

Ranko Gacesa

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

1,749
citations

361413
20
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315739
38
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53
all docs

53
docs citations

53
times ranked

2235
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-term dietary patterns are associated with pro-inflammatory and anti-inflammatory features of the gut microbiome. <i>Gut</i> , 2021, 70, 1287-1298.	12.1	246
2	Environmental factors shaping the gut microbiome in a Dutch population. <i>Nature</i> , 2022, 604, 732-739.	27.8	239
3	The long-term genetic stability and individual specificity of the human gut microbiome. <i>Cell</i> , 2021, 184, 2302-2315.e12.	28.9	166
4	Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project. <i>Nature Genetics</i> , 2022, 54, 143-151.	21.4	132
5	Gut microbial co-abundance networks show specificity in inflammatory bowel disease and obesity. <i>Nature Communications</i> , 2020, 11, 4018.	12.8	80
6	Riboflavin Supplementation in Patients with Crohn's Disease [the RISE-UP study]. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 595-607.	1.3	63
7	Gene duplications are extensive and contribute significantly to the toxic proteome of nematocysts isolated from <i>Acropora digitifera</i> (Cnidaria: Anthozoa: Scleractinia). <i>BMC Genomics</i> , 2015, 16, 774.	2.8	58
8	The mycosporine-like amino acids porphyra-334 and shinorine are antioxidants and direct antagonists of Keap1-Nrf2 binding. <i>Biochimie</i> , 2018, 154, 35-44.	2.6	54
9	Rising levels of atmospheric oxygen and evolution of Nrf2. <i>Scientific Reports</i> , 2016, 6, 27740.	3.3	52
10	KEGG orthology-based annotation of the predicted proteome of <i>Acropora digitifera</i> : ZoophyteBase - an open access and searchable database of a coral genome. <i>BMC Genomics</i> , 2013, 14, 509.	2.8	51
11	Molecular photoprotection of human keratinocytes <i>in vitro</i> by the naturally occurring mycosporine-like amino acid palythine. <i>British Journal of Dermatology</i> , 2018, 178, 1353-1363.	1.5	50
12	O ⁶ -Methyltransferase Is Shared between the Pentose Phosphate and Shikimate Pathways and Is Essential for Mycosporine-Like Amino Acid Biosynthesis in <i>Anabaena variabilis</i> ATCC 29413. <i>ChemBioChem</i> , 2015, 16, 320-327.	2.6	48
13	Bacterial diversity of polluted surface sediments in the northern Adriatic Sea. <i>Systematic and Applied Microbiology</i> , 2015, 38, 189-197.	2.8	45
14	Gut microbial species and metabolic pathways associated with response to treatment with immune checkpoint inhibitors in metastatic melanoma. <i>Melanoma Research</i> , 2020, 30, 235-246.	1.2	42
15	Anti-inflammatory Gut Microbial Pathways Are Decreased During Crohn's Disease Exacerbations. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 1439-1449.	1.3	39
16	Machine learning can differentiate venom toxins from other proteins having non-toxic physiological functions. <i>PeerJ Computer Science</i> , 0, 2, e90.	4.5	38
17	Draft Genome Sequence of <i>Streptomyces rapamycinicus</i> Strain NRRL 5491, the Producer of the Immunosuppressant Rapamycin. <i>Genome Announcements</i> , 2013, 1, .	0.8	37
18	Predicting substrate specificity of adenylation domains of nonribosomal peptide synthetases and other protein properties by latent semantic indexing. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 461-467.	3.0	37

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19	Healthy Cotwins Share Gut Microbiome Signatures With Their Inflammatory Bowel Disease Twins and Unrelated Patients. <i>Gastroenterology</i> , 2021, 160, 1970-1985.	1.3	31
20	Whole exome sequencing analyses reveal gene-microbiota interactions in the context of IBD. <i>Gut</i> , 2021, 70, gutjnl-2019-319706.	12.1	26
21	Comparative proteomics reveals recruitment patterns of some protein families in the venoms of Cnidaria. <i>Toxicon</i> , 2017, 137, 19-26.	1.6	24
22	Databases of the thiotemplate modular systems (CSDB) and their in silico recombinants (r-CSDB). <i>Journal of Industrial Microbiology and Biotechnology</i> , 2013, 40, 653-659.	3.0	22
23	Multi-omics examination of Q fever fatigue syndrome identifies similarities with chronic fatigue syndrome. <i>Journal of Translational Medicine</i> , 2020, 18, 448.	4.4	21
24	The Gut Microbiome Composition Is Altered in Long-standing Type 1 Diabetes and Associates With Glycemic Control and Disease-Related Complications. <i>Diabetes Care</i> , 2022, 45, 2084-2094.	8.6	21
25	Bioinformatics analyses provide insight into distant homology of the Keap1-Nrf2 pathway. <i>Free Radical Biology and Medicine</i> , 2015, 88, 373-380.	2.9	18
26	"Beyond Primary Sequence" Proteomic Data Reveal Complex Toxins in Cnidarian Venoms. <i>Integrative and Comparative Biology</i> , 2019, 59, 777-785.	2.0	18
27	Evolutionary concepts in natural products discovery: what actinomycetes have taught us. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 211-217.	3.0	16
28	Bioprospecting for Genes Encoding Hydrocarbon-Degrading Enzymes from Metagenomic Samples Isolated from Northern Adriatic Sea Sediments. <i>Food Technology and Biotechnology</i> , 2018, 56, 270-277.	2.1	9
29	Genetic and biochemical evidence for redundant pathways leading to mycosporine-like amino acid biosynthesis in the cyanobacterium <i>Sphaerospermopsis torques-reginae</i> ; ITEP-024. <i>Algae</i> , 2020, 35, 177-187.	2.3	7
30	Mycosporine-like amino acid activation of the Keap1-Nrf2 pathway. <i>Free Radical Biology and Medicine</i> , 2017, 108, S21.	2.9	4
31	Donor tobacco smoking is associated with postoperative thrombosis after primary liver transplantation. <i>Journal of Thrombosis and Haemostasis</i> , 2020, 18, 2590-2600.	3.8	4
32	Donor genetic variants as risk factors for thrombosis after liver transplantation: A genome-wide association study. <i>American Journal of Transplantation</i> , 2021, 21, 3133-3147.	4.7	4
33	A combination of fecal calprotectin and human beta-defensin 2 facilitates diagnosis and monitoring of inflammatory bowel disease. <i>Gut Microbes</i> , 2021, 13, 1943288.	9.8	4
34	Long-Term Dietary Patterns Are Reflected in the Plasma Inflammatory Proteome of Patients with Inflammatory Bowel Disease. <i>Nutrients</i> , 2022, 14, 2522.	4.1	4
35	Genome Sequence of <i>Streptomyces caatingaensis</i> CMAA 1322, a New Abiotic Stress-Tolerant Actinomycete Isolated from Dried Lake Bed Sediment in the Brazilian Caatinga Biome. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
36	Predicting Liver Disease Risk Using a Combination of Common Clinical Markers: A Screening Model from Routine Health Check-Up. <i>Disease Markers</i> , 2020, 2020, 1-11.	1.3	2

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37	The Long-Term Genetic Stability and Individual Specificity of the Human Gut Microbiome. SSRN Electronic Journal, 0, , .	0.4	2
38	MEGGASENSE - the Metagenome/Genome Annotated Sequence Natural Language Search Engine: a Platform for the Construction of Sequence Data Warehouses. Food Technology and Biotechnology, 2017, 55, 251-257.	2.1	1
39	Horizontal transfer of a natterin-like toxin encoding gene within the holobiont of the reef building coral (Cnidaria: Anthozoa: Scleractinia) and across multiple animal linages. Journal of Venom Research, 2020, 10, 7-12.	0.6	1
40	Bioprospecting for genes of alkane-degrading enzymes in metagenomic samples from northern Adriatic Sea. Journal of Biotechnology, 2014, 185, S6.	3.8	0
41	OP01 In-depth characterisation of host genetics and gut microbiome unravels novel host-microbiome interactions in inflammatory bowel disease. Journal of Crohn's and Colitis, 2019, 13, S001-S001.	1.3	0
42	Solid-Phase Synthesis and In-Silico Analysis of Iron-Binding Catecholato Chelators. International Journal of Molecular Sciences, 2020, 21, 7498.	4.1	0
43	P006 Host-genetics, dysbiosis, and clinical history explains fecal metabolic alterations in patients with Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2021, 15, S128-S128.	1.3	0