

# Rob Lavigne

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1137994/publications.pdf>

Version: 2024-02-01

243  
papers

15,543  
citations

12330

69  
h-index

25787

108  
g-index

260  
all docs

260  
docs citations

260  
times ranked

11112  
citing authors

#	ARTICLE	IF	CITATIONS
1	Minimum Information about a Biosynthetic Gene cluster. <i>Nature Chemical Biology</i> , 2015, 11, 625-631.	8.0	715
2	Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. <i>Nature Biotechnology</i> , 2019, 37, 632-639.	17.5	569
3	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	17.5	414
4	Quality-Controlled Small-Scale Production of a Well-Defined Bacteriophage Cocktail for Use in Human Clinical Trials. <i>PLoS ONE</i> , 2009, 4, e4944.	2.5	391
5	Targeting mechanisms of tailed bacteriophages. <i>Nature Reviews Microbiology</i> , 2018, 16, 760-773.	28.6	310
6	Engineered Endolysin-Based <i>Artilyns</i> To Combat Multidrug-Resistant Gram-Negative Pathogens. <i>MBio</i> , 2014, 5, e01379-14.	4.1	279
7	Modular approach to customise sample preparation procedures for viral metagenomics: a reproducible protocol for virome analysis. <i>Scientific Reports</i> , 2015, 5, 16532.	3.3	277
8	Unifying classical and molecular taxonomic classification: analysis of the Podoviridae using BLASTP-based tools. <i>Research in Microbiology</i> , 2008, 159, 406-414.	2.1	273
9	The Phage Therapy Paradigm: Pr <sup>o</sup> -Porter or Sur-mesure?. <i>Pharmaceutical Research</i> , 2011, 28, 934-937.	3.5	249
10	Classification of Myoviridae bacteriophages using protein sequence similarity. <i>BMC Microbiology</i> , 2009, 9, 224.	3.3	245
11	The Ever-Expanding <i>Pseudomonas</i> Genus: Description of 43 New Species and Partition of the <i>Pseudomonas putida</i> Group. <i>Microorganisms</i> , 2021, 9, 1766.	3.6	206
12	Learning from Bacteriophages - Advantages and Limitations of Phage and Phage-Encoded Protein Applications. <i>Current Protein and Peptide Science</i> , 2012, 13, 699-722.	1.4	197
13	Position paper: The creation of a rational scheme for the nomenclature of viruses of <i>Bacteria</i> and <i>Archaea</i> . <i>Environmental Microbiology</i> , 2009, 11, 2775-2777.	3.8	184
14	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. <i>Nature Microbiology</i> , 2019, 4, 1727-1736.	13.3	184
15	Pro- and anti-inflammatory responses of peripheral blood mononuclear cells induced by <i>Staphylococcus aureus</i> and <i>Pseudomonas aeruginosa</i> phages. <i>Scientific Reports</i> , 2017, 7, 8004.	3.3	179
16	Quality and Safety Requirements for Sustainable Phage Therapy Products. <i>Pharmaceutical Research</i> , 2015, 32, 2173-2179.	3.5	176
17	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018, 163, 1125-1129.	2.1	172
18	T4-Related Bacteriophage LIMeStone Isolates for the Control of Soft Rot on Potato Caused by <i>Dickeya solani</i> . <i>PLoS ONE</i> , 2012, 7, e33227.	2.5	169

#	ARTICLE	IF	CITATIONS
19	Pseudomonas predators: understanding and exploiting phage-host interactions. Nature Reviews Microbiology, 2017, 15, 517-530.	28.6	156
20	Art-175 Is a Highly Efficient Antibacterial against Multidrug-Resistant Strains and Persists of Pseudomonas aeruginosa. Antimicrobial Agents and Chemotherapy, 2014, 58, 3774-3784.	3.2	152
21	Muralytic activity and modular structure of the endolysins of <i>Pseudomonas aeruginosa</i> bacteriophages $\phi$ KZ and EL. Molecular Microbiology, 2007, 65, 1334-1344.	2.5	150
22	Breaking barriers: expansion of the use of endolysins as novel antibacterials against Gram-negative bacteria. Future Microbiology, 2015, 10, 377-390.	2.0	147
23	The T7-Related Pseudomonas putida Phage $\phi$ 15 Displays Virion-Associated Biofilm Degradation Properties. PLoS ONE, 2011, 6, e18597.	2.5	147
24	Development of Giant Bacteriophage $\phi$ KZ Is Independent of the Host Transcription Apparatus. Journal of Virology, 2014, 88, 10501-10510.	3.4	144
25	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. Archives of Virology, 2020, 165, 1253-1260.	2.1	144
26	A Thermostable Salmonella Phage Endolysin, Lys68, with Broad Bactericidal Properties against Gram-Negative Pathogens in Presence of Weak Acids. PLoS ONE, 2014, 9, e108376.	2.5	143
27	Genomic Analysis of Pseudomonas aeruginosa Phages LKD16 and LKA1: Establishment of the $\phi$ KMV Subgroup within the T7 Supergroup. Journal of Bacteriology, 2006, 188, 6924-6931.	2.2	131
28	High coverage metabolomics analysis reveals phage-specific alterations to <i>Pseudomonas aeruginosa</i> physiology during infection. ISME Journal, 2016, 10, 1823-1835.	9.8	126
29	Predicting <i>In Vivo</i> Efficacy of Therapeutic Bacteriophages Used To Treat Pulmonary Infections. Antimicrobial Agents and Chemotherapy, 2013, 57, 5961-5968.	3.2	125
30	Safety and efficacy of phage therapy in difficult-to-treat infections: a systematic review. Lancet Infectious Diseases, The, 2022, 22, e208-e220.	9.1	125
31	Two Phages, phiPLA-RODI and phiPLA-C1C, Lyse Mono- and Dual-Species Staphylococcal Biofilms. Applied and Environmental Microbiology, 2015, 81, 3336-3348.	3.1	124
32	The role of interactions between phage and bacterial proteins within the infected cell: a diverse and puzzling interactome. Environmental Microbiology, 2009, 11, 2789-2805.	3.8	123
33	Bacteriophage Therapy: Advances in Formulation Strategies and Human Clinical Trials. Annual Review of Virology, 2015, 2, 599-618.	6.7	122
34	The genome of bacteriophage $\phi$ KMV, a T7-like virus infecting Pseudomonas aeruginosa. Virology, 2003, 312, 49-59.	2.4	118
35	Structural and Enzymatic Characterization of ABgp46, a Novel Phage Endolysin with Broad Anti-Gram-Negative Bacterial Activity. Frontiers in Microbiology, 2016, 7, 208.	3.5	118
36	Capsule-Targeting Depolymerase, Derived from Klebsiella KP36 Phage, as a Tool for the Development of Anti-Virulent Strategy. Viruses, 2016, 8, 324.	3.3	117

#	ARTICLE	IF	CITATIONS
37	Genome Comparison of <i>Pseudomonas aeruginosa</i> Large Phages. <i>Journal of Molecular Biology</i> , 2005, 354, 536-545.	4.2	111
38	Experimental phage therapy of burn wound infection: difficult first steps. <i>International Journal of Burns and Trauma</i> , 2014, 4, 66-73.	0.2	111
39	Characterization of Modular Bacteriophage Endolysins from Myoviridae Phages OBP, 2011-2 and PVP-SE1. <i>PLoS ONE</i> , 2012, 7, e36991.	2.5	109
40	Feasibility of spray drying bacteriophages into respirable powders to combat pulmonary bacterial infections. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2013, 84, 578-582.	4.3	101
41	Efficacy of Artilysin Art-175 against Resistant and Persistent <i>Acinetobacter baumannii</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 3480-3488.	3.2	99
42	Bacteriophage Application for Difficult-to-treat Musculoskeletal Infections: Development of a Standardized Multidisciplinary Treatment Protocol. <i>Viruses</i> , 2019, 11, 891.	3.3	98
43	Combination of pre-adapted bacteriophage therapy and antibiotics for treatment of fracture-related infection due to pandrug-resistant <i>Klebsiella pneumoniae</i> . <i>Nature Communications</i> , 2022, 13, 302.	12.8	97
44	Next-Generation "omics" Approaches Reveal a Massive Alteration of Host RNA Metabolism during Bacteriophage Infection of <i>Pseudomonas aeruginosa</i> . <i>PLoS Genetics</i> , 2016, 12, e1006134.	3.5	94
45	Microbiological and Molecular Assessment of Bacteriophage ISP for the Control of <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2011, 6, e24418.	2.5	92
46	The SPO1-related bacteriophages. <i>Archives of Virology</i> , 2010, 155, 1547-1561.	2.1	91
47	From endolysins to Artilysin®: novel enzyme-based approaches to kill drug-resistant bacteria. <i>Biochemical Society Transactions</i> , 2016, 44, 123-128.	3.4	89
48	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020, 69, 110-123.	5.6	89
49	The O-specific polysaccharide lyase from the phage LKA1 tailspike reduces <i>Pseudomonas</i> virulence. <i>Scientific Reports</i> , 2017, 7, 16302.	3.3	88
50	Metagenomic Characterisation of the Viral Community of Lough Neagh, the Largest Freshwater Lake in Ireland. <i>PLoS ONE</i> , 2016, 11, e0150361.	2.5	87
51	Molecular and physiological analysis of three <i>Pseudomonas aeruginosa</i> phages belonging to the "N4-like viruses". <i>Virology</i> , 2010, 405, 26-30.	2.4	86
52	Identification of EPS-degrading activity within the tail spikes of the novel <i>Pseudomonas putida</i> phage AF. <i>Virology</i> , 2012, 434, 251-256.	2.4	86
53	Characterization of Novel Bacteriophages for Biocontrol of Bacterial Blight in Leek Caused by <i>Pseudomonas syringae</i> pv. <i>porri</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 279.	3.5	86
54	A proposed integrated approach for the preclinical evaluation of phage therapy in <i>Pseudomonas</i> infections. <i>Scientific Reports</i> , 2016, 6, 28115.	3.3	86

#	ARTICLE	IF	CITATIONS
55	Comparative analysis of the widespread and conserved PB1-like viruses infecting <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2009, 11, 2874-2883.	3.8	85
56	Massive Activation of Archaeal Defense Genes during Viral Infection. <i>Journal of Virology</i> , 2013, 87, 8419-8428.	3.4	84
57	Bacteriophages of <i>Pseudomonas</i> . <i>Future Microbiology</i> , 2010, 5, 1041-1055.	2.0	83
58	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2016, 161, 1095-1099.	2.1	83
59	Role of the Pre-neck Appendage Protein (Dpo7) from Phage $\nu$ B_SepiS-philPLA7 as an Anti-biofilm Agent in Staphylococcal Species. <i>Frontiers in Microbiology</i> , 2015, 6, 1315.	3.5	81
60	Genomic and Proteomic Characterization of the Broad-Host-Range Salmonella Phage PVP-SE1: Creation of a New Phage Genus. <i>Journal of Virology</i> , 2011, 85, 11265-11273.	3.4	80
61	Introducing yesterday's phage therapy in today's medicine. <i>Future Virology</i> , 2012, 7, 379-390.	1.8	80
62	Characterization of Newly Isolated Lytic Bacteriophages Active against <i>Acinetobacter baumannii</i> . <i>PLoS ONE</i> , 2014, 9, e104853.	2.5	80
63	Food applications of bacterial cell wall hydrolases. <i>Current Opinion in Biotechnology</i> , 2011, 22, 164-171.	6.6	79
64	Romulus and Remus, Two Phage Isolates Representing a Distinct Clade within the Twortlikevirus Genus, Display Suitable Properties for Phage Therapy Applications. <i>Journal of Virology</i> , 2013, 87, 3237-3247.	3.4	79
65	Isolation and Purification of a New Kalimantanacin/Batumin-Related Polyketide Antibiotic and Elucidation of Its Biosynthesis Gene Cluster. <i>Chemistry and Biology</i> , 2010, 17, 149-159.	6.0	78
66	A conserved motif flags acyl carrier proteins for $\beta^2$ -branching in polyketide synthesis. <i>Nature Chemical Biology</i> , 2013, 9, 685-692.	8.0	78
67	A suggested new bacteriophage genus: <i>Viunalikevirus</i> . <i>Archives of Virology</i> , 2012, 157, 2035-2046.	2.1	77
68	The future of phage biocontrol in integrated plant protection for sustainable crop production. <i>Current Opinion in Biotechnology</i> , 2021, 68, 60-71.	6.6	77
69	Complete Genome Sequence of the Giant Virus OBP and Comparative Genome Analysis of the Diverse $\beta$ -KZ-Related Phages. <i>Journal of Virology</i> , 2012, 86, 1844-1852.	3.4	75
70	A PKS/NRPS/FAS Hybrid Gene Cluster from <i>Serratia plymuthica</i> RVH1 Encoding the Biosynthesis of Three Broad Spectrum, Zeamine-Related Antibiotics. <i>PLoS ONE</i> , 2013, 8, e54143.	2.5	75
71	Characterization of five novel endolysins from Gram-negative infecting bacteriophages. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 4369-4375.	3.6	73
72	The Genome and Structural Proteome of YuA, a New <i>Pseudomonas aeruginosa</i> Phage Resembling M6. <i>Journal of Bacteriology</i> , 2008, 190, 1429-1435.	2.2	72

#	ARTICLE	IF	CITATIONS
73	RNA-Sequencing Reveals the Progression of Phage-Host Interactions between $\phi$ R1-37 and <i>Yersinia enterocolitica</i> . <i>Viruses</i> , 2016, 8, 111.	3.3	72
74	Evaluation of the genomic diversity of viruses infecting bacteria, archaea and eukaryotes using a common bioinformatic platform: steps towards a unified taxonomy. <i>Journal of General Virology</i> , 2018, 99, 1331-1343.	2.9	72
75	Bacteriophage endolysins as a response to emerging foodborne pathogens. <i>Trends in Food Science and Technology</i> , 2012, 28, 103-115.	15.1	71
76	Call for a Dedicated European Legal Framework for Bacteriophage Therapy. <i>Archivum Immunologiae Et Therapiae Experimentalis</i> , 2014, 62, 117-129.	2.3	71
77	Phenotypic characterization of an international <i>Pseudomonas aeruginosa</i> reference panel: strains of cystic fibrosis (CF) origin show less in vivo virulence than non-CF strains. <i>Microbiology (United Kingdom)</i> 157:107-116	1.8	63
78	A Novel Hydrolase Identified by Genomic-Proteomic Analysis of Phenylurea Herbicide Mineralization by <i>Variovorax</i> sp. Strain SRS16. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8754-8764.	3.1	70
79	Phenotypic and genotypic variations within a single bacteriophage species. <i>Virology Journal</i> , 2011, 8, 134.	3.4	69
80	Characterization of the Newly Isolated Lytic Bacteriophages KTN6 and KT28 and Their Efficacy against <i>Pseudomonas aeruginosa</i> Biofilm. <i>PLoS ONE</i> , 2015, 10, e0127603.	2.5	69
81	A standardized approach for accurate quantification of murein hydrolase activity in high-throughput assays. <i>Journal of Proteomics</i> , 2007, 70, 531-533.	2.4	68
82	The high-affinity peptidoglycan binding domain of <i>Pseudomonas</i> phage endolysin KZ144. <i>Biochemical and Biophysical Research Communications</i> , 2009, 383, 187-191.	2.1	68
83	A Multifaceted Study of <i>Pseudomonas aeruginosa</i> Shutdown by Virulent Podovirus LUZ19. <i>MBio</i> , 2013, 4, e00061-13.	4.1	68
84	Optimizing the European Regulatory Framework for Sustainable Bacteriophage Therapy in Human Medicine. <i>Archivum Immunologiae Et Therapiae Experimentalis</i> , 2012, 60, 161-172.	2.3	67
85	Substrate specificity of three recombinant $\alpha$ -L-arabinofuranosidases from <i>Bifidobacterium adolescentis</i> and their divergent action on arabinoxylan and arabinoxylan oligosaccharides. <i>Biochemical and Biophysical Research Communications</i> , 2010, 402, 644-650.	2.1	66
86	Instability of bacteriophages in spray-dried trehalose powders is caused by crystallization of the matrix. <i>International Journal of Pharmaceutics</i> , 2014, 472, 202-205.	5.2	66
87	CIM <sup>Å</sup> ® monolithic anion-exchange chromatography as a useful alternative to CsCl gradient purification of bacteriophage particles. <i>Virology</i> , 2012, 434, 265-270.	2.4	65
88	The structural proteome of <i>Pseudomonas aeruginosa</i> bacteriophage $\phi$ KMV. <i>Microbiology (United Kingdom)</i> 157:107-116	1.8	63
89	A suggested classification for two groups of <i>Campylobacter</i> myoviruses. <i>Archives of Virology</i> , 2014, 159, 181-190.	2.1	63
90	Expression of a Novel P22 ORFan Gene Reveals the Phage Carrier State in <i>Salmonella</i> Typhimurium. <i>PLoS Genetics</i> , 2013, 9, e1003269.	3.5	61

#	ARTICLE	IF	CITATIONS
91	Investigating the biocontrol and anti-biofilm potential of a three phage cocktail against <i>Cronobacter sakazakii</i> in different brands of infant formula. <i>International Journal of Food Microbiology</i> , 2017, 253, 1-11.	4.7	60
92	Functional Analysis and Antivirulence Properties of a New Depolymerase from a Myovirus That Infects <i>Acinetobacter baumannii</i> Capsule K45. <i>Journal of Virology</i> , 2019, 93, .	3.4	58
93	Prevalence of Pf1-like (pro)phage genetic elements among <i>Pseudomonas aeruginosa</i> isolates. <i>Virology</i> , 2015, 483, 64-71.	2.4	57
94	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2017, 162, 1153-1157.	2.1	57
95	<i>Sphaerolobus</i> phage <i>SphA</i> 511, a model for the contractile tail machineries of <i>Sphaerolobus</i> -related bacteriophages. <i>Molecular Microbiology</i> , 2014, 92, 84-99.	2.5	55
96	Systematic Identification of Hypothetical Bacteriophage Proteins Targeting Key Protein Complexes of <i>Pseudomonas aeruginosa</i> . <i>Journal of Proteome Research</i> , 2014, 13, 4446-4456.	3.7	54
97	Bacteriophages as drivers of bacterial virulence and their potential for biotechnological exploitation. <i>FEMS Microbiology Reviews</i> , 2021, 45, .	8.6	53
98	Integration of genomic and proteomic analyses in the classification of the Siphoviridae family. <i>Virology</i> , 2015, 477, 144-154.	2.4	52
99	Artisylation™ of endolysin <i>Sa2lys</i> strongly improves its enzymatic and antibacterial activity against streptococci. <i>Scientific Reports</i> , 2016, 6, 35382.	3.3	52
100	Bacteriophages LIMelight and LIMezero of <i>Pantoea agglomerans</i> , Belonging to the $\phi$ KMV-Like Viruses. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3443-3450.	3.1	51
101	The intron-containing genome of the lytic <i>Pseudomonas</i> phage LUZ24 resembles the temperate phage PaP3. <i>Virology</i> , 2008, 377, 233-238.	2.4	50
102	Characterization of two $\beta$ -xylosidases from <i>Bifidobacterium adolescentis</i> and their contribution to the hydrolysis of prebiotic xylooligosaccharides. <i>Applied Microbiology and Biotechnology</i> , 2011, 92, 1179-1185.	3.6	49
103	Phage-host interactions during pseudolysogeny. <i>Bacteriophage</i> , 2013, 3, e25029.	1.9	49
104	DUF3380 Domain from a <i>Salmonella</i> Phage Endolysin Shows Potent N-Acetylmuramidase Activity. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4975-4981.	3.1	49
105	<i>Klebsiella</i> phages representing a novel clade of viruses with an unknown DNA modification and biotechnologically interesting enzymes. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 673-684.	3.6	49
106	Novel N4-Like Bacteriophages of <i>Pectobacterium atrosepticum</i> . <i>Pharmaceuticals</i> , 2018, 11, 45.	3.8	49
107	Selection and Characterization of a Candidate Therapeutic Bacteriophage That Lyses the <i>Escherichia coli</i> O104:H4 Strain from the 2011 Outbreak in Germany. <i>PLoS ONE</i> , 2012, 7, e52709.	2.5	48
108	Identification and comparative analysis of the structural proteomes of $\phi$ KZ and EL, two giant <i>Pseudomonas aeruginosa</i> bacteriophages. <i>Proteomics</i> , 2009, 9, 3215-3219.	2.2	47



#	ARTICLE	IF	CITATIONS
109	The lysis cassette of bacteriophage $\Phi_{KMV}$ encodes a signal-arrest-release endolysin and a pinholin. <i>Bacteriophage</i> , 2011, 1, 25-30.	1.9	47
110	Functional elucidation of antibacterial phage ORFans targeting <i>Pseudomonas aeruginosa</i> . <i>Cellular Microbiology</i> , 2014, 16, 1822-1835.	2.1	47
111	Comparative transcriptomics analyses reveal the conservation of an ancestral infectious strategy in two bacteriophage genera. <i>ISME Journal</i> , 2017, 11, 1988-1996.	9.8	47
112	Structural elucidation of a novel mechanism for the bacteriophage-based inhibition of the RNA degradosome. <i>ELife</i> , 2016, 5, .	6.0	47
113	Functional Genomic Analysis of Two <i>Staphylococcus aureus</i> Phages Isolated from the Dairy Environment. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7663-7673.	3.1	46
114	The adsorption of <i>Pseudomonas aeruginosa</i> bacteriophage $\Phi_{KMV}$ is dependent on expression regulation of type IV pili genes. <i>FEMS Microbiology Letters</i> , 2009, 296, 210-218.	1.8	46
115	Supersize me: <i>Cronobacter sakazakii</i> phage GAP32. <i>Virology</i> , 2014, 460-461, 138-146.	2.4	46
116	Transcriptomic Analysis of the <i>Campylobacter jejuni</i> Response to T4-Like Phage NCTC 12673 Infection. <i>Viruses</i> , 2018, 10, 332.	3.3	46
117	Phage Proteomics: Applications of Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2009, 502, 239-251.	0.9	45
118	Exploring the synthetic biology potential of bacteriophages for engineering non-model bacteria. <i>Nature Communications</i> , 2020, 11, 5294.	12.8	45
119	Phage biocontrol to combat <i>Pseudomonas syringae</i> pathogens causing disease in cherry. <i>Microbial Biotechnology</i> , 2020, 13, 1428-1445.	4.2	44
120	The evolutionary trade-offs in phage-resistant <i>Klebsiella pneumoniae</i> entail cross-phage sensitization and loss of multidrug resistance. <i>Environmental Microbiology</i> , 2021, 23, 7723-7740.	3.8	43
121	Analysis of outer membrane permeability of <i>Pseudomonas aeruginosa</i> and bactericidal activity of endolysins KZ144 and EL188 under high hydrostatic pressure. <i>FEMS Microbiology Letters</i> , 2008, 280, 113-119.	1.8	42
122	High prevalence of IncP-1 plasmids and IS1071 insertion sequences in on-farm biopurification systems and other pesticide-polluted environments. <i>FEMS Microbiology Ecology</i> , 2013, 86, 415-431.	2.7	41
123	A cocktail of in vitro efficient phages is not a guarantee for in vivo therapeutic results against avian colibacillosis. <i>Veterinary Microbiology</i> , 2014, 171, 470-479.	1.9	41
124	Advanced engineering of third-generation lysins and formulation strategies for clinical applications. <i>Critical Reviews in Microbiology</i> , 2020, 46, 548-564.	6.1	41
125	Things Are Getting Hairy: Enterobacteria Bacteriophage $\nu B_{PcaM\_CBB}$ . <i>Frontiers in Microbiology</i> , 2017, 8, 44.	3.5	40
126	Hurdles in bacteriophage therapy: Deconstructing the parameters. <i>Veterinary Microbiology</i> , 2014, 171, 460-469.	1.9	38



#	ARTICLE	IF	CITATIONS
127	A comparative study of different strategies for removal of endotoxins from bacteriophage preparations. <i>Journal of Microbiological Methods</i> , 2017, 132, 153-159.	1.6	37
128	Comparative Analysis of 37 <i>Acinetobacter</i> Bacteriophages. <i>Viruses</i> , 2018, 10, 5.	3.3	37
129	The structural peptidoglycan hydrolase gp181 of bacteriophage $\phi$ KZ. <i>Biochemical and Biophysical Research Communications</i> , 2008, 374, 747-751.	2.1	36
130	New Bacteriophages against Emerging Lineages ST23 and ST258 of <i>Klebsiella pneumoniae</i> and Efficacy Assessment in <i>Galleria mellonella</i> Larvae. <i>Viruses</i> , 2019, 11, 411.	3.3	36
131	SAPPHIRE: a neural network based classifier for $\phi$ 70 promoter prediction in <i>Pseudomonas</i> . <i>BMC Bioinformatics</i> , 2020, 21, 415.	2.6	35
132	Synergistic action of phage phiPLA-RODI and lytic protein CHAPSH3b: a combination strategy to target <i>Staphylococcus aureus</i> biofilms. <i>Npj Biofilms and Microbiomes</i> , 2021, 7, 39.	6.4	34
133	Survey of <i>Pseudomonas aeruginosa</i> and its phages: <i>de novo</i> peptide sequencing as a novel tool to assess the diversity of worldwide collected viruses. <i>Environmental Microbiology</i> , 2009, 11, 1303-1313.	3.8	32
134	Paving a regulatory pathway for phage therapy. <i>EMBO Reports</i> , 2013, 14, 951-954.	4.5	32
135	Viral Transmission Dynamics at Single-Cell Resolution Reveal Transiently Immune Subpopulations Caused by a Carrier State Association. <i>PLoS Genetics</i> , 2015, 11, e1005770.	3.5	32
136	Targeted metagenomics demonstrates the ecological role of IS1071 in bacterial community adaptation to pesticide degradation. <i>Environmental Microbiology</i> , 2018, 20, 4091-4111.	3.8	32
137	Integrative omics analysis of <i>Pseudomonas aeruginosa</i> virus PA5oct highlights the molecular complexity of jumbo phages. <i>Environmental Microbiology</i> , 2020, 22, 2165-2181.	3.8	32
138	Genome-driven elucidation of phage-host interplay and impact of phage resistance evolution on bacterial fitness. <i>ISME Journal</i> , 2022, 16, 533-542.	9.8	32
139	The Kalimantacin/Batumin Biosynthesis Operon Encodes a Self-Resistance Isoform of the FabI Bacterial Target. <i>Chemistry and Biology</i> , 2010, 17, 1067-1071.	6.0	31
140	Antibacterial phage ORFans of <i>Pseudomonas aeruginosa</i> phage LUZ24 reveal a novel MvaT inhibiting protein. <i>Frontiers in Microbiology</i> , 2015, 6, 1242.	3.5	31
141	Representational Difference Analysis (RDA) of bacteriophage genomes. <i>Journal of Microbiological Methods</i> , 2009, 77, 207-213.	1.6	30
142	<i>Pseudomonas aeruginosa</i> PA5oct Jumbo Phage Impacts Planktonic and Biofilm Population and Reduces Its Host Virulence. <i>Viruses</i> , 2019, 11, 1089.	3.3	29
143	The Zeamine Antibiotics Affect the Integrity of Bacterial Membranes. <i>Applied and Environmental Microbiology</i> , 2015, 81, 1139-1146.	3.1	28
144	A combination of polyunsaturated fatty acid, nonribosomal peptide and polyketide biosynthetic machinery is used to assemble the zeamine antibiotics. <i>Chemical Science</i> , 2015, 6, 923-929.	7.4	28

#	ARTICLE	IF	CITATIONS
145	Genomes of <i>φ</i> KMV-like viruses of <i>Pseudomonas aeruginosa</i> contain localized single-strand interruptions. <i>Virology</i> , 2009, 391, 1-4.	2.4	27
146	Indian medicinal plant extracts to control multidrug-resistant <i>S. aureus</i> , including in biofilms. <i>South African Journal of Botany</i> , 2020, 128, 283-291.	2.5	27
147	Characterisation and genome sequence of the lytic <i>Acinetobacter baumannii</i> bacteriophage vB_AbaS_Loki. <i>PLoS ONE</i> , 2017, 12, e0172303.	2.5	26
148	Lysin LysMK34 of <i>Acinetobacter baumannii</i> Bacteriophage PMK34 Has a Turgor Pressure-Dependent Intrinsic Antibacterial Activity and Reverts Colistin Resistance. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	25
149	Bacterial Viruses Subcommittee and Archaeal Viruses Subcommittee of the ICTV: update of taxonomy changes in 2021. <i>Archives of Virology</i> , 2021, 166, 3239-3244.	2.1	24
150	Genome and proteome analysis of 7-7-1, a flagellotropic phage infecting <i>Agrobacterium</i> sp H13-3. <i>Virology Journal</i> , 2012, 9, 102.	3.4	23
151	Characterization and genomic analyses of two newly isolated <i>Morganella</i> phages define distant members among <i>Tevenvirinae</i> and <i>Autographivirinae</i> subfamilies. <i>Scientific Reports</i> , 2017, 7, 46157.	3.3	23
152	Larger Than Life: Isolation and Genomic Characterization of a Jumbo Phage That Infects the Bacterial Plant Pathogen, <i>Agrobacterium tumefaciens</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 1861.	3.5	23
153	<i>σ</i> <sup>Drc</sup> <sup>TM</sup> , a structurally novel ssDNA-binding transcription regulator of N4-related bacterial viruses. <i>Nucleic Acids Research</i> , 2020, 48, 445-459.	14.5	23
154	Three proposed new bacteriophage genera of staphylococcal phages: <i>φ</i> 3alikevirus, <i>φ</i> 77likevirus and <i>φ</i> Phietalikevirus. <i>Archives of Virology</i> , 2014, 159, 389-398.	2.1	22
155	Selection of Potential Therapeutic Bacteriophages that Lyse a CTX-M-15 Extended Spectrum $\beta$ -Lactamase Producing <i>Salmonella enterica</i> Serovar Typhi Strain from the Democratic Republic of the Congo. <i>Viruses</i> , 2018, 10, 172.	3.3	22
156	Phage S144, a New Polyvalent Phage Infecting <i>Salmonella</i> spp. and <i>Cronobacter sakazakii</i> . <i>International Journal of Molecular Sciences</i> , 2020, 21, 5196.	4.1	22
157	A Tailspike with Exopolysaccharide Depolymerase Activity from a New <i>Providencia stuartii</i> Phage Makes Multidrug-Resistant Bacteria Susceptible to Serum-Mediated Killing. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	22
158	A Grad-seq View of RNA and Protein Complexes in <i>Pseudomonas aeruginosa</i> under Standard and Bacteriophage Predation Conditions. <i>MBio</i> , 2021, 12, .	4.1	22
159	Host RNA polymerase inhibitors encoded by <i>φ</i> KMV-like phages of <i>pseudomonas</i> . <i>Virology</i> , 2013, 436, 67-74.	2.4	21
160	<i>Pectobacterium atrosepticum</i> Phage vB_PatP_CB5: A Member of the Proposed Genus <i>φ</i> Phimunavirus <sup>TM</sup> . <i>Viruses</i> , 2018, 10, 394.	3.3	21
161	Isolation and Characterization of <i>Pectobacterium</i> Phage vB_PatM_CB7: New Insights into the Genus <i>Cervivirus</i> . <i>Antibiotics</i> , 2020, 9, 352.	3.7	21
162	Bacteriophage Therapy for Difficult-to-Treat Infections: The Implementation of a Multidisciplinary Phage Task Force (The PHAGEFORCE Study Protocol). <i>Viruses</i> , 2021, 13, 1543.	3.3	21

#	ARTICLE	IF	CITATIONS
163	Digital phagograms: predicting phage infectivity through a multilayer machine learning approach. <i>Current Opinion in Virology</i> , 2022, 52, 174-181.	5.4	21
164	Elucidation of the relative and absolute stereochemistry of the kalimantacin/batumin antibiotics. <i>Chemical Science</i> , 2017, 8, 6196-6201.	7.4	20
165	Completed Genomic Sequence of <i>Bacillus thuringiensis</i> HER1410 Reveals a Cry-Containing Chromosome, Two Megaplasms, and an Integrative Plasmidial Prophage. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2927-2939.	1.8	20
166	The Kalimantacin Polyketide Antibiotics Inhibit Fatty Acid Biosynthesis in <i>Staphylococcus aureus</i> by Targeting the Enoyl- $\beta$ -Acyl Carrier Protein Binding Site of FabI. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 10549-10556.	13.8	20
167	Metabolic reprogramming of <i>Pseudomonas aeruginosa</i> by phage-based quorum sensing modulation. <i>Cell Reports</i> , 2022, 38, 110372.	6.4	20
168	Catabolic task division between two near-isogenic subpopulations co-existing in a herbicide-degrading bacterial consortium: consequences for the interspecies consortium metabolic model. <i>Environmental Microbiology</i> , 2018, 20, 85-96.	3.8	19
169	Introducing differential RNA-seq mapping to track the early infection phase for <i>Pseudomonas</i> phage $\phi$ KZ. <i>RNA Biology</i> , 2021, 18, 1099-1110.	3.1	19
170	Phage-based target discovery and its exploitation towards novel antibacterial molecules. <i>Current Opinion in Biotechnology</i> , 2021, 68, 1-7.	6.6	19
171	Reliable Identification of Environmental <i>Pseudomonas</i> Isolates Using the <i>rpoD</i> Gene. <i>Microorganisms</i> , 2020, 8, 1166.	3.6	18
172	Metabolite profiling and peptidoglycan analysis of transient cell wall-deficient bacteria in a new <i>Escherichia coli</i> model system. <i>Environmental Microbiology</i> , 2015, 17, 1586-1599.	3.8	17
173	Community-led comparative genomic and phenotypic analysis of the aquaculture pathogen <i>Pseudomonas baetica</i> a390T sequenced by Ion semiconductor and Nanopore technologies. <i>FEMS Microbiology Letters</i> , 2018, 365, .	1.8	17
174	Characterization of the Bacteriophage-Derived Endolysins PlySs2 and PlySs9 with In Vitro Lytic Activity against Bovine Mastitis <i>Streptococcus uberis</i> . <i>Antibiotics</i> , 2020, 9, 621.	3.7	17
175	Host Range Expansion of <i>Pseudomonas</i> Virus LUZ7 Is Driven by a Conserved Tail Fiber Mutation. <i>Phage</i> , 2020, 1, 87-90.	1.7	17
176	Preparing for the KIL: Receptor Analysis of <i>Pseudomonas syringae</i> pv. <i>porri</i> Phages and Their Impact on Bacterial Virulence. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2930.	4.1	17
177	Combining sequencing approaches to fully resolve a carbapenemase-encoding megaplasmid in a <i>Pseudomonas shirazica</i> clinical strain. <i>Emerging Microbes and Infections</i> , 2019, 8, 1186-1194.	6.5	16
178	SEVAtile: a standardised DNA assembly method optimised for <i>Pseudomonas</i> . <i>Microbial Biotechnology</i> , 2022, 15, 370-386.	4.2	16
179	The potential of bacteriophages to control <i>Xanthomonas campestris</i> pv. <i>campestris</i> at different stages of disease development. <i>Microbial Biotechnology</i> , 2022, 15, 1762-1782.	4.2	16
180	A procedure for systematic identification of bacteriophage-host interactions of <i>P. aeruginosa</i> phages. <i>Virology</i> , 2009, 387, 50-58.	2.4	15

#	ARTICLE	IF	CITATIONS
181	The temperate Burkholderia phage AP3 of the Peduovirinae shows efficient antimicrobial activity against <i>B. cenocepacia</i> of the IIIA lineage. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1203-1216.	3.6	15
182	Catabolism of the groundwater micropollutant 2,6-dichlorobenzamide beyond 2,6-dichlorobenzoate is plasmid encoded in <i>Aminobacter</i> sp. MSH1. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 7963-7979.	3.6	15
183	Protection of Phage Applications in Crop Production: A Patent Landscape. <i>Viruses</i> , 2019, 11, 277.	3.3	15
184	First Report of Filamentous Phages Isolated from Tunisian Orchards to Control <i>Erwinia amylovora</i> . <i>Microorganisms</i> , 2020, 8, 1762.	3.6	15
185	Characterization of Salmonella Isolates from Various Geographical Regions of the Caucasus and Their Susceptibility to Bacteriophages. <i>Viruses</i> , 2020, 12, 1418.	3.3	15
186	The bacteriophage LUZ24 $\alpha$ -peptide inhibits the <i>Pseudomonas</i> DNA gyrase. <i>Cell Reports</i> , 2021, 36, 109567.	6.4	15
187	Shopping for phages? Unpacking design rules for therapeutic phage cocktails. <i>Current Opinion in Virology</i> , 2022, 52, 236-243.	5.4	15
188	Bacteriophage Therapy for the Prevention and Treatment of Fracture-Related Infection Caused by <i>Staphylococcus aureus</i> : a Preclinical Study. <i>Microbiology Spectrum</i> , 2021, 9, e0173621.	3.0	15
189	Bacteriophage-mediated interference of the cAMP-GMP signalling pathway in <i>Pseudomonas aeruginosa</i> . <i>Microbial Biotechnology</i> , 2021, 14, 967-978.	4.2	14
190	Differential transcription profiling of the phage LUZ19 infection process in different growth media. <i>RNA Biology</i> , 2021, 18, 1778-1790.	3.1	14
191	A Lytic <i>Providencia rettgeri</i> Virus of Potential Therapeutic Value Is a Deep-Branching Member of the $\tau$ 5virus Genus. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	13
192	Characterization of a new podovirus infecting <i>Paenibacillus</i> larvae. <i>Scientific Reports</i> , 2019, 9, 20355.	3.3	13
193	Structural Analysis of Jumbo Coliphage phAPEC6. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3119.	4.1	13
194	Group I introns in <i>Staphylococcus</i> bacteriophages. <i>Future Virology</i> , 2013, 8, 997-1005.	1.8	12
195	Viral interference of the bacterial RNA metabolism machinery. <i>RNA Biology</i> , 2017, 14, 6-10.	3.1	12
196	Biology and Genomics of an Historic Therapeutic <i>Escherichia coli</i> Bacteriophage Collection. <i>Frontiers in Microbiology</i> , 2017, 8, 1652.	3.5	12
197	Preparing cDNA Libraries from Lytic Phage-Infected Cells for Whole Transcriptome Analysis by RNA-Seq. <i>Methods in Molecular Biology</i> , 2018, 1681, 185-194.	0.9	12
198	Natural and Induced Antibodies Against Phages in Humans: Induction Kinetics and Immunogenicity for Structural Proteins of PB1-Related Phages. <i>Phage</i> , 2020, 1, 91-99.	1.7	12

#	ARTICLE	IF	CITATIONS
199	Molecular Characterization and Taxonomic Assignment of Three Phage Isolates from a Collection Infecting <i>Pseudomonas</i> ssp. <i>actinidiae</i> and <i>P. ssp. phaseolicola</i> from Northern Italy. <i>Viruses</i> , 2021, 13, 2083.	3.3	12
200	Deconstructing the Phage-Bacterial Biofilm Interaction as a Basis to Establish New Antibiofilm Strategies. <i>Viruses</i> , 2022, 14, 1057.	3.3	12
201	Novel Bacteriophage Specific against <i>Staphylococcus epidermidis</i> and with Antibiofilm Activity. <i>Viruses</i> , 2022, 14, 1340.	3.3	12
202	Biochemical characterization of malate synthase G of <i>P. aeruginosa</i> . <i>BMC Biochemistry</i> , 2009, 10, 20.	4.4	11
203	The Phage-Encoded N-Acetyltransferase Rac Mediates Inactivation of <i>Pseudomonas aeruginosa</i> Transcription by Cleavage of the RNA Polymerase Alpha Subunit. <i>Viruses</i> , 2020, 12, 976.	3.3	11
204	Genomics of an endemic cystic fibrosis <i>Burkholderia multivorans</i> strain reveals low within-patient evolution but high between-patient diversity. <i>PLoS Pathogens</i> , 2021, 17, e1009418.	4.7	11
205	DNA-Interacting Characteristics of the Archaeal Rudiviral Protein SIRV2_Gp1. <i>Viruses</i> , 2017, 9, 190.	3.3	10
206	Design and Selection of Engineered Lytic Proteins With <i>Staphylococcus aureus</i> Decolonizing Activity. <i>Frontiers in Microbiology</i> , 2021, 12, 723834.	3.5	10
207	Iterative Chemical Engineering of Vancomycin Leads to Novel Vancomycin Analogs With a High in Vitro Therapeutic Index. <i>Frontiers in Microbiology</i> , 2018, 9, 1175.	3.5	9
208	Phage Biocontrol of Bacterial Leaf Blight Disease on Welsh Onion Caused by <i>Xanthomonas axonopodis</i> pv. <i>allii</i> . <i>Antibiotics</i> , 2021, 10, 517.	3.7	9
209	Development of ONT-cappable-seq to unravel the transcriptional landscape of <i>Pseudomonas</i> phages. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2624-2638.	4.1	9
210	A theoretical and experimental proteome map of <i>Pseudomonas aeruginosa</i> PAO1. <i>MicrobiologyOpen</i> , 2012, 1, 169-181.	3.0	8
211	Rapid and High-Throughput Evaluation of Diverse Configurations of Engineered Lysins Using the VersaTile Technique. <i>Antibiotics</i> , 2021, 10, 293.	3.7	8
212	Genome Sequence of <i>Serratia plymuthica</i> RVH1, Isolated from a Raw Vegetable-Processing Line. <i>Genome Announcements</i> , 2014, 2, .	0.8	7
213	Dip-a-Dee-Doo-Dah: Bacteriophage-Mediated Rescoring of a Harmoniously Orchestrated RNA Metabolism. <i>Annual Review of Virology</i> , 2019, 6, 199-213.	6.7	7
214	Bioluminescent avian pathogenic <i>Escherichia coli</i> for monitoring colibacillosis in experimentally infected chickens. <i>Veterinary Journal</i> , 2016, 216, 87-92.	1.7	6
215	The Kalimantacin Polyketide Antibiotics Inhibit Fatty Acid Biosynthesis in <i>Staphylococcus aureus</i> by Targeting the Enoyl Carrier Protein Binding Site of FabI. <i>Angewandte Chemie</i> , 2020, 132, 10636-10643.	2.0	6
216	The Potential Role of Bacteriophages in the Treatment of Recalcitrant Chronic Rhinosinusitis. <i>Antibiotics</i> , 2021, 10, 675.	3.7	6

#	ARTICLE	IF	CITATIONS
217	Total Synthesis of Septocylindrin B and C-Terminus Modified Analogues. PLoS ONE, 2012, 7, e51708.	2.5	5
218	Systematic analysis of the kalimantacin assembly line <scp>NRPS</scp> module using an adapted targeted mutagenesis approach. MicrobiologyOpen, 2016, 5, 279-286.	3.0	5
219	Phenolic Composition, Antimicrobial and Antioxidant Properties of Belgian Apple Wood Extracts. Journal of Biologically Active Products From Nature, 2019, 9, 24-38.	0.3	5
220	Total Synthesis of Kalimantacin A. Organic Letters, 2020, 22, 6349-6353.	4.6	5
221	The complete genome of 2,6-dichlorobenzamide (BAM) degrader Aminobacter sp. MSH1 suggests a polyploid chromosome, phylogenetic reassignment, and functions of plasmids. Scientific Reports, 2021, 11, 18943.	3.3	5
222	Experimental evidence for proteins constituting virion components and particle morphogenesis of bacteriophage ZF40. FEMS Microbiology Letters, 2016, 363, fnw042.	1.8	4
223	High-Throughput Sequencing of Phage Display Libraries Reveals Parasitic Enrichment of Indel Mutants Caused by Amplification Bias. International Journal of Molecular Sciences, 2021, 22, 5513.	4.1	4
224	Two Complete and One Draft Genome Sequence of Nonproteolytic Clostridium botulinum Type E Strains NCTC 8266, NCTC 8550, and NCTC 11219. Genome Announcements, 2015, 3, .	0.8	3
225	A Protein Interaction Map of the Kalimantacin Biosynthesis Assembly Line. Frontiers in Microbiology, 2016, 7, 1726.	3.5	3
226	Identification of Protein-Protein Interactions Using Pool-Array-Based Yeast Two-Hybrid Screening. Methods in Molecular Biology, 2018, 1794, 29-48.	0.9	3
227	Innovative teaching in the digital age goes viral. Nature Microbiology, 2019, 4, 562-564.	13.3	3
228	In silico Characterization of DNA Motifs with Particular Reference to Promoters and Terminators. Methods in Molecular Biology, 2009, 502, 113-129.	0.9	3
229	In Vitro Evaluation of the Therapeutic Potential of Phage VA7 against Enterotoxigenic Bacteroides fragilis Infection. Viruses, 2021, 13, 2044.	3.3	3
230	STORM towards protein function: systematic tailored ORF-data retrieval and management. Applied Bioinformatics, 2003, 2, 177-9.	1.6	3
231	Superinfection exclusion factors drive a history-dependent switch from vertical to horizontal phage transmission. Cell Reports, 2022, 39, 110804.	6.4	3
232	Characterization and Genomic Analysis of a New Phage Infecting Helicobacter pylori. International Journal of Molecular Sciences, 2022, 23, 7885.	4.1	3
233	Structural analysis of bacteriophage-encoded peptidoglycan hydrolase domain KMV36C: crystallization and preliminary X-ray diffraction. Acta Crystallographica Section F: Structural Biology Communications, 2008, 64, 263-265.	0.7	2
234	Quality control and statistical evaluation of combinatorial DNA libraries using nanopore sequencing. BioTechniques, 2020, 69, 379-383.	1.8	2

#	ARTICLE	IF	CITATIONS
235	qDNase assay: A quantitative method for real-time assessment of DNase activity on coated surfaces. <i>Biochemical and Biophysical Research Communications</i> , 2021, 534, 1003-1006.	2.1	2
236	Editorial overview: Phage therapy in the 21st century – inspired by biotechnology!. <i>Current Opinion in Biotechnology</i> , 2021, 68, vi-vii.	6.6	2
237	Transcriptional Organization of the Salmonella Typhimurium Phage P22 pid ORFan Locus. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1253.	4.1	2
238	P22 mediated recombination of <i>frt</i> -sites. <i>Virology</i> , 2014, 462-463, 340-342.	2.4	1
239	Phage Therapy. <i>Wikijournal of Medicine</i> , 2021, 8, 4.	1.0	1
240	Long-Range PCR Reveals the Genetic Cargo of IncP-1 Plasmids in the Complex Microbial Community of an On-Farm Biopurification System Treating Pesticide-Contaminated Wastewater. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0164821.	3.1	1
241	Unraveling Protein Interactions between the Temperate Virus Bam35 and Its <i>Bacillus</i> Host Using an Integrative Yeast Two Hybrid – High Throughput Sequencing Approach. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11105.	4.1	0
242	VIROPLANT in a Nutshell. <i>Phage</i> , 2020, 1, 174-175.	1.7	0
243	SASpector: analysis of missing genomic regions in draft genomes of prokaryotes. <i>Bioinformatics</i> , 2022, , .	4.1	0