

Jochen Klumpp

List of Publications by Year in descending order

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Version: 2024-02-01

91
papers

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citations

94381

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#	ARTICLE	IF	CITATIONS
1	Gene gain and loss and recombination shape evolution of <i>Listeria</i> bacteriophages of the genus <i>Pecentumvirus</i> . <i>Genomics</i> , 2021, 113, 411-419.	1.3	3
2	Isolation and Characterization of vB_MsmS_Celfi: A New <i>Mycobacterium tuberculosis</i> Bacteriophage. <i>Phage</i> , 2021, 2, 43-49.	0.8	1
3	Genome Sequence and Characterization of <i>Lactobacillus casei</i> Phage, vB_LcaM_Lbab1 Isolated from Raw Milk. <i>Phage</i> , 2021, 2, 57-63.	0.8	2
4	<i>Campylobacter</i> phages use hypermutable polyG tracts to create phenotypic diversity and evade bacterial resistance. <i>Cell Reports</i> , 2021, 35, 109214.	2.9	15
5	Identification of Novel Phage Resistance Mechanisms in <i>Campylobacter jejuni</i> by Comparative Genomics. <i>Frontiers in Microbiology</i> , 2021, 12, 780559.	1.5	7
6	Analysis of Spounaviruses as a Case Study for the Overdue Reclassification of Tailed Phages. <i>Systematic Biology</i> , 2020, 69, 110-123.	2.7	89
7	Bacteriophages: a Panacea in Neuro-Urology?. <i>European Urology Focus</i> , 2020, 6, 518-521.	1.6	11
8	Taxonomy of prokaryotic viruses: 2018-2019 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2020, 165, 1253-1260.	0.9	144
9	Development of a broad-spectrum <i>Salmonella</i> phage cocktail containing Viunalike and Jerseylike viruses isolated from Thailand. <i>Food Microbiology</i> , 2020, 92, 103586.	2.1	31
10	Differential transcriptome analysis of enterohemorrhagic <i>Escherichia coli</i> strains reveals differences in response to plant-derived compounds. <i>BMC Microbiology</i> , 2019, 19, 212.	1.3	6
11	A major-capsid-protein-based multiplex PCR assay for rapid identification of selected virulent bacteriophage types. <i>Archives of Virology</i> , 2019, 164, 819-830.	0.9	17
12	Characterization of Flagellotropic, Chi-Like <i>Salmonella</i> Phages Isolated from Thai Poultry Farms. <i>Viruses</i> , 2019, 11, 520.	1.5	28
13	Whole-genome-based phylogeny of <i>Bacillus cytotoxicus</i> reveals different clades within the species and provides clues on ecology and evolution. <i>Scientific Reports</i> , 2019, 9, 1984.	1.6	35
14	Structure and transformation of bacteriophage A511 baseplate and tail upon infection of <i>Listeria</i> cells. <i>EMBO Journal</i> , 2019, 38, .	3.5	34
15	Complete nucleotide sequences of six blaCTX-M-1-encoding plasmids from <i>Escherichia coli</i> isolated from urinary tract and wound infections in dogs. <i>Journal of Global Antimicrobial Resistance</i> , 2019, 16, 117-119.	0.9	0
16	Taxonomy of prokaryotic viruses: 2017 update from the ICTV Bacterial and Archaeal Viruses Subcommittee. <i>Archives of Virology</i> , 2018, 163, 1125-1129.	0.9	172
17	Cross-genus rebooting of custom-made, synthetic bacteriophage genomes in L-form bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 567-572.	3.3	155
18	Growth advantage of <i>Escherichia coli</i> O104:H4 strains on 5- N -acetyl-9- O -acetyl neuraminic acid as a carbon source is dependent on heterogeneous phage-Borne nanS-p esterases. <i>International Journal of Medical Microbiology</i> , 2018, 308, 459-468.	1.5	18

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19	Chromosomal Sil system contributes to silver resistance in <i>E. coli</i> ATCC 8739. <i>BioMetals</i> , 2018, 31, 1101-1114.	1.8	12
20	Salmonella Phage S16 Tail Fiber Adhesin Features a Rare Polyglycine Rich Domain for Host Recognition. <i>Structure</i> , 2018, 26, 1573-1582.e4.	1.6	69
21	Molecular Basis of Bacterial Host Interactions by Gram-Positive Targeting Bacteriophages. <i>Viruses</i> , 2018, 10, 397.	1.5	76
22	A functional type II-A CRISPR-Cas system from <i>Listeria</i> enables efficient genome editing of large non-integrating bacteriophage. <i>Nucleic Acids Research</i> , 2018, 46, 6920-6933.	6.5	58
23	Modified Bacteriophage S16 Long Tail Fiber Proteins for Rapid and Specific Immobilization and Detection of Salmonella Cells. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	59
24	Complete and Assembled Genome Sequence of <i>Lactobacillus plantarum</i> RI-113 Isolated from Salami. <i>Genome Announcements</i> , 2017, 5, .	0.8	6
25	Full-Genome Sequence of <i>Listeria monocytogenes</i> Strain H34, Isolated from a Newborn with Sepsis in Uruguay. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
26	TetR-dependent gene regulation in intracellular <i>Listeria monocytogenes</i> demonstrates the spatiotemporal surface distribution of ActA. <i>Molecular Microbiology</i> , 2017, 105, 413-425.	1.2	4
27	Stable core virome despite variable microbiome after fecal transfer. <i>Gut Microbes</i> , 2017, 8, 214-220.	4.3	60
28	Complete Genome Sequence of <i>Citrobacter freundii</i> 705SK3, an OXA-48-Encoding Wastewater Isolate. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
29	Complete Genome Sequence of <i>Escherichia coli</i> ABWA45, an rmtB-Encoding Wastewater Isolate. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
30	Complete Genome Sequence of <i>Enterobacter cloacae</i> 704SK10, an OXA-48-Encoding Wastewater Isolate. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
31	Draft Genome Sequence of <i>Klebsiella pneumoniae</i> 704SK6, an OXA-48- and CTX-M-15-Encoding Wastewater Isolate. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
32	Draft Genome Sequences of Five Shiga Toxin-Producing <i>Escherichia coli</i> Isolates Harboring the New and Recently Described Subtilase Cytotoxin Allelic Variant subAB 2-3. <i>Genome Announcements</i> , 2017, 5, .	0.8	7
33	Taxonomy of prokaryotic viruses: 2016 update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2017, 162, 1153-1157.	0.9	57
34	Complete Genome Sequence of <i>Anoxybacillus flavithermus</i> Strain 52-1A Isolated from a Heat-Processed Powdered Milk Concentrate. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
35	Key features of mcr-1-bearing plasmids from <i>Escherichia coli</i> isolated from humans and food. <i>Antimicrobial Resistance and Infection Control</i> , 2017, 6, 91.	1.5	64
36	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.	1.5	86

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37	Complete Genome Sequence of <i>Staphylococcus carnosus</i> LTH 3730. <i>Genome Announcements</i> , 2016, 4, .	0.8	2
38	Long-term microbiota and virome in a Z ^{1/4} rich patient after fecal transplantation against <i>Clostridium difficile</i> infection. <i>Annals of the New York Academy of Sciences</i> , 2016, 1372, 29-41.	1.8	38
39	Genome Sequences of <i>Listeria monocytogenes</i> Strains Responsible for Cheese- and Cooked Ham Product-Associated Swiss Listeriosis Outbreaks in 2005 and 2011. <i>Genome Announcements</i> , 2016, 4, .	0.8	17
40	Long-term changes of bacterial and viral compositions in the intestine of a recovered <i>Clostridium difficile</i> patient after fecal microbiota transplantation. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a000448.	0.5	50
41	Genome Sequences of Five Nonvirulent <i>Listeria monocytogenes</i> Serovar 4 Strains. <i>Genome Announcements</i> , 2016, 4, .	0.8	4
42	<i>Escherichia coli</i> O157:H7 Strain EDL933 Harbors Multiple Functional Prophage-Associated Genes Necessary for the Utilization of 5-N-Acetyl-9-O-Acetyl Neuraminic Acid as a Growth Substrate. <i>Applied and Environmental Microbiology</i> , 2016, 82, 5940-5950.	1.4	40
43	Full-Length Nucleotide Sequences of <i>mcr-1</i> -Harboring Plasmids Isolated from Extended-Spectrum- β -Lactamase-Producing <i>Escherichia coli</i> Isolates of Different Origins. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 5589-5591.	1.4	72
44	Taxonomy of prokaryotic viruses: update from the ICTV bacterial and archaeal viruses subcommittee. <i>Archives of Virology</i> , 2016, 161, 1095-1099.	0.9	83
45	Potential of phage cocktails in the inactivation of <i>Enterobacter cloacae</i> – An in vitro study in a buffer solution and in urine samples. <i>Virus Research</i> , 2016, 211, 199-208.	1.1	38
46	Analyses of the Distribution Patterns of <i>Burkholderia pseudomallei</i> and Associated Phages in Soil Samples in Thailand Suggest That Phage Presence Reduces the Frequency of Bacterial Isolation. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005005.	1.3	21
47	Prevalence of subtilase cytotoxin-encoding subAB variants among Shiga toxin-producing <i>Escherichia coli</i> strains isolated from wild ruminants and sheep differs from that of cattle and pigs and is predominated by the new allelic variant subAB2-2. <i>International Journal of Medical Microbiology</i> , 2015, 305, 124-128.	1.5	15
48	Genome Sequences of the <i>Listeria ivanovii</i> subsp. <i>ivanovii</i> Type Strain and Two <i>Listeria ivanovii</i> subsp. <i>londoniensis</i> Strains. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
49	Receptor binding proteins of <i>Listeria monocytogenes</i> bacteriophages A118 and P35 recognize serovar-specific teichoic acids. <i>Virology</i> , 2015, 477, 110-118.	1.1	47
50	Complete Genome Sequence of <i>Listeria monocytogenes</i> N2306, a Strain Associated with the 2013-2014 Listeriosis Outbreak in Switzerland. <i>Genome Announcements</i> , 2015, 3, .	0.8	14
51	Taxonomic reassessment of N4-like viruses using comparative genomics and proteomics suggests a new subfamily - ϵ Enquartavirinae. <i>Archives of Virology</i> , 2015, 160, 3053-3062.	0.9	36
52	Putative type 1 thymidylate synthase and dihydrofolate reductase as signature genes of a novel bastille-like group of phages in the subfamily Spounavirinae. <i>BMC Genomics</i> , 2015, 16, 582.	1.2	26
53	Complete genome sequence analysis and identification of putative metallo-beta-lactamase and SpoIIIE homologs in <i>Bacillus cereus</i> group phage BCP8-2, a new member of the proposed Bastille-like group. <i>Archives of Virology</i> , 2015, 160, 2647-2650.	0.9	3
54	<i>Bifidobacterium pseudolongum</i> Strain PV8-2, Isolated from a Stool Sample of an Anemic Kenyan Infant. <i>Genome Announcements</i> , 2015, 3, .	0.8	9

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55	Complete and Assembled Genome Sequence of Bifidobacterium kashiwanohense PV20-2, Isolated from the Feces of an Anemic Kenyan Infant. Genome Announcements, 2015, 3, .	0.8	10
56	A Novel Tn3-Like Composite Transposon Harboring blaVIM-1 in Klebsiella pneumoniae spp. pneumoniae isolated from River Water. Microbial Drug Resistance, 2015, 21, 43-49.	0.9	10
57	Vertical transmission of highly similar blaCTX-M-1-harboring IncI1 plasmids in Escherichia coli with different MLST types in the poultry production pyramid. Frontiers in Microbiology, 2014, 5, 519.	1.5	74
58	Genome Sequences of Three Frequently Used Listeria monocytogenes and Listeria ivanovii Strains. Genome Announcements, 2014, 2, .	0.8	9
59	Complete Genome Sequence of Listeria monocytogenes Lm60, a Strain with an Enhanced Cold Adaptation Capacity. Genome Announcements, 2014, 2, .	0.8	2
60	Methyltransferases acquired by lactococcal 936-type phage provide protection against restriction endonuclease activity. BMC Genomics, 2014, 15, 831.	1.2	26
61	The tail-associated depolymerase of <i>Escherichia amylovora</i> phage <i>L1</i> mediates host cell adsorption and enzymatic capsule removal, which can enhance infection by other phage. Environmental Microbiology, 2014, 16, 2168-2180.	1.8	45
62	A cocktail of in vitro efficient phages is not a guarantee for in vivo therapeutic results against avian colibacillosis. Veterinary Microbiology, 2014, 171, 470-479.	0.8	41
63	<i>Escherichia coli</i> phage <i>A511</i> , a model for the contractile tail machineries of <i>SPO</i> -related bacteriophages. Molecular Microbiology, 2014, 92, 84-99.	1.2	55
64	The odd one out: Bacillus ACT bacteriophage CP-51 exhibits unusual properties compared to related Spounavirinae W.Ph. and Bastille. Virology, 2014, 462-463, 299-308.	1.1	15
65	Detection of Bacteria with Bioluminescent Reporter Bacteriophage. Advances in Biochemical Engineering/Biotechnology, 2014, 144, 155-171.	0.6	10
66	Novel Giant Siphovirus from Bacillus anthracis Features Unusual Genome Characteristics. PLoS ONE, 2014, 9, e85972.	1.1	22
67	Whole genome sequencing and comparative genomic analyses of two Vibrio cholerae O139 Bengal-specific Podoviruses to other N4-like phages reveal extensive genetic diversity. Virology Journal, 2013, 10, 165.	1.4	38
68	Feasibility of spray drying bacteriophages into respirable powders to combat pulmonary bacterial infections. European Journal of Pharmaceutics and Biopharmaceutics, 2013, 84, 578-582.	2.0	101
69	Bacteriophage functional genomics and its role in bacterial pathogen detection. Briefings in Functional Genomics, 2013, 12, 354-365.	1.3	20
70	Genome Sequence of Salmonella bongori Strain N268-08, a Rare Clinical Isolate. Genome Announcements, 2013, 1, .	0.8	2
71	Analysis of the Intestinal Microbiome of a Recovered & Clostridium difficile Patient after Fecal Transplantation. Digestion, 2013, 88, 243-251.	1.2	33
72	Long tail fibres of the novel broad-host-range <i>T-even</i> bacteriophage <i>S</i> 16 specifically recognize <i>Salmonella</i> <i>OmpC</i> . Molecular Microbiology, 2013, 87, 818-834.	1.2	102

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73	<i>Listeria</i> phages. <i>Bacteriophage</i> , 2013, 3, e26861.	1.9	70
74	Complete Genome Sequence of the Novel <i>Escherichia coli</i> Phage phAPEC8. <i>Journal of Virology</i> , 2012, 86, 13117-13118.	1.5	22
75	Inducible <i>Clostridium perfringens</i> bacteriophages ϕ S9 and ϕ S63. <i>Bacteriophage</i> , 2012, 2, 89-97.	1.9	16
76	Next generation sequencing technologies and the changing landscape of phage genomics. <i>Bacteriophage</i> , 2012, 2, 190-199.	1.9	57
77	Endolysins as Antimicrobials. <i>Advances in Virus Research</i> , 2012, 83, 299-365.	0.9	291
78	Bacteriophage P70: Unique Morphology and Unrelatedness to Other <i>Listeria</i> Bacteriophages. <i>Journal of Virology</i> , 2012, 86, 13099-13102.	1.5	27
79	Biocontrol of <i>Salmonella</i> Typhimurium in RTE foods with the virulent bacteriophage FO1-E2. <i>International Journal of Food Microbiology</i> , 2012, 154, 66-72.	2.1	178
80	Genome Sequence of <i>Listeria monocytogenes</i> Scott A, a Clinical Isolate from a Food-Borne Listeriosis Outbreak. <i>Journal of Bacteriology</i> , 2011, 193, 4284-4285.	1.0	74
81	The SPO1-related bacteriophages. <i>Archives of Virology</i> , 2010, 155, 1547-1561.	0.9	91
82	<i>Brochothrix thermosphacta</i> Bacteriophages Feature Heterogeneous and Highly Mosaic Genomes and Utilize Unique Prophage Insertion Sites. <i>Journal of Bacteriology</i> , 2010, 192, 5441-5453.	1.0	39
83	Complete Nucleotide Sequence and Molecular Characterization of <i>Bacillus</i> Phage TP21 and its Relatedness to Other Phages with the Same Name. <i>Viruses</i> , 2010, 2, 961-971.	1.5	20
84	Comparative Genome Analysis of <i>Listeria</i> Bacteriophages Reveals Extensive Mosaicism, Programmed Translational Frameshifting, and a Novel Prophage Insertion Site. <i>Journal of Bacteriology</i> , 2009, 191, 7206-7215.	1.0	133
85	Role of Cold Shock Proteins in Growth of <i>Listeria monocytogenes</i> under Cold and Osmotic Stress Conditions. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1621-1627.	1.4	189
86	PEGylation of bacteriophages increases blood circulation time and reduces T _H 1 immune response. <i>Microbial Biotechnology</i> , 2008, 1, 247-257.	2.0	93
87	The Terminally Redundant, Nonpermuted Genome of <i>Listeria</i> Bacteriophage A511: a Model for the SPO1-Like Myoviruses of Gram-Positive Bacteria. <i>Journal of Bacteriology</i> , 2008, 190, 5753-5765.	1.0	122
88	Pathogenomics of <i>Listeria</i> spp.. <i>International Journal of Medical Microbiology</i> , 2007, 297, 541-557.	1.5	84
89	<i>Enterobacter sakazakii</i> bacteriophages can prevent bacterial growth in reconstituted infant formula. <i>International Journal of Food Microbiology</i> , 2007, 115, 195-203.	2.1	101
90	Identification of novel genes in genomic islands that contribute to <i>Salmonella typhimurium</i> replication in macrophages. <i>Microbiology (United Kingdom)</i> , 2007, 153, 1207-1220.	0.7	98

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91	Insertion-duplication mutagenesis of <i>Salmonella enterica</i> and related species using a novel thermosensitive vector. <i>Plasmid</i> , 2006, 55, 39-49.	0.4	6