

Joerg Graf

List of Publications by Year in descending order

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97
papers

5,094
citations

117453

34
h-index

98622

67
g-index

106
all docs

106
docs citations

106
times ranked

6293
citing authors

#	ARTICLE	IF	CITATIONS
1	Detecting Flavobacterial Fish Pathogens in the Environment via High-Throughput Community Analysis. Applied and Environmental Microbiology, 2022, 88, AEM0209221.	1.4	6
2	Simultaneous Single-Cell Genome and Transcriptome Sequencing of Termite Hindgut Protists Reveals Metabolic and Evolutionary Traits of Their Endosymbionts. MSphere, 2022, 7, e0002122.	1.3	1
3	Insights from shotgun metagenomics into bacterial species and metabolic pathways associated with NAFLD in obese youth. Hepatology Communications, 2022, 6, 1962-1974.	2.0	20
4	High-Resolution Differentiation of Enteric Bacteria in Premature Infant Fecal Microbiomes Using a Novel rRNA Amplicon. MBio, 2021, 12, .	1.8	23
5	Systematic Detection of Large-Scale Multigene Horizontal Transfer in Prokaryotes. Molecular Biology and Evolution, 2021, 38, 2639-2659.	3.5	10
6	<i>Macrobodella decora</i> : Old World Leech Gut Microbial Community Structure Conserved in a New World Leech. Applied and Environmental Microbiology, 2021, 87, .	1.4	4
7	Draft Genome Sequence of <i>Aeromonas popoffii</i> ID682, Isolated from a Natural Water Source in Idaho. Microbiology Resource Announcements, 2021, 10, e0044521.	0.3	1
8	Draft Genome Sequence of <i>Janthinobacterium lividum</i> ID1246, Isolated from a Rainbow Trout Hatchery Biofilm. Microbiology Resource Announcements, 2021, 10, e0044421.	0.3	1
9	Effects of Host Species Identity and Diet on the Biodiversity of the Microbiota in Puerto Rican Bats. Current Microbiology, 2021, 78, 3526-3540.	1.0	2
10	Draft Genome Sequences of <i>Dysgonomonas</i> sp. Strains BGC7 and HGC4, Isolated from the Hindgut of a Lower Termite. Microbiology Resource Announcements, 2021, 10, .	0.3	4
11	PmtA Regulates Pyocyanin Expression and Biofilm Formation in <i>Pseudomonas aeruginosa</i> . Frontiers in Microbiology, 2021, 12, 789765.	1.5	10
12	Closed Genome Sequence of <i>Aeromonas veronii</i> Strain Hm21, an Isolate from the Medicinal Leech <i>Hirudo verbana</i> . Microbiology Resource Announcements, 2020, 9, .	0.3	1
13	Gut Microbiota-Derived Short-Chain Fatty Acids Promote Poststroke Recovery in Aged Mice. Circulation Research, 2020, 127, 453-465.	2.0	263
14	Effect of Gut Microbiota and <i>PNPLA3</i> rs738409 Variant on Nonalcoholic Fatty Liver Disease (NAFLD) in Obese Youth. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e3575-e3585.	1.8	51
15	Comparative and Evolutionary Genomics of Isolates Provide Insight into the Pathoadaptation of <i>Aeromonas</i> . Genome Biology and Evolution, 2020, 12, 535-552.	1.1	10
16	1819-P: Gut Microbiota and <i>PNPLA3</i> RS738409 Associated with Nonalcoholic Fatty Liver Disease in Obese Youth. Diabetes, 2020, 69, 1819-P.	0.3	0
17	Identification and characterization of putative <i>Aeromonas</i> spp. T3SS effectors. PLoS ONE, 2019, 14, e0214035.	1.1	20
18	Flagellar regulation mediated by the Rcs pathway is required for virulence in the fish pathogen <i>Yersinia ruckeri</i> . Fish and Shellfish Immunology, 2019, 91, 306-314.	1.6	12

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19	Evaluation of strategies for the assembly of diverse bacterial genomes using MinION long-read sequencing. <i>BMC Genomics</i> , 2019, 20, 23.	1.2	110
20	Oxidized Derivatives of Linoleic Acid in Pediatric Metabolic Syndrome: Is Their Pathogenic Role Modulated by the Genetic Background and the Gut Microbiota?. <i>Antioxidants and Redox Signaling</i> , 2019, 30, 241-250.	2.5	30
21	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
22	Early-life antibiotics attenuate regulatory T cell generation and increase the severity of murine house dust mite-induced asthma. <i>Pediatric Research</i> , 2018, 84, 426-434.	1.1	23
23	Low-Level Antimicrobials in the Medicinal Leech Select for Resistant Pathogens That Spread to Patients. <i>MBio</i> , 2018, 9, .	1.8	25
24	Microbiome Analyses for Toxicological Studies. <i>Current Protocols in Toxicology / Editorial Board</i> , Mahin D Maines (editor-in-chief) [et Al], 2018, 77, e53.	1.1	11
25	Age-related changes in the gut microbiota influence systemic inflammation and stroke outcome. <i>Annals of Neurology</i> , 2018, 84, 23-36.	2.8	293
26	Low-abundant bacteria drive compositional changes in the gut microbiota after dietary alteration. <i>Microbiome</i> , 2018, 6, 86.	4.9	82
27	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.	1.1	6
28	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
29	Factors influencing bacterial microbiome composition in a wild non-human primate community in Taï National Park, Côte d'Ivoire. <i>ISME Journal</i> , 2018, 12, 2559-2574.	4.4	31
30	Draft Genome Sequence of the Fish Pathogen <i>Flavobacterium columnare</i> Strain CSF-298-10. <i>Genome Announcements</i> , 2017, 5, .	0.8	12
31	Influence of Feeding Type on Gut Microbiome Development in Hospitalized Preterm Infants. <i>Nursing Research</i> , 2017, 66, 123-133.	0.8	89
32	The flagellar master operon <i>flhDC</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.	1.4	15
33	Delineation of Taxonomic Species within Complex of Species: <i>Aeromonas media</i> and Related Species as a Test Case. <i>Frontiers in Microbiology</i> , 2017, 8, 621.	1.5	27
34	Characterization of the Core and Caste-Specific Microbiota in the Termite, <i>Reticulitermes flavipes</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 171.	1.5	71
35	Host Matters: Medicinal Leech Digestive-Tract Symbionts and Their Pathogenic Potential. <i>Frontiers in Microbiology</i> , 2016, 7, 1569.	1.5	25
36	Ischemic stroke induces gut permeability and enhances bacterial translocation leading to sepsis in aged mice. <i>Aging</i> , 2016, 8, 1049-1063.	1.4	127

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37	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
38	Lessons from Digestive-Tract Symbioses Between Bacteria and Invertebrates. <i>Annual Review of Microbiology</i> , 2016, 70, 375-393.	2.9	28
39	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.	1.8	124
40	Metabolite Overproduction through Engineering and Optimization of Microbiome Composition Dynamics. , 2016, , .		0
41	Meeting report: GenBank microbial genomic taxonomy workshop (12–13 May, 2015). <i>Standards in Genomic Sciences</i> , 2016, 11, .	1.5	81
42	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.	4.8	47
43	Gut Microbiome Developmental Patterns in Early Life of Preterm Infants: Impacts of Feeding and Gender. <i>PLoS ONE</i> , 2016, 11, e0152751.	1.1	184
44	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
45	Early Life Experience and Gut Microbiome. <i>Advances in Neonatal Care</i> , 2015, 15, 314-323.	0.5	66
46	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.	1.5	19
47	Exposure to pairs of <i>Aeromonas</i> strains enhances virulence in the <i>Caenorhabditis elegans</i> infection model. <i>Frontiers in Microbiology</i> , 2015, 6, 1218.	1.5	30
48	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
49	Complete Genome Sequence of the Novel Leech Symbiont <i>Mucinivorans hirudinis</i> M3 ^T . <i>Genome Announcements</i> , 2015, 3, .	0.8	6
50	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.	1.7	104
51	<i>Mucinivorans hirudinis</i> gen. nov., sp. nov., an anaerobic, mucin-degrading bacterium isolated from the digestive tract of the medicinal leech <i>Hirudo verbana</i> . <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 990-995.	0.8	32
52	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.	1.7	9
53	<i>Aeromonas</i> , a Multifaceted Microbe: Beneficial Associations with Animals. , 2015, , 109-116.		0
54	Metagenomic analysis of the medicinal leech gut microbiota. <i>Frontiers in Microbiology</i> , 2014, 5, 151.	1.5	27

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55	Bioinformatic Genome Comparisons for Taxonomic and Phylogenetic Assignments Using <i>Aeromonas</i> as a Test Case. MBio, 2014, 5, e02136.	1.8	209
56	Analysis, Optimization and Verification of Illumina-Generated 16S rRNA Gene Amplicon Surveys. PLoS ONE, 2014, 9, e94249.	1.1	287
57	Seasonal and spatial variations in microbial activity at various phylogenetic resolutions at a groundwater – surface water interface. Canadian Journal of Microbiology, 2014, 60, 277-286.	0.8	1
58	Characterization of the Digestive Tract Microbiota of <i>Hirudo orientalis</i> (Medicinal Leech) and Antibiotic Resistance Profile. Plastic and Reconstructive Surgery, 2014, 133, 408e-418e.	0.7	19
59	The Family Rikenellaceae. , 2014, , 857-859.		43
60	Draft Genome Sequence of <i>Aeromonas veronii</i> Hm21, a Symbiotic Isolate from the Medicinal Leech Digestive Tract. Genome Announcements, 2013, 1, .	0.8	22
61	Bacterial symbioses of the medicinal leech <i>Hirudo verbana</i> . Gut Microbes, 2012, 3, 322-331.	4.3	34
62	Investigation into the Physiologies of <i>Aeromonas veronii</i> in vitro and Inside the Digestive Tract of the Medicinal Leech Using RNA-seq. Biological Bulletin, 2012, 223, 155-166.	0.7	10
63	Knowing your friends: invertebrate innate immunity fosters beneficial bacterial symbioses. Nature Reviews Microbiology, 2012, 10, 815-827.	13.6	186
64	Medicinal leeches and the microsurgeon: A four-year study, clinical series and risk benefit review. Microsurgery, 2011, 31, 281-287.	0.6	44
65	The Type II Secretion System Is Essential for Erythrocyte Lysis and Gut Colonization by the Leech Digestive Tract Symbiont <i>Aeromonas veronii</i> . Applied and Environmental Microbiology, 2011, 77, 597-603.	1.4	45
66	Shifting Paradigm on <i>Bacillus thuringiensis</i> Toxin and a Natural Model for <i>Enterococcus faecalis</i> Septicemia. MBio, 2011, 2, .	1.8	20
67	Directed Culturing of Microorganisms Using Metatranscriptomics. MBio, 2011, 2, e00012-11.	1.8	125
68	Complex Evolutionary History of the <i>Aeromonas veronii</i> Group Revealed by Host Interaction and DNA Sequence Data. PLoS ONE, 2011, 6, e16751.	1.1	61
69	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.	0.9	28
70	Symbiont Succession during Embryonic Development of the European Medicinal Leech, <i>Hirudo verbana</i> . Applied and Environmental Microbiology, 2009, 75, 6890-6895.	1.4	22
71	Preventing infective complications following leech therapy: Is practice keeping pace with current research?. Microsurgery, 2009, 29, 619-625.	0.6	35
72	Stratified bacterial community in the bladder of the medicinal leech, <i>Hirudo verbana</i> . Environmental Microbiology, 2009, 11, 2758-2770.	1.8	35

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73	Virulence factor-activity relationships (VFAR) with specific emphasis on <i>Aeromonas</i> species (spp.). <i>Journal of Water and Health</i> , 2009, 07, S29.	1.1	27
74	An improved cell recovery method for iron oxidizing bacterial (IOB) enrichments. <i>Journal of Microbiological Methods</i> , 2008, 72, 235-240.	0.7	5
75	Characterization of the Digestive-Tract Microbiota of <i>Hirudo orientalis</i> , a European Medicinal Leech. <i>Applied and Environmental Microbiology</i> , 2008, 74, 6151-6154.	1.4	34
76	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.	3.3	79
77	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.	1.0	41
78	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.	1.4	20
79	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.	1.4	53
80	Characterization of a catalase gene from <i>Aeromonas veronii</i> , the digestive-tract symbiont of the medicinal leech. <i>Microbiology (United Kingdom)</i> , 2007, 153, 1897-1906.	0.7	23
81	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.	1.3	65
82	Soil DNA Typing in Forensic Science. <i>International Forensic Science and Investigation Series</i> , 2007, , 167-183.	0.0	0
83	Genome Sequence of <i>Aeromonas hydrophila</i> ATCC 7966 T : Jack of All Trades. <i>Journal of Bacteriology</i> , 2006, 188, 8272-8282.	1.0	317
84	Leeches and their microbiota: naturally simple symbiosis models. <i>Trends in Microbiology</i> , 2006, 14, 365-371.	3.5	89
85	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.	1.4	72
86	Molecular Requirements for the Colonization of <i>Hirudo medicinalis</i> by <i>Aeromonas veronii</i> . , 2006, 41, 291-303.		7
87	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.	1.0	89
88	Complement Resistance Is Essential for Colonization of the Digestive Tract of <i>Hirudo medicinalis</i> by <i>Aeromonas</i> Strains. <i>Applied and Environmental Microbiology</i> , 2003, 69, 4268-4271.	1.4	29
89	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.	0.3	18
90	<i>Helicobacter</i> sp. <i>Flexispira</i> Bacteremia in an Immunocompetent Young Adult. <i>Journal of Clinical Microbiology</i> , 2001, 39, 1716-1720.	1.8	19

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91	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.	1.2	60
92	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.	1.4	44
93	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.	1.0	118
94	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. <i>Journal of Clinical Microbiology</i> , 1999, 37, 3194-3197.	1.8	33
95	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.	1.2	16
96	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.	3.3	168
97	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.	1.0	223