

Robert Hertel

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

424
citations

686830

13
h-index

839053

18
g-index

34
all docs

34
docs citations

34
times ranked

418
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA-Seq of <i>Bacillus licheniformis</i> : active regulatory RNA features expressed within a productive fermentation. <i>BMC Genomics</i> , 2013, 14, 667.	1.2	40
2	A CRISPR-Cas9-Based Toolkit for Fast and Precise In Vivo Genetic Engineering of <i>Bacillus subtilis</i> Phages. <i>Viruses</i> , 2018, 10, 241.	1.5	38
3	Nitrile-Degrading Bacteria Isolated from Compost. <i>Frontiers in Environmental Science</i> , 2017, 5, .	1.5	33
4	Tripartite species interaction: eukaryotic hosts suffer more from phage susceptible than from phage resistant bacteria. <i>BMC Evolutionary Biology</i> , 2017, 17, 98.	3.2	27
5	The life cycle of SP ¹² and related phages. <i>Archives of Virology</i> , 2021, 166, 2119-2130.	0.9	27
6	Characterization of <i>Bacillus subtilis</i> Viruses vB_BsuM-Goe2 and vB_BsuM-Goe3. <i>Viruses</i> , 2017, 9, 146.	1.5	26
7	Genome-Based Identification of Active Prophage Regions by Next Generation Sequencing in <i>Bacillus licheniformis</i> DSM13. <i>PLoS ONE</i> , 2015, 10, e0120759.	1.1	22
8	Living in a Puddle of Mud: Isolation and Characterization of Two Novel Caulobacteraceae Strains <i>Brevundimonas pondensis</i> sp. nov. and <i>Brevundimonas goettingensis</i> sp. nov.. <i>Applied Microbiology</i> , 2021, 1, 38-59.	0.7	20
9	The <i>Bacillus</i> phage <scp>SP ¹² </scp> and its relatives: a temperate phage model system reveals new strains, species, prophage integration loci, conserved proteins and lysogeny management components. <i>Environmental Microbiology</i> , 2022, 24, 2098-2118.	1.8	19
10	Impact of Nitriles on Bacterial Communities. <i>Frontiers in Environmental Science</i> , 2019, 7, .	1.5	18
11	First Complete Genome Sequences of <i>Janthinobacterium lividum</i> EIF1 and EIF2 and Their Comparative Genome Analysis. <i>Genome Biology and Evolution</i> , 2020, 12, 1782-1788.	1.1	15
12	Molecular Identification and In Vitro Plant Growth-Promoting Activities of Culturable Potato (<i>Solanum tuberosum</i> L.) Rhizobacteria in Tanzania. <i>Potato Research</i> , 2021, 64, 67-95.	1.2	15
13	Small RNA mediated repression of subtilisin production in <i>Bacillus licheniformis</i> . <i>Scientific Reports</i> , 2017, 7, 5699.	1.6	13
14	Genomic Analysis of the Recent Viral Isolate vB_BthP-Goe4 Reveals Increased Diversity of ϕ 29-Like Phages. <i>Viruses</i> , 2018, 10, 624.	1.5	13
15	Closely Related <i>Vibrio alginolyticus</i> Strains Encode an Identical Repertoire of Caudovirales-Like Regions and Filamentous Phages. <i>Viruses</i> , 2020, 12, 1359.	1.5	13
16	Phage vB_BsuP-Goe1: the smallest identified lytic phage of <i>Bacillus subtilis</i> . <i>FEMS Microbiology Letters</i> , 2016, 363, fnw208.	0.7	12
17	From sequence to function: a new workflow for nitrilase identification. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 4957-4970.	1.7	9
18	A CRISPR-Cas9 tool to explore the genetics of <i>Bacillus subtilis</i> phages. <i>Letters in Applied Microbiology</i> , 2020, 71, 588-595.	1.0	8

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19	Down in the pond: Isolation and characterization of a new <i>Serratia marcescens</i> strain (LVF3) from the surface water near frog's lettuce (<i>Groenlandia densa</i>). <i>PLoS ONE</i> , 2021, 16, e0259673.	1.1	8
20	Complete genome sequence of the virus isolate vB_BthM-Goe5 infecting <i>Bacillus thuringiensis</i> . <i>Archives of Virology</i> , 2019, 164, 1485-1488.	0.9	6
21	Conjugative reporter system for the use in <i>Bacillus licheniformis</i> and closely related <i>Bacilli</i> . <i>Letters in Applied Microbiology</i> , 2015, 60, 162-167.	1.0	5
22	Complete Genome Sequence of vB_BveP-Goe6, a Virus Infecting <i>Bacillus velezensis</i> FZB42. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
23	Chances and limitations when uncovering essential and non-essential genes of <i>Bacillus subtilis</i> phages with CRISPR-Cas9. <i>Environmental Microbiology Reports</i> , 2021, 13, 934-944.	1.0	5
24	Phage vB_BmeM-Goe8 infecting <i>Bacillus megaterium</i> DSM319. <i>Archives of Virology</i> , 2020, 165, 515-517.	0.9	4
25	Complete Genome Sequence of the Prototrophic <i>Bacillus subtilis</i> subsp. <i>subtilis</i> Strain SP1. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
26	Draft Genome Sequence of the Type Strain <i>Bacillus subtilis</i> subsp. <i>subtilis</i> DSM10. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	4
27	Phage vB_BveM-Goe7 represents a new genus in the subfamily Bastillevirinae. <i>Archives of Virology</i> , 2020, 165, 959-962.	0.9	3
28	Whole-Genome Sequences of Three Plant Growth-Promoting Rhizobacteria Isolated from <i>Solanum tuberosum</i> L. Rhizosphere in Tanzania. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
29	Complete Genome Sequence of <i>Stenotrophomonas indicatrix</i> DAIF1. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
30	Complete Genome Sequence of <i>Kinneretia</i> sp. Strain DAIF2, Isolated from a Freshwater Pond. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.3	2
31	Manufacturing triple-isotopically labeled microbial necromass to track C, N and P cycles in terrestrial ecosystems. <i>Applied Soil Ecology</i> , 2022, 171, 104322.	2.1	2