

Joerg Graf

List of Publications by Year in descending order

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97
papers

5,094
citations

117625

34
h-index

98798

67
g-index

106
all docs

106
docs citations

106
times ranked

6293
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome Sequence of <i>Aeromonas hydrophila</i> ATCC 7966 T : Jack of All Trades. <i>Journal of Bacteriology</i> , 2006, 188, 8272-8282.	2.2	317
2	Age-related changes in the gut microbiota influence systemic inflammation and stroke outcome. <i>Annals of Neurology</i> , 2018, 84, 23-36.	5.3	293
3	Analysis, Optimization and Verification of Illumina-Generated 16S rRNA Gene Amplicon Surveys. <i>PLoS ONE</i> , 2014, 9, e94249.	2.5	287
4	Gut Microbiota-Derived Short-Chain Fatty Acids Promote Poststroke Recovery in Aged Mice. <i>Circulation Research</i> , 2020, 127, 453-465.	4.5	263
5	Effect of transposon-induced motility mutations on colonization of the host light organ by <i>Vibrio fischeri</i> . <i>Journal of Bacteriology</i> , 1994, 176, 6986-6991.	2.2	223
6	Bioinformatic Genome Comparisons for Taxonomic and Phylogenetic Assignments Using <i>Aeromonas</i> as a Test Case. <i>MBio</i> , 2014, 5, e02136.	4.1	209
7	Knowing your friends: invertebrate innate immunity fosters beneficial bacterial symbioses. <i>Nature Reviews Microbiology</i> , 2012, 10, 815-827.	28.6	186
8	Gut Microbiome Developmental Patterns in Early Life of Preterm Infants: Impacts of Feeding and Gender. <i>PLoS ONE</i> , 2016, 11, e0152751.	2.5	184
9	Host-derived amino acids support the proliferation of symbiotic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 1818-1822.	7.1	168
10	Ischemic stroke induces gut permeability and enhances bacterial translocation leading to sepsis in aged mice. <i>Aging</i> , 2016, 8, 1049-1063.	3.1	127
11	Directed Culturing of Microorganisms Using Metatranscriptomics. <i>MBio</i> , 2011, 2, e00012-11.	4.1	125
12	Role of Gut Microbiota and Short Chain Fatty Acids in Modulating Energy Harvest and Fat Partitioning in Youth. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 4367-4376.	3.6	124
13	Symbiosis of <i>Aeromonas veronii</i> Biovar <i>sobria</i> and <i>Hirudo medicinalis</i> , the Medicinal Leech: a Novel Model for Digestive Tract Associations. <i>Infection and Immunity</i> , 1999, 67, 1-7.	2.2	118
14	Evaluation of strategies for the assembly of diverse bacterial genomes using MinION long-read sequencing. <i>BMC Genomics</i> , 2019, 20, 23.	2.8	110
15	Comparison of the microbial communities in solid-state anaerobic digestion (SS-AD) reactors operated at mesophilic and thermophilic temperatures. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 969-980.	3.6	104
16	Evolutionary and Diagnostic Implications of Intragenomic Heterogeneity in the 16S rRNA Gene in <i>Aeromonas</i> Strains. <i>Journal of Bacteriology</i> , 2005, 187, 6561-6564.	2.2	89
17	Leeches and their microbiota: naturally simple symbiosis models. <i>Trends in Microbiology</i> , 2006, 14, 365-371.	7.7	89
18	Influence of Feeding Type on Gut Microbiome Development in Hospitalized Preterm Infants. <i>Nursing Research</i> , 2017, 66, 123-133.	1.7	89

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19	Low-abundant bacteria drive compositional changes in the gut microbiota after dietary alteration. <i>Microbiome</i> , 2018, 6, 86.	11.1	82
20	Meeting report: GenBank microbial genomic taxonomy workshop (12–13 May, 2015). <i>Standards in Genomic Sciences</i> , 2016, 11, .	1.5	81
21	Interaction between innate immune cells and a bacterial type III secretion system in mutualistic and pathogenic associations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 9481-9486.	7.1	79
22	Culture-Independent Characterization of the Digestive-Tract Microbiota of the Medicinal Leech Reveals a Tripartite Symbiosis. <i>Applied and Environmental Microbiology</i> , 2006, 72, 4775-4781.	3.1	72
23	Characterization of the Core and Caste-Specific Microbiota in the Termite, <i>Reticulitermes flavipes</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 171.	3.5	71
24	Early Life Experience and Gut Microbiome. <i>Advances in Neonatal Care</i> , 2015, 15, 314-323.	1.1	66
25	Further characterization of a type III secretion system (T3SS) and of a new effector protein from a clinical isolate of <i>Aeromonas hydrophila</i> —Part I. <i>Microbial Pathogenesis</i> , 2007, 43, 127-146.	2.9	65
26	Complex Evolutionary History of the <i>Aeromonas veronii</i> Group Revealed by Host Interaction and DNA Sequence Data. <i>PLoS ONE</i> , 2011, 6, e16751.	2.5	61
27	Novel effects of a transposon insertion in the <i>Vibrio fischeri</i> <i>glnD</i> gene: defects in iron uptake and symbiotic persistence in addition to nitrogen utilization. <i>Molecular Microbiology</i> , 2000, 37, 168-179.	2.5	60
28	Spatial and Temporal Population Dynamics of a Naturally Occurring Two-Species Microbial Community inside the Digestive Tract of the Medicinal Leech. <i>Applied and Environmental Microbiology</i> , 2007, 73, 1984-1991.	3.1	53
29	Effect of Gut Microbiota and <i>PNPLA3</i> rs738409 Variant on Nonalcoholic Fatty Liver Disease (NAFLD) in Obese Youth. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e3575-e3585.	3.6	51
30	Impact of different ratios of feedstock to liquid anaerobic digestion effluent on the performance and microbiome of solid-state anaerobic digesters digesting corn stover. <i>Bioresource Technology</i> , 2016, 200, 744-752.	9.6	47
31	The Type II Secretion System Is Essential for Erythrocyte Lysis and Gut Colonization by the Leech Digestive Tract Symbiont <i>Aeromonas veronii</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 597-603.	3.1	45
32	Ingested Blood Contributes to the Specificity of the Symbiosis of <i>Aeromonas veronii</i> Biovar <i>Sobria</i> and <i>Hirudo medicinalis</i> , the Medicinal Leech. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4735-4741.	3.1	44
33	Medicinal leeches and the microsurgeon: A four-year study, clinical series and risk benefit review. <i>Microsurgery</i> , 2011, 31, 281-287.	1.3	44
34	The Family Rikenellaceae. , 2014, , 857-859.		43
35	Identification of <i>Aeromonas veronii</i> Genes Required for Colonization of the Medicinal Leech, <i>Hirudo verbana</i> . <i>Journal of Bacteriology</i> , 2007, 189, 6763-6772.	2.2	41
36	Preventing infective complications following leech therapy: Is practice keeping pace with current research?. <i>Microsurgery</i> , 2009, 29, 619-625.	1.3	35

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37	Stratified bacterial community in the bladder of the medicinal leech, <i>Hirudo verbana</i> . Environmental Microbiology, 2009, 11, 2758-2770.	3.8	35
38	Characterization of the Digestive-Tract Microbiota of <i>Hirudo orientalis</i> , a European Medicinal Leech. Applied and Environmental Microbiology, 2008, 74, 6151-6154.	3.1	34
39	Bacterial symbioses of the medicinal leech <i>Hirudo verbana</i> . Gut Microbes, 2012, 3, 322-331.	9.8	34
40	Diverse Restriction Fragment Length Polymorphism Patterns of the PCR-Amplified 16S rRNA Genes in <i>Aeromonas veronii</i> Strains and Possible Misidentification of <i>Aeromonas</i> Species. Journal of Clinical Microbiology, 1999, 37, 3194-3197.	3.9	33
41	Mucinivorans hirudinis gen. nov., sp. nov., an anaerobic, mucin-degrading bacterium isolated from the digestive tract of the medicinal leech <i>Hirudo verbana</i> . International Journal of Systematic and Evolutionary Microbiology, 2015, 65, 990-995.	1.7	32
42	Factors influencing bacterial microbiome composition in a wild non-human primate community in Taï National Park, Côte d'Ivoire. ISME Journal, 2018, 12, 2559-2574.	9.8	31
43	Exposure to pairs of <i>Aeromonas</i> strains enhances virulence in the <i>Caenorhabditis elegans</i> infection model. Frontiers in Microbiology, 2015, 6, 1218.	3.5	30
44	Oxidized Derivatives of Linoleic Acid in Pediatric Metabolic Syndrome: Is Their Pathogenic Role Modulated by the Genetic Background and the Gut Microbiota?. Antioxidants and Redox Signaling, 2019, 30, 241-250.	5.4	30
45	Complement Resistance Is Essential for Colonization of the Digestive Tract of <i>Hirudo medicinalis</i> by <i>Aeromonas</i> Strains. Applied and Environmental Microbiology, 2003, 69, 4268-4271.	3.1	29
46	Prevalence of Genes Encoding the Type Three Secretion System and the Effectors AexT and AexU in the <i>Aeromonas veronii</i> Group. DNA and Cell Biology, 2009, 28, 383-388.	1.9	28
47	Lessons from Digestive-Tract Symbioses Between Bacteria and Invertebrates. Annual Review of Microbiology, 2016, 70, 375-393.	7.3	28
48	Virulence factor-activity relationships (VFAR) with specific emphasis on <i>Aeromonas</i> species (spp.). Journal of Water and Health, 2009, 07, S29.	2.6	27
49	Metagenomic analysis of the medicinal leech gut microbiota. Frontiers in Microbiology, 2014, 5, 151.	3.5	27
50	Delineation of Taxonomic Species within Complex of Species: <i>Aeromonas media</i> and Related Species as a Test Case. Frontiers in Microbiology, 2017, 8, 621.	3.5	27
51	Host Matters: Medicinal Leech Digestive-Tract Symbionts and Their Pathogenic Potential. Frontiers in Microbiology, 2016, 7, 1569.	3.5	25
52	Low-Level Antimicrobials in the Medicinal Leech Select for Resistant Pathogens That Spread to Patients. MBio, 2018, 9, .	4.1	25
53	Characterization of a catalase gene from <i>Aeromonas veronii</i> , the digestive-tract symbiont of the medicinal leech. Microbiology (United Kingdom), 2007, 153, 1897-1906.	1.8	23
54	Early-life antibiotics attenuate regulatory T cell generation and increase the severity of murine house dust mite-induced asthma. Pediatric Research, 2018, 84, 426-434.	2.3	23

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55	High-Resolution Differentiation of Enteric Bacteria in Premature Infant Fecal Microbiomes Using a Novel rRNA Amplicon. <i>MBio</i> , 2021, 12, .	4.1	23
56	Symbiont Succession during Embryonic Development of the European Medicinal Leech, <i>Hirudo verbana</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 6890-6895.	3.1	22
57	Draft Genome Sequence of <i>Aeromonas veronii</i> Hm21, a Symbiotic Isolate from the Medicinal Leech Digestive Tract. <i>Genome Announcements</i> , 2013, 1, .	0.8	22
58	Complete Genome Sequence of <i>Yersinia ruckeri</i> Strain CSF007-82, Etiologic Agent of Red Mouth Disease in Salmonid Fish. <i>Genome Announcements</i> , 2015, 3, .	0.8	21
59	Novel Role for <i>Aeromonas jandaei</i> as a Digestive Tract Symbiont of the North American Medicinal Leech. <i>Applied and Environmental Microbiology</i> , 2007, 73, 655-658.	3.1	20
60	Shifting Paradigm on <i>Bacillus thuringiensis</i> Toxin and a Natural Model for <i>Enterococcus faecalis</i> Septicemia. <i>MBio</i> , 2011, 2, .	4.1	20
61	Identification and characterization of putative <i>Aeromonas</i> spp. T3SS effectors. <i>PLoS ONE</i> , 2019, 14, e0214035.	2.5	20
62	Insights from shotgun metagenomics into bacterial species and metabolic pathways associated with NAFLD in obese youth. <i>Hepatology Communications</i> , 2022, 6, 1962-1974.	4.3	20
63	<i>Helicobacter</i> sp. <i>Flexispira</i> Bacteremia in an Immunocompetent Young Adult. <i>Journal of Clinical Microbiology</i> , 2001, 39, 1716-1720.	3.9	19
64	Characterization of the Digestive Tract Microbiota of <i>Hirudo orientalis</i> (Medicinal Leech) and Antibiotic Resistance Profile. <i>Plastic and Reconstructive Surgery</i> , 2014, 133, 408e-418e.	1.4	19
65	Identification of iron and heme utilization genes in <i>Aeromonas</i> and their role in the colonization of the leech digestive tract. <i>Frontiers in Microbiology</i> , 2015, 6, 763.	3.5	19
66	The effect of symbionts on the physiology of <i>Hirudo medicinalis</i> , the medicinal leech. <i>Invertebrate Reproduction and Development</i> , 2002, 41, 269-275.	0.8	18
67	Isolation and Identification of Sulphite- and Iron Reducing, Hydrogenase Positive Facultative Anaerobes from Cooling Water Systems. <i>Systematic and Applied Microbiology</i> , 1998, 21, 297-305.	2.8	16
68	The flagellar master operon <i>flh</i> is a pleiotropic regulator involved in motility and virulence of the fish pathogen <i>Yersinia ruckeri</i> . <i>Journal of Applied Microbiology</i> , 2017, 122, 578-588.	3.1	15
69	Draft Genome Sequence of the Fish Pathogen <i>Flavobacterium columnare</i> Strain CSF-298-10. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
70	Flagellar regulation mediated by the Rcs pathway is required for virulence in the fish pathogen <i>Yersinia ruckeri</i> . <i>Fish and Shellfish Immunology</i> , 2019, 91, 306-314.	3.6	12
71	Draft Genome Sequence of <i>Lactococcus garvieae</i> Strain PAQ102015-99, an Outbreak Strain Isolated from a Commercial Trout Farm in the Northwestern United States. <i>Genome Announcements</i> , 2016, 4, .	0.8	11
72	Microbiome Analyses for Toxicological Studies. <i>Current Protocols in Toxicology</i> / Editorial Board, Mahin D Maines (editor-in-chief) [et Al], 2018, 77, e53.	1.1	11

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73	Investigation into the Physiologies of <i>Aeromonas veronii</i> in vitro and Inside the Digestive Tract of the Medicinal Leech Using RNA-seq. <i>Biological Bulletin</i> , 2012, 223, 155-166.	1.8	10
74	Comparative and Evolutionary Genomics of Isolates Provide Insight into the Pathoadaptation of <i>Aeromonas</i> . <i>Genome Biology and Evolution</i> , 2020, 12, 535-552.	2.5	10
75	Systematic Detection of Large-Scale Multigene Horizontal Transfer in Prokaryotes. <i>Molecular Biology and Evolution</i> , 2021, 38, 2639-2659.	8.9	10
76	PmtA Regulates Pyocyanin Expression and Biofilm Formation in <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 789765.	3.5	10
77	Effect of organic loading on the microbiota in a temperature-phased anaerobic digestion (TPAD) system co-digesting dairy manure and waste whey. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 8777-8792.	3.6	9
78	Molecular Requirements for the Colonization of <i>Hirudo medicinalis</i> by <i>Aeromonas veronii</i> . , 2006, 41, 291-303.		7
79	Complete Genome Sequence of the Novel Leech Symbiont <i>Mucinivorans hirudinis</i> M3 . <i>Genome Announcements</i> , 2015, 3, .	0.8	6
80	Genome-driven evaluation and redesign of PCR tools for improving the detection of virulence-associated genes in aeromonads. <i>PLoS ONE</i> , 2018, 13, e0201428.	2.5	6
81	Detecting Flavobacterial Fish Pathogens in the Environment via High-Throughput Community Analysis. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0209221.	3.1	6
82	An improved cell recovery method for iron oxidizing bacterial (IOB) enrichments. <i>Journal of Microbiological Methods</i> , 2008, 72, 235-240.	1.6	5
83	<i>Macrobdella decora</i> : Old World Leech Gut Microbial Community Structure Conserved in a New World Leech. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	4
84	Draft Genome Sequences of <i>Dysgonomonas</i> sp. Strains BGC7 and HGC4, Isolated from the Hindgut of a Lower Termite. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	4
85	Effects of Host Species Identity and Diet on the Biodiversity of the Microbiota in Puerto Rican Bats. <i>Current Microbiology</i> , 2021, 78, 3526-3540.	2.2	2
86	Seasonal and spatial variations in microbial activity at various phylogenetic resolutions at a groundwater – surface water interface. <i>Canadian Journal of Microbiology</i> , 2014, 60, 277-286.	1.7	1
87	Draft Genome Sequence of <i>Aeromonas lusitana</i> sp. nov. Strain DSM 24905 T , Isolated from a Hot Spring in Vila-Real, Portugal. <i>Genome Announcements</i> , 2018, 6, .	0.8	1
88	Closed Genome Sequence of <i>Aeromonas veronii</i> Strain Hm21, an Isolate from the Medicinal Leech <i>Hirudo verbana</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
89	Draft Genome Sequence of <i>Aeromonas popoffii</i> ID682, Isolated from a Natural Water Source in Idaho. <i>Microbiology Resource Announcements</i> , 2021, 10, e0044521.	0.6	1
90	Draft Genome Sequence of <i>Janthinobacterium lividum</i> ID1246, Isolated from a Rainbow Trout Hatchery Biofilm. <i>Microbiology Resource Announcements</i> , 2021, 10, e0044421.	0.6	1

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91	Simultaneous Single-Cell Genome and Transcriptome Sequencing of Termite Hindgut Protists Reveals Metabolic and Evolutionary Traits of Their Endosymbionts. <i>MSphere</i> , 2022, 7, e0002122.	2.9	1
92	Draft Genome Sequence of <i>Pedobacter</i> sp. Strain Hv1, an Isolate from Medicinal Leech Mucosal Castings. <i>Genome Announcements</i> , 2015, 3, .	0.8	0
93	Metabolite Overproduction through Engineering and Optimization of Microbiome Composition Dynamics. , 2016, , .		0
94	Draft Genome Sequence of <i>Aeromonas cavernicola</i> sp. nov. DSM 24474 ^T , Isolated from a Cavern Brook in the Moravia Region of the Czech Republic. <i>Genome Announcements</i> , 2018, 6, .	0.8	0
95	Soil DNA Typing in Forensic Science. <i>International Forensic Science and Investigation Series</i> , 2007, , 167-183.	0.0	0
96	<i>Aeromonas</i> , a Multifaceted Microbe: Beneficial Associations with Animals. , 2015, , 109-116.		0
97	1819-P: Gut Microbiota and PNPLA3 RS738409 Associated with Nonalcoholic Fatty Liver Disease in Obese Youth. <i>Diabetes</i> , 2020, 69, 1819-P.	0.6	0