

Steve Petrovski

List of Publications by Year in descending order

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Version: 2024-02-01

68
papers

1,788
citations

331259

21
h-index

301761

39
g-index

68
all docs

68
docs citations

68
times ranked

1745
citing authors

#	ARTICLE	IF	CITATIONS
1	Elevated atmospheric CO ₂ alters the microbial community composition and metabolic potential to mineralize organic phosphorus in the rhizosphere of wheat. <i>Microbiome</i> , 2022, 10, 12.	4.9	24
2	MiDAS 4: A global catalogue of full-length 16S rRNA gene sequences and taxonomy for studies of bacterial communities in wastewater treatment plants. <i>Nature Communications</i> , 2022, 13, 1908.	5.8	114
3	Biological control of problematic bacterial populations causing foaming in activated sludge wastewater treatment plants—phage therapy and beyond. <i>Letters in Applied Microbiology</i> , 2022, 75, 776-784.	1.0	3
4	The phylogeny, ecology and ecophysiology of the glycogen accumulating organism (GAO) <i>DeFluviicoccus</i> in wastewater treatment plants. <i>Water Research</i> , 2022, 221, 118729.	5.3	25
5	Variants of <i>Streptococcus pneumoniae</i> Serotype 14 from Papua New Guinea with the Potential to Be Mistyped and Escape Vaccine-Induced Protection. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	5
6	Lytic Bacteriophage EFA1 Modulates HCT116 Colon Cancer Cell Growth and Upregulates ROS Production in an <i>Enterococcus faecalis</i> Co-culture System. <i>Frontiers in Microbiology</i> , 2021, 12, 650849.	1.5	16
7	Cocultivation of an ultrasmall environmental parasitic bacterium with lytic ability against bacteria associated with wastewater foams. <i>Nature Microbiology</i> , 2021, 6, 703-711.	5.9	43
8	Environmental hotspots for antibiotic resistance genes. <i>MicrobiologyOpen</i> , 2021, 10, e1197.	1.2	56
9	Draft Genome Sequence of <i>Enterobacter mori</i> Strain NSE2, Isolated from the Rhizosphere of a <i>Sedum</i> sp.. <i>Microbiology Resource Announcements</i> , 2021, 10, e0048721.	0.3	3
10	Isolation and Characterisation of the Bundooravirus Genus and Phylogenetic Investigation of the <i>Salasmaviridae</i> Bacteriophages. <i>Viruses</i> , 2021, 13, 1557.	1.5	7
11	Novel <i>Drexelviriidae</i> bacteriophage KMI8 with specific lytic activity against <i>Klebsiella michiganensis</i> and its biofilms. <i>PLoS ONE</i> , 2021, 16, e0257102.	1.1	9
12	Genetic characterisation of antibiotic resistance transposons Tn6608 and Tn6609 isolated from clinical <i>Pseudomonas</i> strains in Cyprus. <i>Journal of Global Antimicrobial Resistance</i> , 2021, 26, 330-334.	0.9	2
13	Draft Genome Sequence of <i>Enterobacter asburiae</i> NCR1, a Plant Growth-Promoting Rhizobacterium Isolated from a Cadmium-Contaminated Environment. <i>Microbiology Resource Announcements</i> , 2021, 10, e0047821.	0.3	4
14	Towards Identifying Genetic Biomarkers for Gastrointestinal Dysfunction in Autism. <i>Journal of Autism and Developmental Disorders</i> , 2020, 50, 76-86.	1.7	8
15	Molecular characterisation of a novel pathogenic avipoxvirus from the Australian magpie (<i>Gymnorhina tibicen</i>). <i>Virology</i> , 2020, 540, 1-16.	1.1	24
16	Potential Determinants of Gastrointestinal Dysfunction in Autism Spectrum Disorders. <i>Review Journal of Autism and Developmental Disorders</i> , 2020, 7, 182-196.	2.2	2
17	The community compositions of three nitrogen removal wastewater treatment plants of different configurations in Victoria, Australia, over a 12-month operational period. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 9839-9852.	1.7	22
18	Exploring the operating factors controlling <i>Kouleothrix</i> (type 1851), the dominant filamentous bacterial population, in a full-scale A2O plant. <i>Scientific Reports</i> , 2020, 10, 6809.	1.6	16

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19	Characterization of Novel Lytic Bacteriophages of <i>Achromobacter marplantis</i> Isolated from a Pneumonia Patient. <i>Viruses</i> , 2020, 12, 1138.	1.5	8
20	Tn6603, a Carrier of Tn5053 Family Transposons, Occurs in the Chromosome and in a Genomic Island of <i>Pseudomonas aeruginosa</i> Clinical Strains. <i>Microorganisms</i> , 2020, 8, 1997.	1.6	1
21	Complete Genome Sequence of <i>Moraxella osloensis</i> Strain YV1, Isolated from an Australian Wastewater Treatment Plant. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
22	Novel Bacteriophages Capable of Disrupting Biofilms From Clinical Strains of <i>Aeromonas hydrophila</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 194.	1.5	22
23	A preliminary study of pharmacogenetic biomarkers for individuals with autism and gastrointestinal dysfunction. <i>Research in Autism Spectrum Disorders</i> , 2020, 71, 101516.	0.8	0
24	Comparative Analysis of Structural Variations Due to Genome Shuffling of <i>Bacillus Subtilis</i> VS15 for Improved Cellulase Production. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1299.	1.8	12
25	Adaptive Evolution of <i>Geobacter sulfurreducens</i> in Coculture with <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2020, 11, .	1.8	5
26	The varying effects of a range of preservatives on <i>Myoviridae</i> and <i>Siphoviridae</i> bacteriophages formulated in a semi-solid cream preparation. <i>Letters in Applied Microbiology</i> , 2020, 71, 203-209.	1.0	6
27	Whole-genome analyses reveal gene content differences between nontypeable <i>Haemophilus influenzae</i> isolates from chronic obstructive pulmonary disease compared to other clinical phenotypes. <i>Microbial Genomics</i> , 2020, 6, .	1.0	10
28	Draft Genome Sequence of an Isolate of Nontypeable <i>Haemophilus influenzae</i> from an Acute Exacerbation of Chronic Obstructive Pulmonary Disease in Tasmania. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	2
29	Bacteriophages in Natural and Artificial Environments. <i>Pathogens</i> , 2019, 8, 100.	1.2	124
30	The Phylogeny, Biodiversity, and Ecology of the Chloroflexi in Activated Sludge. <i>Frontiers in Microbiology</i> , 2019, 10, 2015.	1.5	159
31	Genomic, morphological and functional characterisation of novel bacteriophage FNU1 capable of disrupting <i>Fusobacterium nucleatum</i> biofilms. <i>Scientific Reports</i> , 2019, 9, 9107.	1.6	34
32	Isolation and characterization of bacteriophage NTR1 infectious for <i>Nocardia transvalensis</i> and other <i>Nocardia</i> species. <i>Virus Genes</i> , 2019, 55, 257-265.	0.7	8
33	Reviewing microbial electrical systems and bacteriophage biocontrol as targeted novel treatments for reducing hydrogen sulfide emissions in urban sewer systems. <i>Reviews in Environmental Science and Biotechnology</i> , 2018, 17, 749-764.	3.9	4
34	Activated sludge foaming: can phage therapy provide a control strategy?. <i>Microbiology Australia</i> , 2018, 39, 162.	0.1	7
35	Semi-Solid and Solid Dosage Forms for the Delivery of Phage Therapy to Epithelia. <i>Pharmaceuticals</i> , 2018, 11, 26.	1.7	20
36	Bacteriophage formulated into a range of semisolid and solid dosage forms maintain lytic capacity against isolated cutaneous and opportunistic oral bacteria. <i>Journal of Pharmacy and Pharmacology</i> , 2017, 69, 244-253.	1.2	17

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37	Dynamic interactions between prophages induce lysis in <i>Propionibacterium acnes</i> . <i>Research in Microbiology</i> , 2017, 168, 103-112.	1.0	5
38	Characterization and formulation into solid dosage forms of a novel bacteriophage lytic against <i>Klebsiella oxytoca</i> . <i>PLoS ONE</i> , 2017, 12, e0183510.	1.1	21
39	The Formulation of Bacteriophage in a Semi Solid Preparation for Control of <i>Propionibacterium acnes</i> Growth. <i>PLoS ONE</i> , 2016, 11, e0151184.	1.1	49
40	Locating and Activating Molecular "Time Bombs": Induction of Mycolata Prophages. <i>PLoS ONE</i> , 2016, 11, e0159957.	1.1	4
41	Genome Sequences of <i>Pseudomonas oryzae</i> Phage POR1 and <i>Pseudomonas aeruginosa</i> Phage PAE1. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
42	Isolation and characterization of bacteriophage SPI1, which infects the activated-sludge-foaming bacterium <i>Skermania piniformis</i> . <i>Archives of Virology</i> , 2016, 161, 149-158.	0.9	11
43	Innovative biological approaches for monitoring and improving water quality. <i>Frontiers in Microbiology</i> , 2015, 6, 826.	1.5	29
44	Three of a Kind: Genetically Similar <i>Tsukamurella</i> Phages TIN2, TIN3, and TIN4. <i>Applied and Environmental Microbiology</i> , 2015, 81, 6767-6772.	1.4	6
45	Lysis to Kill: Evaluation of the Lytic Abilities, and Genomics of Nine Bacteriophages Infective for <i>Gordonia</i> spp. and Their Potential Use in Activated Sludge Foam Biocontrol. <i>PLoS ONE</i> , 2015, 10, e0134512.	1.1	39
46	Isolation and characterization of two plasmids in a clinical <i>Acinetobacter nosocomialis</i> strain. <i>BMC Research Notes</i> , 2014, 7, 732.	0.6	4
47	Genome sequence of the <i>Nocardia</i> bacteriophage NBR1. <i>Archives of Virology</i> , 2014, 159, 167-173.	0.9	12
48	Characterization and whole genome sequences of the <i>Rhodococcus</i> bacteriophages RGL3 and RER2. <i>Archives of Virology</i> , 2013, 158, 601-609.	0.9	20
49	Genome sequence and characterization of a <i>Rhodococcus equi</i> phage REQ1. <i>Virus Genes</i> , 2013, 46, 588-590.	0.7	21
50	A metabolic model for members of the genus <i>Tetrasphaera</i> involved in enhanced biological phosphorus removal. <i>ISME Journal</i> , 2013, 7, 543-554.	4.4	188
51	Synthesis Characterization and Antibacterial, Antifungal Activity of N-(Benzyl Carbamoyl or Tj ETQq1 1 0.784314 rgBT /Overlock 10 TFS International Journal of Medicinal Chemistry, 2013, 2013, 1-20.	2.2	8
52	Metagenomics of rumen bacteriophage from thirteen lactating dairy cattle. <i>BMC Microbiology</i> , 2013, 13, 242.	1.3	51
53	Resolvase. , 2013, , 179.		0
54	Resolvase Mediated Deletion. , 2013, , 180-182.		1

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55	Genome Sequences and Characterization of the Related <i>Gordonia</i> Phages GTE5 and GRU1 and Their Use as Potential Biocontrol Agents. <i>Applied and Environmental Microbiology</i> , 2012, 78, 42-47.	1.4	34
56	Small but Sufficient: the <i>Rhodococcus</i> Phage RRH1 Has the Smallest Known Siphoviridae Genome at 14.2 Kilobases. <i>Journal of Virology</i> , 2012, 86, 358-363.	1.5	36
57	Isolation and complete genome sequence of a bacteriophage lysing <i>Tetrasphaera jenkinsii</i> , a filamentous bacteria responsible for bulking in activated sludge. <i>Virus Genes</i> , 2012, 45, 380-388.	0.7	15
58	Back to the kitchen: Food-grade agar is a low-cost alternative to bacteriological agar. <i>Analytical Biochemistry</i> , 2012, 429, 140-141.	1.1	12
59	An examination of the mechanisms for stable foam formation in activated sludge systems. <i>Water Research</i> , 2011, 45, 2146-2154.	5.3	87
60	The activated sludge bulking filament Eikelboom morphotype 0914 is a member of the <i>Chloroflexi</i> . <i>Environmental Microbiology Reports</i> , 2011, 3, 159-165.	1.0	26
61	Non-target sites with single nucleotide insertions or deletions are frequently found in 16S rRNA sequences and can lead to false positives in fluorescence <i>in situ</i> hybridization (FISH). <i>Environmental Microbiology</i> , 2011, 13, 33-47.	1.8	23
62	Mercury(II)-resistance transposons Tn502 and Tn512, from <i>Pseudomonas</i> clinical strains, are structurally different members of the Tn5053 family. <i>Plasmid</i> , 2011, 65, 58-64.	0.4	9
63	Characterization of the Genome of the Polyvalent Lytic Bacteriophage GTE2, Which Has Potential for Biocontrol of <i>Gordonia</i> -, <i>Rhodococcus</i> -, and <i>Nocardia</i> -Stabilized Foams in Activated Sludge Plants. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3923-3929.	1.4	69
64	Prevention of <i>Gordonia</i> and <i>Nocardia</i> Stabilized Foam Formation by Using Bacteriophage GTE7. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7864-7867.	1.4	65
65	Genome Sequence and Characterization of the <i>Tsukamurella</i> Bacteriophage TPA2. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1389-1398.	1.4	59
66	Embedded elements in the IncP β plasmids R772 and R906 can be mobilized and can serve as a source of diverse and novel elements. <i>Microbiology (United Kingdom)</i> , 2011, 157, 1714-1725.	0.7	10
67	Tn502 and Tn512 Are <i>res</i> Site Hunters That Provide Evidence of Resolvase-Independent Transposition to Random Sites. <i>Journal of Bacteriology</i> , 2010, 192, 1865-1874.	1.0	33
68	Phylogeny and <i>in situ</i> identification of a novel gammaproteobacterium in activated sludge. <i>FEMS Microbiology Letters</i> , 2009, 297, 157-163.	0.7	12