>) Spathe De Novo Transcriptome Assembly. <i>PLoS ONE</i> , 2014, 9, e90487.	2.5	16
28	Inositol 1, 4, 5-trisphosphate-dependent nuclear calcium signals regulate angiogenesis and cell motility in triple negative breast cancer. <i>PLoS ONE</i> , 2017, 12, e0175041.	2.5	15
29	Oral delivery of pancreatitis-associated protein by <i>Lactococcus lactis</i> displays protective effects in dinitrobenzenesulfonic acid-induced colitis model and is able to modulate the composition of the microbiota. <i>Environmental Microbiology</i> , 2019, 21, 4020-4031.	3.8	15
30	Soil Acidobacteria Strain AB23 Resistance to Oxidative Stress Through Production of Carotenoids. <i>Microbial Ecology</i> , 2021, 81, 169-179.	2.8	15
31	An Integrative Approach Uncovers Biomarkers that Associate with Clinically Relevant Disease Outcomes in Vulvar Carcinoma. <i>Molecular Cancer Research</i> , 2016, 14, 720-729.	3.4	11
32	Identification of a novel subtype of feline immunodeficiency virus in a population of naturally infected felines in the Brazilian Federal District. <i>Virus Genes</i> , 2013, 46, 546-550.	1.6	8
33	Draft Genome Sequence of <i>Acidibacillus ferrooxidans</i> ITV01, a Novel Acidophilic Firmicute Isolated from a Chalcopyrite Mine Drainage Site in Brazil. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
34	HD5 and HBD1 variants™ solvation potential energy correlates with their antibacterial activity against <i>Escherichia coli</i> . <i>Biopolymers</i> , 2016, 106, 43-50.	2.4	8
35	Single-cell sequencing unveils the lifestyle and CRISPR-based population history of <i>Hydrothalea</i> sp. in acid mine drainage. <i>Molecular Ecology</i> , 2017, 26, 5541-5551.	3.9	8
36	Unraveling the xylanolytic potential of Acidobacteria bacterium AB60 from Cerrado soils. <i>FEMS Microbiology Letters</i> , 2020, 367, .	1.8	8

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37	Changes in antennal gene expression underlying sensory system maturation in <i>Rhodnius prolixus</i> . <i>Insect Biochemistry and Molecular Biology</i> , 2022, 140, 103704.	2.7	8
38	Comparative transcriptome analyses of magainin I-susceptible and -resistant <i>Escherichia coli</i> strains. <i>Microbiology (United Kingdom)</i> , 2018, 164, 1383-1393.	1.8	7
39	Preimplantation development regulatory pathway construction through a text-mining approach. <i>BMC Genomics</i> , 2011, 12, S3.	2.8	6
40	Whole-Genome Sequence of <i>Leptospira interrogans</i> Serovar Hardjo Subtype Hardjoprajitno Strain Norma, Isolated from Cattle in a Leptospirosis Outbreak in Brazil. <i>Genome Announcements</i> , 2015, 3, .	0.8	6
41	The TLR1 gene is associated with higher protection from leprosy in women. <i>PLoS ONE</i> , 2018, 13, e0205234.	2.5	6
42	A procedure to recruit members to enlarge protein family databases - the building of UECOG (UniRef-Enriched COG Database) as a model. <i>Genetics and Molecular Research</i> , 2008, 7, 910-924.	0.2	6
43	Associations of <i>Blautia</i> Genus With Early-Life Events and Later Phenotype in the NutriHS. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, .	3.9	6
44	Methotrexate promotes recovery of arthritis-induced alveolar bone loss and modifies the composition of the oral-gut microbiota. <i>Anaerobe</i> , 2022, 75, 102577.	2.1	6
45	Insights into the Genome Sequence of <i>Chromobacterium amazonense</i> Isolated from a Tropical Freshwater Lake. <i>International Journal of Genomics</i> , 2018, 2018, 1-10.	1.6	5
46	Draft Genome Sequence of <i>Hydrotaea flava</i> Strain CCUG 51397 T. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
47	Genomic Comparison among Lethal Invasive Strains of <i>Streptococcus pyogenes</i> Serotype M1. <i>Frontiers in Microbiology</i> , 2017, 8, 1993.	3.5	2
48	Testing the performance of automated annotation of ESTs with the Kegg Orthology (KO) database demonstrates lack of completeness of clusters. <i>Genetics and Molecular Research</i> , 2008, 7, 948-957.	0.2	1