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## List of Publications by Year in descending order

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Version: 2024-02-01

63  
papers

2,967  
citations

331538

21  
h-index

175177

52  
g-index

65  
all docs

65  
docs citations

65  
times ranked

4969  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of a carbapenem-resistant <i>Escherichia coli</i> from dairy cattle harbouring bla <sub>NDM-1</sub> in an IncC plasmid. <i>Journal of Antimicrobial Chemotherapy</i> , 2022, 77, 843-845.	1.3	7
2	Mitochondrial complex I dysfunction alters the balance of soluble and membrane-bound TNF during chronic experimental colitis. <i>Scientific Reports</i> , 2022, 12, .	1.6	2
3	<i>Borrelia burgdorferi</i> infection induces long-term memory-like responses in macrophages with tissue-wide consequences in the heart. <i>PLoS Biology</i> , 2021, 19, e3001062.	2.6	7
4	The commensal bacterium <i>Lactiplantibacillus plantarum</i> imprints innate memory-like responses in mononuclear phagocytes. <i>Gut Microbes</i> , 2021, 13, 1939598.	4.3	8
5	Whole genome-based characterisation of antimicrobial resistance and genetic diversity in <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> from ruminants. <i>Scientific Reports</i> , 2021, 11, 8998.	1.6	25
6	A conserved rRNA switch is central to decoding site maturation on the small ribosomal subunit. <i>Science Advances</i> , 2021, 7, .	4.7	23
7	Evaluating the Inclusion of Cold-Pressed Rapeseed Cake in the Concentrate for Dairy Cows upon Ruminant Biohydrogenation Process, Ruminant Microbial Community and Milk Production and Acceptability. <i>Animals</i> , 2021, 11, 2553.	1.0	4
8	Identification of loci associated with susceptibility to bovine paratuberculosis and with the dysregulation of the MECOM, eEF1A2, and U1 spliceosomal RNA expression. <i>Scientific Reports</i> , 2021, 11, 313.	1.6	10
9	Draft Genome Sequence of <i>Escherichia marmotae</i> E690, Isolated from Beef Cattle. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	5
10	Secretomes of medically important fungi reflect morphological and phylogenetic diversity. <i>Fungal Biology</i> , 2020, 124, 915-923.	1.1	2
11	Cross-sectional study of human coding- and non-coding RNAs in progressive stages of <i>Helicobacter pylori</i> infection. <i>Scientific Data</i> , 2020, 7, 296.	2.4	1
12	Spent Coffee Grounds Alter Bacterial Communities in Latxa Dairy Ewes. <i>Microorganisms</i> , 2020, 8, 1961.	1.6	6
13	A structurally unique <i>Fusobacterium nucleatum</i> tannase provides detoxicant activity against gallotannins and pathogen resistance. <i>Microbial Biotechnology</i> , 2020, .	2.0	3
14	Editorial: Macrophage Metabolism and Immune Responses. <i>Frontiers in Immunology</i> , 2020, 11, 1078.	2.2	4
15	Patients with Cholangiocarcinoma Present Specific RNA Profiles in Serum and Urine Extracellular Vesicles Mirroring the Tumor Expression: Novel Liquid Biopsy Biomarkers for Disease Diagnosis. <i>Cells</i> , 2020, 9, 721.	1.8	63
16	The mitochondrial negative regulator MCJ modulates the interplay between microbiota and the host during ulcerative colitis. <i>Scientific Reports</i> , 2020, 10, 572.	1.6	17
17	Extracellular Vesicles From Liver Progenitor Cells Downregulates Fibroblast Metabolic Activity and Increase the Expression of Immune-Response Related Molecules. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 613583.	1.8	0
18	HuR/ELAVL1 drives malignant peripheral nerve sheath tumor growth and metastasis. <i>Journal of Clinical Investigation</i> , 2020, 130, 3848-3864.	3.9	38

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19	Gut microbiome and serum metabolome analyses identify molecular biomarkers and altered glutamate metabolism in fibromyalgia. <i>EBioMedicine</i> , 2019, 46, 499-511.	2.7	128
20	Signal Integration and Transcriptional Regulation of the Inflammatory Response Mediated by the GM-/M-CSF Signaling Axis in Human Monocytes. <i>Cell Reports</i> , 2019, 29, 860-872.e5.	2.9	29
21	Intestinal epithelial deletion of the glucocorticoid receptor NR3C1 alters expression of inflammatory mediators and barrier function. <i>FASEB Journal</i> , 2019, 33, 14067-14082.	0.2	16
22	Effect of Feeding Cold-Pressed Sunflower Cake on Ruminal Fermentation, Lipid Metabolism and Bacterial Community in Dairy Cows. <i>Animals</i> , 2019, 9, 755.	1.0	15
23	Host-microbiome interactions in response to a high-saturated fat diet and fish-oil supplementation in zebrafish adult. <i>Journal of Functional Foods</i> , 2019, 60, 103416.	1.6	10
24	ANP32E, a Protein Involved in Steroid-Refractoriness in Ulcerative Colitis, Identified by a Systems Biology Approach. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 351-361.	0.6	30
25	A multi-omic analysis reveals the regulatory role of CD180 during the response of macrophages to <i>Borrelia burgdorferi</i> . <i>Emerging Microbes and Infections</i> , 2018, 7, 1-13.	3.0	9
26	Cluster Locator, online analysis and visualization of gene clustering. <i>Bioinformatics</i> , 2018, 34, 3377-3379.	1.8	20
27	Quantum DNA Sequencing: A Peek Into a Dystopic Future?. <i>BioEssays</i> , 2018, 40, 1700248.	1.2	2
28	Identification of a highly active tannase enzyme from the oral pathogen <i>Fusobacterium nucleatum</i> subsp. <i>polymorphum</i> . <i>Microbial Cell Factories</i> , 2018, 17, 33.	1.9	17
29	Progressive loss of hybrid histidine kinase genes during the evolution of budding yeasts ( <i>Saccharomycotina</i> ). <i>Current Genetics</i> , 2018, 64, 841-851.	0.8	7
30	MiR-873-5p acts as an epigenetic regulator in early stages of liver fibrosis and cirrhosis. <i>Cell Death and Disease</i> , 2018, 9, 958.	2.7	38
31	Metabolomic Identification of Subtypes of Nonalcoholic Steatohepatitis. <i>Gastroenterology</i> , 2017, 152, 1449-1461.e7.	0.6	209
32	SOX17 regulates cholangiocyte differentiation and acts as a tumor suppressor in cholangiocarcinoma. <i>Journal of Hepatology</i> , 2017, 67, 72-83.	1.8	81
33	Aramchol reduces established fibrosis in MCD diet animal model. <i>Journal of Hepatology</i> , 2017, 66, S432.	1.8	0
34	The Expression of mir-19b-3p and HIPK3 is Highly Correlated in Patients with Precancerous Lesions of Gastric Cancer. <i>Gastroenterology</i> , 2017, 152, S664-S665.	0.6	0
35	A synbiotic composed of <i>Lactobacillus fermentum</i> CECT5716 and FOS prevents the development of fatty acid liver and glycemic alterations in rats fed a high fructose diet associated with changes in the microbiota. <i>Molecular Nutrition and Food Research</i> , 2017, 61, 1600622.	1.5	37
36	A fistful of tips for a fruitful high throughput sequencing experiment. <i>BioEssays</i> , 2017, 39, 1700037.	1.2	1

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37	Epigenetic Networks Regulate the Transcriptional Program in Memory and Terminally Differentiated CD8+ T Cells. <i>Journal of Immunology</i> , 2017, 198, 937-949.	0.4	55
38	Role of aramchol in steatohepatitis and fibrosis in mice. <i>Hepatology Communications</i> , 2017, 1, 911-927.	2.0	84
39	The immunosuppressive effect of the tick protein, Salp15, is long-lasting and persists in a murine model of hematopoietic transplant. <i>Scientific Reports</i> , 2017, 7, 10740.	1.6	14
40	Potyvirus virion structure shows conserved protein fold and RNA binding site in ssRNA viruses. <i>Science Advances</i> , 2017, 3, eaao2182.	4.7	84
41	Inverse Correlation of Pleckstrin mRNA and miR-200a in the Antrum of Helicobacter Pylori Infected Patients. <i>Gastroenterology</i> , 2017, 152, S665.	0.6	0
42	VerSeDa: vertebrate secretome database. <i>Database: the Journal of Biological Databases and Curation</i> , 2017, 2017, .	1.4	19
43	Comparative and transcriptional analysis of the predicted secretome in the lignocellulose-degrading basidiomycete fungus <i>Pleurotus ostreatus</i> . <i>Environmental Microbiology</i> , 2016, 18, 4710-4726.	1.8	77
44	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	1.8	175
45	SOX17 Regulates Cholangiocyte Differentiation and Acts as a Tumour Suppressor in Cholangiocarcinoma. <i>Journal of Hepatology</i> , 2016, 64, S569-S570.	1.8	1
46	Sa1741 The Antrum and Corpus mRNA and Small-RNA Profile of the Human Healthy Stomach. <i>Gastroenterology</i> , 2015, 148, S-319.	0.6	0
47	Genomewide analysis of phytochrome proteins in the phylum Basidiomycota. <i>Journal of Basic Microbiology</i> , 2015, 55, 1141-1147.	1.8	2
48	PECAS: prokaryotic and eukaryotic classical analysis of secretome. <i>Amino Acids</i> , 2015, 47, 2659-2663.	1.2	7
49	SECRETOOL: integrated secretome analysis tool for fungi. <i>Amino Acids</i> , 2014, 46, 471-473.	1.2	46
50	Dual-histidine kinases in basidiomycete fungi. <i>Comptes Rendus - Biologies</i> , 2014, 337, 111-116.	0.1	7
51	S-adenosylmethionine Levels Regulate the Schwann Cell DNA Methylome. <i>Neuron</i> , 2014, 81, 1024-1039.	3.8	67
52	Complete Genome Sequence of the Multiresistant <i>Acinetobacter baumannii</i> Strain AbH120-A2, Isolated during a Large Outbreak in Spain. <i>Genome Announcements</i> , 2014, 2, .	0.8	19
53	FUNGALOXPHOS: An integrated database for oxidative phosphorylation in fungi. <i>Mitochondrion</i> , 2013, 13, 357-359.	1.6	3
54	Two-component signal transduction in <i>Agaricus bisporus</i> : A comparative genomic analysis with other basidiomycetes through the web-based tool BASID2CS. <i>Fungal Genetics and Biology</i> , 2013, 55, 77-84.	0.9	6

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55	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5458-5463.	3.3	259
56	The Plant Cell Wall “Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
57	Genomics and transcriptomics characterization of genes expressed during postharvest at 4°C by the edible basidiomycete <i>Pleurotus ostreatus</i> . <i>International Microbiology</i> , 2011, 14, 111-20.	1.1	17
58	Differences in two-component signal transduction proteins among the genus <i>Brucella</i> : Implications for host preference and pathogenesis. <i>Veterinary Microbiology</i> , 2010, 144, 478-483.	0.8	9
59	Genomic Analysis of Two-Component Signal Transduction Proteins in Basidiomycetes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010, 18, 63-73.	1.0	14
60	Genome, transcriptome, and secretome analysis of wood decay fungus <i>Postia placenta</i> supports unique mechanisms of lignocellulose conversion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1954-1959.	3.3	530
61	Comparative genomics of the oxidative phosphorylation system in fungi. <i>Fungal Genetics and Biology</i> , 2008, 45, 1248-1256.	0.9	28
62	Genetic networks for the functional study of genomes. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2008, 7, 249-263.	3.8	12
63	Comparative genomic analysis of two-component regulatory proteins in <i>Pseudomonas syringae</i> . <i>BMC Genomics</i> , 2007, 8, 397.	1.2	33