

Pã;raic Ã“ CuÃ-v

List of Publications by Year in descending order

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39
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42
docs citations

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times ranked

2826
citing authors

#	ARTICLE	IF	CITATIONS
1	Secreted NF-ÎB suppressive microbial metabolites modulate gut inflammation. <i>Cell Reports</i> , 2022, 39, 110646.	6.4	22
2	<i>Streptococcus</i> species enriched in the oral cavity of patients with RA are a source of peptidoglycan-polysaccharide polymers that can induce arthritis in mice. <i>Annals of the Rheumatic Diseases</i> , 2021, 80, 573-581.	0.9	24
3	Plasmacytoid dendritic cells protect from viral bronchiolitis and asthma through semaphorin 4a-mediated T reg expansion. <i>Journal of Experimental Medicine</i> , 2018, 215, 537-557.	8.5	65
4	Colonic thioguanine pro-drug: Investigation of microbiome and novel host metabolism. <i>Gut Microbes</i> , 2018, 9, 175-178.	9.8	11
5	Food Starch Structure Impacts Gut Microbiome Composition. <i>MSphere</i> , 2018, 3, .	2.9	106
6	Culture- and metagenomics-enabled analyses of the <i>Methanosphaera</i> genus reveals their monophyletic origin and differentiation according to genome size. <i>ISME Journal</i> , 2018, 12, 2942-2953.	9.8	24
7	<i>Enterococcus faecalis</i> AHG0090 is a Genetically Tractable Bacterium and Produces a Secreted Peptidic Bioactive that Suppresses Nuclear Factor Kappa B Activation in Human Gut Epithelial Cells. <i>Frontiers in Immunology</i> , 2018, 9, 790.	4.8	15
8	Diet and the Microbiome. <i>Gastroenterology Clinics of North America</i> , 2017, 46, 49-60.	2.2	27
9	Colonic microbiota can promote rapid local improvement of murine colitis by thioguanine independently of T lymphocytes and host metabolism. <i>Gut</i> , 2017, 66, 59-69.	12.1	65
10	The gut bacterium and pathobiont <i>Bacteroides vulgatus</i> activates NF-ÎB in a human gut epithelial cell line in a strain and growth phase dependent manner. <i>Anaerobe</i> , 2017, 47, 209-217.	2.1	55
11	The Influence of the Microbiome on Early-Life Severe Viral Lower Respiratory Infections and Asthma—Food for Thought?. <i>Frontiers in Immunology</i> , 2017, 8, 156.	4.8	40
12	Methane matters: from blue-tinged moos, to boozy roos, and the health of humans too. <i>Animal Frontiers</i> , 2016, 6, 15-21.	1.7	1
13	Exploring the Bioactive Landscape of the Gut Microbiota to Identify Metabolites Underpinning Human Health. , 2016, , 49-82.		0
14	Differences down-under: alcohol-fueled methanogenesis by archaea present in Australian macropodids. <i>ISME Journal</i> , 2016, 10, 2376-2388.	9.8	41
15	Microbial metabolism of thiopurines: A method to measure thioguanine nucleotides. <i>Journal of Microbiological Methods</i> , 2016, 128, 102-107.	1.6	14
16	High Fat Diets Induce Colonic Epithelial Cell Stress and Inflammation that is Reversed by IL-22. <i>Scientific Reports</i> , 2016, 6, 28990.	3.3	243
17	971d Colonic Microbiota Can Promote Rapid Improvement of Murine Colitis by Thioguanine Independently of T-Lymphocytes and Host Metabolism. <i>Gastroenterology</i> , 2016, 150, S196-S197.	1.3	1
18	An (Anti)-Inflammatory Microbiota: Defining the Role in Inflammatory Bowel Disease?. <i>Digestive Diseases</i> , 2016, 34, 64-71.	1.9	13

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19	Towards an integrated understanding of the therapeutic utility of exclusive enteral nutrition in the treatment of Crohn's disease. <i>Food and Function</i> , 2016, 7, 1741-1751.	4.6	16
20	Isolation of Genetically Tractable Most-Wanted Bacteria by Metaparental Mating. <i>Scientific Reports</i> , 2015, 5, 13282.	3.3	23
21	Draft Genome Sequence of <i>Enterococcus faecium</i> PC4.1, a Clade B Strain Isolated from Human Feces. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
22	Draft Genome Sequence of <i>Enterococcus faecalis</i> PC1.1, a Candidate Probiotic Strain Isolated from Human Feces. <i>Genome Announcements</i> , 2013, 1, .	0.8	9
23	Genome Sequence of <i>Stenotrophomonas maltophilia</i> Strain AU12-09, Isolated from an Intravascular Catheter. <i>Genome Announcements</i> , 2013, 1, .	0.8	11
24	Extending the Cellulosome Paradigm: the Modular <i>Clostridium thermocellum</i> Cellulosomal Serpin PinA Is a Broad-Spectrum Inhibitor of Subtilisin-Like Proteases. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6173-6175.	3.1	11
25	Genome Sequence of <i>Staphylococcus epidermidis</i> Strain AU12-03, Isolated from an Intravascular Catheter. <i>Journal of Bacteriology</i> , 2012, 194, 6639-6639.	2.2	2
26	Draft Genome Sequence of <i>Treponema</i> sp. Strain JC4, a Novel Spirochete Isolated from the Bovine Rumen. <i>Journal of Bacteriology</i> , 2012, 194, 4130-4130.	2.2	33
27	Numerical ecology validates a biogeographical distribution and gender-based effect on mucosa-associated bacteria along the human colon. <i>ISME Journal</i> , 2011, 5, 801-809.	9.8	78
28	High-Yield and Phylogenetically Robust Methods of DNA Recovery for Analysis of Microbial Biofilms Adherent to Plant Biomass in the Herbivore Gut. <i>Microbial Ecology</i> , 2011, 61, 448-454.	2.8	33
29	The Effects from DNA Extraction Methods on the Evaluation of Microbial Diversity Associated with Human Colonic Tissue. <i>Microbial Ecology</i> , 2011, 61, 353-362.	2.8	55
30	Draft Genome Sequence of <i>Turicibacter sanguinis</i> PC909, Isolated from Human Feces. <i>Journal of Bacteriology</i> , 2011, 193, 1288-1289.	2.2	58
31	Draft Genome Sequence of <i>Bacteroides vulgatus</i> PC510, a Strain Isolated from Human Feces. <i>Journal of Bacteriology</i> , 2011, 193, 4025-4026.	2.2	12
32	The <i>hmuUV</i> genes of <i>Sinorhizobium meliloti</i> 2011 encode the permease and ATPase components of an ABC transport system for the utilization of both haem and the hydroxamate siderophores, ferrichrome and ferrioxamine B. <i>Molecular Microbiology</i> , 2008, 70, 1261-1273.	2.5	26
33	FoxB of <i>Pseudomonas aeruginosa</i> Functions in the Utilization of the Xenosiderophores Ferrichrome, Ferrioxamine B, and Schizokinen: Evidence for Transport Redundancy at the Inner Membrane. <i>Journal of Bacteriology</i> , 2007, 189, 284-287.	2.2	33
34	Cloning and heterologous expression of bovine pyroglutamyl peptidase type-1 in <i>Escherichia coli</i> : purification, biochemical and kinetic characterisation. <i>Molecular and Cellular Biochemistry</i> , 2007, 297, 189-197.	3.1	1
35	Identification and characterization of an iron-regulated gene, <i>chtA</i> , required for the utilization of the xenosiderophores aerobactin, rhizobactin 1021 and schizokinen by <i>Pseudomonas aeruginosa</i> . <i>Microbiology (United Kingdom)</i> , 2006, 152, 945-954.	1.8	47
36	Novel mobilizable prokaryotic two-hybrid system vectors for high-throughput protein interaction mapping in <i>Escherichia coli</i> by bacterial conjugation. <i>Nucleic Acids Research</i> , 2005, 33, e18-e18.	14.5	16

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37	RirA is the iron response regulator of the rhizobactin 1021 biosynthesis and transport genes in <i>Sinorhizobium meliloti</i> . FEMS Microbiology Letters, 2005, 246, 235-242.	1.8	51
38	Identification of <i>rhtX</i> and <i>fptX</i> , Novel Genes Encoding Proteins That Show Homology and Function in the Utilization of the Siderophores Rhizobactin 1021 by <i>Sinorhizobium meliloti</i> and Pyochelin by <i>Pseudomonas aeruginosa</i> , Respectively. Journal of Bacteriology, 2004, 186, 2996-3005.	2.2	78
39	Genetic Organization of the Region Encoding Regulation, Biosynthesis, and Transport of Rhizobactin 1021, a Siderophore Produced by <i>Sinorhizobium meliloti</i> . Journal of Bacteriology, 2001, 183, 2576-2585.	2.2	191