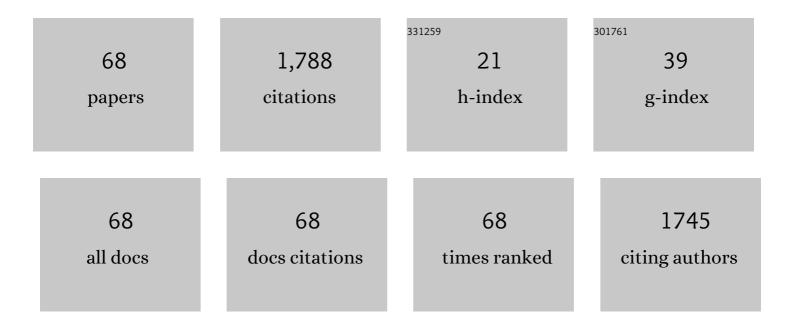
Steve Petrovski

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A metabolic model for members of the genus <i>Tetrasphaera</i> involved in enhanced biological phosphorus removal. ISME Journal, 2013, 7, 543-554.	4.4	188
2	The Phylogeny, Biodiversity, and Ecology of the Chloroflexi in Activated Sludge. Frontiers in Microbiology, 2019, 10, 2015.	1.5	159
3	Bacteriophages in Natural and Artificial Environments. Pathogens, 2019, 8, 100.	1.2	124
4	MiDAS 4: A global catalogue of full-length 16S rRNA gene sequences and taxonomy for studies of bacterial communities in wastewater treatment plants. Nature Communications, 2022, 13, 1908.	5.8	114
5	An examination of the mechanisms for stable foam formation in activated sludge systems. Water Research, 2011, 45, 2146-2154.	5.3	87
6	Characterization of the Genome of the Polyvalent Lytic Bacteriophage GTE2, Which Has Potential for Biocontrol of Gordonia-, Rhodococcus-, and Nocardia-Stabilized Foams in Activated Sludge Plants. Applied and Environmental Microbiology, 2011, 77, 3923-3929.	1.4	69
7	Prevention of Gordonia and Nocardia Stabilized Foam Formation by Using Bacteriophage GTE7. Applied and Environmental Microbiology, 2011, 77, 7864-7867.	1.4	65
8	Genome Sequence and Characterization of the <i>Tsukamurella</i> Bacteriophage TPA2. Applied and Environmental Microbiology, 2011, 77, 1389-1398.	1.4	59
9	Environmental hotspots for antibiotic resistance genes. MicrobiologyOpen, 2021, 10, e1197.	1.2	56
10	Metagenomics of rumen bacteriophage from thirteen lactating dairy cattle. BMC Microbiology, 2013, 13, 242.	1.3	51
11	The Formulation of Bacteriophage in a Semi Solid Preparation for Control of Propionibacterium acnes Growth. PLoS ONE, 2016, 11, e0151184.	1.1	49
12	Cocultivation of an ultrasmall environmental parasitic bacterium with lytic ability against bacteria associated with wastewater foams. Nature Microbiology, 2021, 6, 703-711.	5.9	43
13	Lysis to Kill: Evaluation of the Lytic Abilities, and Genomics of Nine Bacteriophages Infective for Gordonia spp. and Their Potential Use in Activated Sludge Foam Biocontrol. PLoS ONE, 2015, 10, e0134512.	1.1	39
14	Small but Sufficient: the Rhodococcus Phage RRH1 Has the Smallest Known Siphoviridae Genome at 14.2 Kilobases. Journal of Virology, 2012, 86, 358-363.	1.5	36
15	Genome Sequences and Characterization of the Related Gordonia Phages GTE5 and GRU1 and Their Use as Potential Biocontrol Agents. Applied and Environmental Microbiology, 2012, 78, 42-47.	1.4	34
16	Genomic, morphological and functional characterisation of novel bacteriophage FNU1 capable of disrupting Fusobacterium nucleatum biofilms. Scientific Reports, 2019, 9, 9107.	1.6	34
17	Tn <i>502</i> and Tn <i>512</i> Are <i>res</i> Site Hunters That Provide Evidence of Resolvase-Independent Transposition to Random Sites. Journal of Bacteriology, 2010, 192, 1865-1874.	1.0	33
18	Innovative biological approaches for monitoring and improving water quality. Frontiers in Microbiology, 2015, 6, 826.	1.5	29

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19	The activated sludge bulking filament Eikelboom morphotype 0914 is a member of the <i>Chloroflexi</i> . Environmental Microbiology Reports, 2011, 3, 159-165.	1.0	26
20	The phylogeny, ecology and ecophysiology of the glycogen accumulating organism (GAO) Defluviicoccus in wastewater treatment plants. Water Research, 2022, 221, 118729.	5.3	25
21	Molecular characterisation of a novel pathogenic avipoxvirus from the Australian magpie (Gymnorhina tibicen). Virology, 2020, 540, 1-16.	1.1	24
22	Elevated atmospheric CO2 alters the microbial community composition and metabolic potential to mineralize organic phosphorus in the rhizosphere of wheat. Microbiome, 2022, 10, 12.	4.9	24
23	Nonâ€ŧarget 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). Environmental Microbiology, 2011, 13, 33-47.	1.8	23
24	The community compositions of three nitrogen removal wastewater treatment plants of different configurations in Victoria, Australia, over a 12-month operational period. Applied Microbiology and Biotechnology, 2020, 104, 9839-9852.	1.7	22
25	Novel Bacteriophages Capable of Disrupting Biofilms From Clinical Strains of Aeromonas hydrophila. Frontiers in Microbiology, 2020, 11, 194.	1.5	22
26	Genome sequence and characterization of a Rhodococcus equi phage REQ1. Virus Genes, 2013, 46, 588-590.	0.7	21
27	Characterization and formulation into solid dosage forms of a novel bacteriophage lytic against Klebsiella oxytoca. PLoS ONE, 2017, 12, e0183510.	1.1	21
28	Characterization and whole genome sequences of the Rhodococcus bacteriophages RGL3 and RER2. Archives of Virology, 2013, 158, 601-609.	0.9	20
29	Semi-Solid and Solid Dosage Forms for the Delivery of Phage Therapy to Epithelia. Pharmaceuticals, 2018, 11, 26.	1.7	20
30	Bacteriophage formulated into a range of semisolid and solid dosage forms maintain lytic capacity against isolated cutaneous and opportunistic oral bacteria. Journal of Pharmacy and Pharmacology, 2017, 69, 244-253.	1.2	17
31	Exploring the operating factors controlling Kouleothrix (type 1851), the dominant filamentous bacterial population, in a full-scale A2O plant. Scientific Reports, 2020, 10, 6809.	1.6	16
32	Lytic Bacteriophage EFA1 Modulates HCT116 Colon Cancer Cell Growth and Upregulates ROS Production in an Enterococcus faecalis Co-culture System. Frontiers in Microbiology, 2021, 12, 650849.	1.5	16
33	Isolation and complete genome sequence of a bacteriophage lysing Tetrasphaera jenkinsii, a filamentous bacteria responsible for bulking in activated sludge. Virus Genes, 2012, 45, 380-388.	0.7	15
34	Phylogeny and <i>in situ</i> identification of a novel gammaproteobacterium in activated sludge. FEMS Microbiology Letters, 2009, 297, 157-163.	0.7	12
35	Back to the kitchen: Food-grade agar is a low-cost alternative to bacteriological agar. Analytical Biochemistry, 2012, 429, 140-141.	1.1	12
36	Genome sequence of the Nocardia bacteriophage NBR1. Archives of Virology, 2014, 159, 167-173.	0.9	12

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37	Comparative Analysis of Structural Variations Due to Genome Shuffling of Bacillus Subtilis VS15 for Improved Cellulase Production. International Journal of Molecular Sciences, 2020, 21, 1299.	1.8	12
38	Isolation and characterization of bacteriophage SPI1, which infects the activated-sludge-foaming bacterium Skermania piniformis. Archives of Virology, 2016, 161, 149-158.	0.9	11
39	Whole-genome analyses reveal gene content differences between nontypeable Haemophilus influenzae isolates from chronic obstructive pulmonary disease compared to other clinical phenotypes. Microbial Genomics, 2020, 6, .	1.0	10
40	Embedded elements in the IncPβ plasmids R772 and R906 can be mobilized and can serve as a source of diverse and novel elements. Microbiology (United Kingdom), 2011, 157, 1714-1725.	0.7	10
41	Mercury(II)-resistance transposons Tn502 and Tn512, from Pseudomonas clinical strains, are structurally different members of the Tn5053 family. Plasmid, 2011, 65, 58-64.	0.4	9
42	Novel Drexlerviridae bacteriophage KMI8 with specific lytic activity against Klebsiella michiganensis and its biofilms. PLoS ONE, 2021, 16, e0257102.	1.1	9
43	Synthesis Characterization and Antibacterial, Antifungal Activity of N-(Benzyl Carbamoyl or) Tj ETQq1 1 0.7843 International Journal of Medicinal Chemistry, 2013, 2013, 1-20.	14 rgBT /O 2.2	verlock 10 Tf 8
44	Isolation and characterization of bacteriophage NTR1 infectious for Nocardia transvalensis and other Nocardia species. Virus Genes, 2019, 55, 257-265.	0.7	8
45	Towards Identifying Genetic Biomarkers for Gastrointestinal Dysfunction in Autism. Journal of Autism and Developmental Disorders, 2020, 50, 76-86.	1.7	8
46	Characterization of Novel Lytic Bacteriophages of Achromobacter marplantensis Isolated from a Pneumonia Patient. Viruses, 2020, 12, 1138.	1.5	8
47	Activated sludge foaming: can phage therapy provide a control strategy?. Microbiology Australia, 2018, 39, 162.	0.1	7
48	Isolation and Characterisation of the Bundooravirus Genus and Phylogenetic Investigation of the Salasmaviridae Bacteriophages. Viruses, 2021, 13, 1557.	1.5	7
49	Three of a Kind: Genetically Similar Tsukamurella Phages TIN2, TIN3, and TIN4. Applied and Environmental Microbiology, 2015, 81, 6767-6772.	1.4	6
50	The varying effects of a range of preservatives on <i>Myoviridae</i> and <i>Siphoviridae</i> bacteriophages formulated in a semiâ€solid cream preparation. Letters in Applied Microbiology, 2020, 71, 203-209.	1.0	6
51	Genome Sequences of Pseudomonas oryzihabitans Phage POR1 and Pseudomonas aeruginosa Phage PAE1. Genome Announcements, 2016, 4, .	0.8	5
52	Dynamic interactions between prophages induce lysis in Propionibacterium acnes. Research in Microbiology, 2017, 168, 103-112.	1.0	5
53	Adaptive Evolution of Geobacter sulfurreducens in Coculture with Pseudomonas aeruginosa. MBio, 2020, 11, .	1.8	5
54	Variants of Streptococcus pneumoniae Serotype 14 from Papua New Guinea with the Potential to Be Mistyped and Escape Vaccine-Induced Protection. Microbiology Spectrum, 2022, 10, .	1.2	5

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55	Isolation and characterization of two plasmids in a clinical Acinetobacter nosocomialis strain. BMC Research Notes, 2014, 7, 732.	0.6	4
56	Locating and Activating Molecular â€~Time Bombs': Induction of Mycolata Prophages. PLoS ONE, 2016, 11, e0159957.	1.1	4
57	Reviewing microbial electrical systems and bacteriophage biocontrol as targeted novel treatments for reducing hydrogen sulfide emissions in urban sewer systems. Reviews in Environmental Science and Biotechnology, 2018, 17, 749-764.	3.9	4
58	Draft Genome Sequence of Enterobacter asburiae NCR1, a Plant Growth-Promoting Rhizobacterium Isolated from a Cadmium-Contaminated Environment. Microbiology Resource Announcements, 2021, 10, e0047821.	0.3	4
59	Draft Genome Sequence of Enterobacter mori Strain NSE2, Isolated from the Rhizosphere of a <i>Sedum</i> sp Microbiology Resource Announcements, 2021, 10, e0048721.	0.3	3
60	Biological control of problematic bacterial populations causing foaming in activated sludge wastewater treatment plants—phage therapy and beyond. Letters in Applied Microbiology, 2022, 75, 776-784.	1.0	3
61	Potential Determinants of Gastrointestinal Dysfunction in Autism Spectrum Disorders. Review Journal of Autism and Developmental Disorders, 2020, 7, 182-196.	2.2	2
62	Complete Genome Sequence of Moraxella osloensis Strain YV1, Isolated from an Australian Wastewater Treatment Plant. Microbiology Resource Announcements, 2020, 9, .	0.3	2
63	Genetic characterisation of antibiotic resistance transposons Tn6608 and Tn6609 isolated from clinical Pseudomonas strains in Cyprus. Journal of Global Antimicrobial Resistance, 2021, 26, 330-334.	0.9	2
64	Draft Genome Sequence of an Isolate of Nontypeable Haemophilus influenzae from an Acute Exacerbation of Chronic Obstructive Pulmonary Disease in Tasmania. Microbiology Resource Announcements, 2020, 9, .	0.3	2
65	Tn6603, a Carrier of Tn5053 Family Transposons, Occurs in the Chromosome and in a Genomic Island of Pseudomonas aeruginosa Clinical Strains. Microorganisms, 2020, 8, 1997.	1.6	1
66	Resolvase Mediated Deletion. , 2013, , 180-182.		1
67	A preliminary study of pharmacogenetic biomarkers for individuals with autism and gastrointestinal dysfunction. Research in Autism Spectrum Disorders, 2020, 71, 101516.	0.8	0

68 Resolvase. , 2013, , 179.

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