

Henning Sedorf

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

7,196
citations

304743

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330143

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42
all docs

42
docs citations

42
times ranked

10087
citing authors

#	ARTICLE	IF	CITATIONS
1	The Long-Term Stability of the Human Gut Microbiota. <i>Science</i> , 2013, 341, 1237439.	12.6	1,696
2	Methanogenic archaea: ecologically relevant differences in energy conservation. <i>Nature Reviews Microbiology</i> , 2008, 6, 579-591.	28.6	1,674
3	Characterizing a model human gut microbiota composed of members of its two dominant bacterial phyla. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5859-5864.	7.1	612
4	The genome of <i>Clostridium kluyveri</i> , a strict anaerobe with unique metabolic features. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2128-2133.	7.1	409
5	Coupled Ferredoxin and Crotonyl Coenzyme A (CoA) Reduction with NADH Catalyzed by the Butyryl-CoA Dehydrogenase/Etf Complex from <i>Clostridium kluyveri</i> . <i>Journal of Bacteriology</i> , 2008, 190, 843-850.	2.2	379
6	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	5.5	332
7	Bacteria from Diverse Habitats Colonize and Compete in the Mouse Gut. <i>Cell</i> , 2014, 159, 253-266.	28.9	324
8	Simultaneous Amplicon Sequencing to Explore Co-Occurrence Patterns of Bacterial, Archaeal and Eukaryotic Microorganisms in Rumen Microbial Communities. <i>PLoS ONE</i> , 2013, 8, e47879.	2.5	304
9	Two Different Bacterial Community Types Are Linked with the Low-Methane Emission Trait in Sheep. <i>PLoS ONE</i> , 2014, 9, e103171.	2.5	246
10	The Genome Sequence of <i>Methanosphaera stadtmanae</i> Reveals Why This Human Intestinal Archaeon Is Restricted to Methanol and H ₂ for Methane Formation and ATP Synthesis. <i>Journal of Bacteriology</i> , 2006, 188, 642-658.	2.2	245
11	RIM-DB: a taxonomic framework for community structure analysis of methanogenic archaea from the rumen and other intestinal environments. <i>PeerJ</i> , 2014, 2, e494.	2.0	140
12	More Than 200 Genes Required for Methane Formation from H ₂ and CO ₂ and Energy Conservation Are Present in <i>Methanothermobacter marburgensis</i> and <i>Methanothermobacter thermoautotrophicus</i> . <i>Archaea</i> , 2011, 2011, 1-23.	2.3	107
13	F420H ₂ oxidase (FprA) from <i>Methanobrevibacter arboriphilus</i> , a coenzyme F420-dependent enzyme involved in O ₂ detoxification. <i>Archives of Microbiology</i> , 2004, 182, 126-37.	2.2	100
14	Few Highly Abundant Operational Taxonomic Units Dominate within Rumen Methanogenic Archaeal Species in New Zealand Sheep and Cattle. <i>Applied and Environmental Microbiology</i> , 2015, 81, 986-995.	3.1	72
15	Structure of coenzyme F420H ₂ oxidase (FprA), a di-iron flavoprotein from methanogenic Archaea catalyzing the reduction of O ₂ to H ₂ O. <i>FEBS Journal</i> , 2007, 274, 1588-1599.	4.7	65
16	Phylogeny of Intestinal Ciliates, Including <i>Charonina ventriculi</i> , and Comparison of Microscopy and 18S rRNA Gene Pyrosequencing for Rumen Ciliate Community Structure Analysis. <i>Applied and Environmental Microbiology</i> , 2015, 81, 2433-2444.	3.1	65
17	Re -Citrate Synthase from <i>Clostridium kluyveri</i> Is Phylogenetically Related to Homocitrate Synthase and Isopropylmalate Synthase Rather Than to Si -Citrate Synthase. <i>Journal of Bacteriology</i> , 2007, 189, 4299-4304.	2.2	63
18	Characterizing the Interactions between a Naturally Primed Immunoglobulin A and Its Conserved <i>Bacteroides thetaiotaomicron</i> Species-specific Epitope in Gnotobiotic Mice. <i>Journal of Biological Chemistry</i> , 2015, 290, 12630-12649.	3.4	52

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19	Conformational Similarities in the $\hat{\nu}^2$ -Ionone Ring Region of the Rhodopsin Chromophore in Its Ground State and after Photoactivation to the Metarhodopsin-I Intermediate. <i>Biochemistry</i> , 2003, 42, 13371-13378.	2.5	46
20	Emergence of tigecycline- and eravacycline-resistant Tet(X4)-producing Enterobacteriaceae in the gut microbiota of healthy Singaporeans. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3480-3484.	3.0	34
21	Complete Genome Sequence of <i>Methanothermobacter marburgensis</i> , a Methanoarchaeon Model Organism. <i>Journal of Bacteriology</i> , 2010, 192, 5850-5851.	2.2	32
22	Insights into the microbiome of farmed Asian sea bass (<i>Lates calcarifer</i>) with symptoms of tenacibaculosis and description of <i>Tenacibaculum singaporense</i> sp. nov.. <i>Antonie Van Leeuwenhoek</i> , 2020, 113, 737-752.	1.7	28
23	Nutrient-based diet modifications impact on the gut microbiome of the Javan slow loris (<i>Nycticebus</i>) Tj ETQq1 1 0.784314 rgBT /Over	3.3	24
24	Cultivation and description of <i>Duncaniella dubosii</i> sp. nov., <i>Duncaniella freteri</i> sp. nov. and emended description of the species <i>Duncaniella muris</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 3105-3110.	1.7	23
25	<i>Muribaculum gordoncarteri</i> sp. nov., an anaerobic bacterium from the faeces of C57BL/6J mice. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2020, 70, 4725-4729.	1.7	19
26	Comparative Genomic Analysis of Members of the Genera <i>Methanosphaera</i> and <i>Methanobrevibacter</i> Reveals Distinct Clades with Specific Potential Metabolic Functions. <i>Archaea</i> , 2018, 2018, 1-9.	2.3	17
27	<i>Schaedlerella arabinosiphila</i> gen. nov., sp. nov., a D-arabinose-utilizing bacterium isolated from faeces of C57BL/6J mice that is a close relative of <i>Clostridium</i> species ASF 502. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 3616-3622.	1.7	12
28	Longitudinal Changes in Diet Cause Repeatable and Largely Reversible Shifts in Gut Microbial Communities of Laboratory Mice and Are Observed across Segments of the Entire Intestinal Tract. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5981.	4.1	10
29	Extended-Spectrum $\hat{\nu}^2$ -Lactamase-Producing and <i>mcr-1</i> -Positive <i>Escherichia coli</i> from the Gut Microbiota of Healthy Singaporeans. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0048821.	3.1	10
30	The Draft Genome of the Non-Host-Associated <i>Methanobrevibacter arboriphilus</i> Strain DH1 Encodes a Large Repertoire of Adhesin-Like Proteins. <i>Archaea</i> , 2017, 2017, 1-9.	2.3	7
31	Complete Genome Sequence of <i>Duncaniella muris</i> Strain B8, Isolated from the Feces of C57/BL6 Mice. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
32	Natural variation in methane emission of sheep fed on a lucerne pellet diet is unrelated to rumen ciliate community type. <i>Microbiology (United Kingdom)</i> , 2016, 162, 459-465.	1.8	7
33	Host Age Prediction from Fecal Microbiota Composition in Male C57BL/6J Mice. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	7
34	Si-face stereospecificity at C5 of coenzyme F420 for F420H2 oxidase from methanogenic Archaea as determined by mass spectrometry. <i>FEBS Journal</i> , 2005, 272, 5337-5342.	4.7	6
35	Mutual Exclusion of <i>Methanobrevibacter</i> Species in the Human Gut Microbiota Facilitates Directed Cultivation of a <i>Candidatus</i> <i>Methanobrevibacter Intestini</i> Representative. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	6
36	Draft Genome Sequences of <i>Methanobrevibacter curvatus</i> DSM11111, <i>Methanobrevibacter cuticularis</i> DSM11139, <i>Methanobrevibacter filiformis</i> DSM11501, and <i>Methanobrevibacter oralis</i> DSM7256. <i>Genome Announcements</i> , 2016, 4, .	0.8	3

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37	Complete Genome Sequence of Sponge-Associated <i>Tenacibaculum mesophilum</i> DSM 13764 ^T . Microbiology Resource Announcements, 2019, 8, .	0.6	2