

Jens A Hammerl

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5712448/publications.pdf>

Version: 2024-02-01

130
papers

4,660
citations

101543

36
h-index

118850

62
g-index

134
all docs

134
docs citations

134
times ranked

5153
citing authors

#	ARTICLE	IF	CITATIONS
1	Slaughterhouse wastewater as a reservoir for extended-spectrum β -lactamase (ESBL)-producing, and colistin-resistant <i>Klebsiella</i> spp. and their impact in a "One Health"-perspective. <i>Science of the Total Environment</i> , 2022, 804, 150000.	8.0	15
2	Global colistin use: a review of the emergence of resistant <i>Enterobacterales</i> and the impact on their genetic basis. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	8.6	79
3	<i>Mammaliicoccus</i> spp. from German Dairy Farms Exhibit a Wide Range of Antimicrobial Resistance Genes and Non-Wildtype Phenotypes to Several Antibiotic Classes. <i>Biology</i> , 2022, 11, 152.	2.8	8
4	Editorial for the Special Issue: "Antimicrobial Resistance and Molecular Tracing of Foodborne Pathogens". <i>Microorganisms</i> , 2022, 10, 390.	3.6	0
5	Practical Assessment of an Interdisciplinary Bacteriophage Delivery Pipeline for Personalized Therapy of Gram-Negative Bacterial Infections. <i>Pharmaceuticals</i> , 2022, 15, 186.	3.8	8
6	Genetic Characterization of Carbapenem-Resistant <i>Klebsiella</i> spp. from Municipal and Slaughterhouse Wastewater. <i>Antibiotics</i> , 2022, 11, 435.	3.7	9
7	Multicentre evaluation of a selective isolation protocol for detection of <i>Mycobacterium tuberculosis</i> complex and <i>Salmonella</i> spp. in food-producing animals and meat. <i>Letters in Applied Microbiology</i> , 2022, , .	2.2	4
8	Different <i>fosA</i> genes were found on mobile genetic elements in <i>Escherichia coli</i> from wastewaters of hospitals and municipals in Turkey. <i>Science of the Total Environment</i> , 2022, 824, 153928.	8.0	6
9	Characterization of <i>qnrB</i> -carrying plasmids from ESBL- and non-ESBL-producing <i>Escherichia coli</i> . <i>BMC Genomics</i> , 2022, 23, 365.	2.8	6
10	Occurrence and Genomic Characterization of Clone ST1193 Clonotype 14-64 in Uncomplicated Urinary Tract Infections Caused by <i>Escherichia coli</i> in Spain. <i>Microbiology Spectrum</i> , 2022, 10, .	3.0	12
11	Host Range, Morphology and Sequence Analysis of Ten Temperate Phages Isolated from Pathogenic <i>Yersinia enterocolitica</i> Strains. <i>International Journal of Molecular Sciences</i> , 2022, 23, 6779.	4.1	4
12	Co-occurrence of the <i>bla</i> _{VIM-1} and <i>bla</i> _{SHV-12} genes on an IncHI2 plasmid of an <i>Escherichia coli</i> isolate recovered from German livestock. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 531-533.	3.0	8
13	Draft Genome Sequences of <i>Pseudomonas</i> sp. Isolates Recovered from Ghanaian Fish Food Samples in 2018. <i>Microbiology Resource Announcements</i> , 2021, 10, .	0.6	1
14	Outcome of Different Sequencing and Assembly Approaches on the Detection of Plasmids and Localization of Antimicrobial Resistance Genes in Commensal <i>Escherichia coli</i> . <i>Microorganisms</i> , 2021, 9, 598.	3.6	36
15	Genetic but No Phenotypic Associations between Biocide Tolerance and Antibiotic Resistance in <i>Escherichia coli</i> from German Broiler Fattening Farms. <i>Microorganisms</i> , 2021, 9, 651.	3.6	21
16	Multidrug-resistant <i>Staphylococcus cohnii</i> and <i>Staphylococcus urealyticus</i> isolates from German dairy farms exhibit resistance to beta-lactam antibiotics and divergent penicillin-binding proteins. <i>Scientific Reports</i> , 2021, 11, 6075.	3.3	10
17	Clinically Relevant <i>Escherichia coli</i> Isolates from Process Waters and Wastewater of Poultry and Pig Slaughterhouses in Germany. <i>Microorganisms</i> , 2021, 9, 698.	3.6	17
18	Genome-Based Analysis of <i>Klebsiella</i> spp. Isolates from Animals and Food Products in Germany, 2013–2017. <i>Pathogens</i> , 2021, 10, 573.	2.8	22

#	ARTICLE	IF	CITATIONS
19	Analysis of <i>Yersinia pseudotuberculosis</i> Isolates Recovered from Deceased Mammals of a German Zoo Animal Collection. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	3.9	9
20	Isolation Procedure for CP <i>E. coli</i> from Caeca Samples under Review towards an Increased Sensitivity. <i>Microorganisms</i> , 2021, 9, 1105.	3.6	0
21	Phenotypic and Genotypic Properties of Fluoroquinolone-Resistant, qnr-Carrying <i>Escherichia coli</i> Isolated from the German Food Chain in 2017. <i>Microorganisms</i> , 2021, 9, 1308.	3.6	7
22	Comparison of MICs in <i>Escherichia coli</i> isolates from human health surveillance with MICs obtained for the same isolates by broth microdilution. <i>JAC-Antimicrobial Resistance</i> , 2021, 3, dlab145.	2.1	2
23	Antibiotic-resistant bacteria, antibiotic resistance genes, and antibiotic residues in wastewater from a poultry slaughterhouse after conventional and advanced treatments. <i>Scientific Reports</i> , 2021, 11, 16622.	3.3	22
24	The Lytic Siphophage vB_StyS-LmqSP1 Reduces the Number of <i>Salmonella enterica</i> Serovar Typhimurium Isolates on Chicken Skin. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0142421.	3.1	7
25	Characterization of <i>E. coli</i> Isolates Producing Extended Spectrum Beta-Lactamase SHV-Variants from the Food Chain in Germany. <i>Microorganisms</i> , 2021, 9, 1926.	3.6	6
26	Dissection of Highly Prevalent qnrS1-Carrying IncX Plasmid Types in Commensal <i>Escherichia coli</i> from German Food and Livestock. <i>Antibiotics</i> , 2021, 10, 1236.	3.7	4
27	Properties of Two Broad Host Range Phages of <i>Yersinia enterocolitica</i> Isolated from Wild Animals. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11381.	4.1	8
28	Identification of a blaVIM-1-Carrying IncA/C2 Multiresistance Plasmid in an <i>Escherichia coli</i> Isolate Recovered from the German Food Chain. <i>Microorganisms</i> , 2021, 9, 29.	3.6	5
29	The Acquisition of the scr Gene Cluster Encoding Sucrose Metabolization Enzymes Enables Strains of <i>Vibrio parahaemolyticus</i> and <i>Vibrio vulnificus</i> to Utilize Sucrose as Carbon Source. <i>Frontiers in Microbiology</i> , 2021, 12, 754464.	3.5	0
30	Birds Kept in the German Zoo "Tierpark Berlin" Are a Common Source for Polyvalent <i>Yersinia pseudotuberculosis</i> Phages. <i>Frontiers in Microbiology</i> , 2021, 12, 634289.	3.5	2
31	Isolation and Characterization of Group III <i>Campylobacter jejuni</i> -Specific Bacteriophages From Germany and Their Suitability for Use in Food Production. <i>Frontiers in Microbiology</i> , 2021, 12, 761223.	3.5	9
32	ChromID® CARBA Agar Fails to Detect Carbapenem-Resistant Enterobacteriaceae With Slightly Reduced Susceptibility to Carbapenems. <i>Frontiers in Microbiology</i> , 2020, 11, 1678.	3.5	7
33	Colistin-Resistant Enterobacteriaceae Isolated From Process Waters and Wastewater From German Poultry and Pig Slaughterhouses. <i>Frontiers in Microbiology</i> , 2020, 11, 575391.	3.5	26
34	A Proof of Principle for the Detection of Viable <i>Brucella</i> spp. in Raw Milk by qPCR Targeting Bacteriophages. <i>Microorganisms</i> , 2020, 8, 1326.	3.6	3
35	Phenotypic and Genotypic Properties of <i>Vibrio cholerae</i> non-O1, non-O139 Isolates Recovered from Domestic Ducks in Germany. <i>Microorganisms</i> , 2020, 8, 1104.	3.6	10
36	First Detection of GES-5-Producing <i>Escherichia coli</i> from Livestock "An Increasing Diversity of Carbapenemases Recognized from German Pig Production. <i>Microorganisms</i> , 2020, 8, 1593.	3.6	13

#	ARTICLE	IF	CITATIONS
37	Phenotypic and Genotypic Characterization of Veterinary <i>Vibrio cincinnatiensis</i> Isolates. <i>Microorganisms</i> , 2020, 8, 739.	3.6	10
38	Antibiotic-resistant bacteria and antimicrobial residues in wastewater and process water from German pig slaughterhouses and their receiving municipal wastewater treatment plants. <i>Science of the Total Environment</i> , 2020, 727, 138788.	8.0	57
39	The <i>Burkholderia thailandensis</i> Phages ϕ E058 and ϕ E067 Represent Distinct Prototypes of a New Subgroup of Temperate <i>Burkholderia</i> Myoviruses. <i>Frontiers in Microbiology</i> , 2020, 11, 1120.	3.5	3
40	Spill-Over from Public Health? First Detection of an OXA-48-Producing <i>Escherichia coli</i> in a German Pig Farm. <i>Microorganisms</i> , 2020, 8, 855.	3.6	24
41	Development of a Novel <i>mcr-6</i> to <i>mcr-9</i> Multiplex PCR and Assessment of <i>mcr-1</i> to <i>mcr-9</i> Occurrence in Colistin-Resistant <i>Salmonella enterica</i> Isolates From Environment, Feed, Animals and Food (2011–2018) in Germany. <i>Frontiers in Microbiology</i> , 2020, 11, 80.	3.5	118
42	Typing methods based on whole genome sequencing data. <i>One Health Outlook</i> , 2020, 2, 3.	3.4	90
43	ESKAPE Bacteria and Extended-Spectrum- β -Lactamase-Producing <i>Escherichia coli</i> Isolated from Wastewater and Process Water from German Poultry Slaughterhouses. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	67
44	Wildlife as Sentinels of Antimicrobial Resistance in Germany?. <i>Frontiers in Veterinary Science</i> , 2020, 7, 627821.	2.2	71
45	Genomic Distinctions of LA-MRSA ST398 on Dairy Farms From Different German Federal States With a Low Risk of Severe Human Infections. <i>Frontiers in Microbiology</i> , 2020, 11, 575321.	3.5	16
46	Draft Genome Sequences of <i>Vibrio cholerae</i> Non-O1, Non-O139 Isolates from Common Tern Chicks (<i>T. t. ETQq0000rgBT/Overlock 10 Tf</i>) 2020, 9, .	0.6	4
47	Fishing in the Soup – Pathogen Detection in Food Safety Using Metabarcoding and Metagenomic Sequencing. <i>Frontiers in Microbiology</i> , 2019, 10, 1805.	3.5	49
48	Biocide-Tolerant <i>Listeria monocytogenes</i> Isolates from German Food Production Plants Do Not Show Cross-Resistance to Clinically Relevant Antibiotics. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	37
49	Draft Genome Sequences of <i>Acinetobacter baumannii</i> Isolates Recovered from Sewage Water from a Poultry Slaughterhouse in Germany. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	3
50	Characterization of VIM-1-Producing <i>E. coli</i> Isolated From a German Fattening Pig Farm by an Improved Isolation Procedure. <i>Frontiers in Microbiology</i> , 2019, 10, 2256.	3.5	31
51	Environmental and Clinical Strains of <i>Vibrio cholerae</i> Non-O1, Non-O139 From Germany Possess Similar Virulence Gene Profiles. <i>Frontiers in Microbiology</i> , 2019, 10, 733.	3.5	47
52	Characterization of <i>mcr-5</i> -Harboring <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar Typhimurium Isolates from Animal and Food Origin in Germany. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	41
53	<i>Campylobacter</i> Phage Isolation and Characterization: What We Have Learned So Far. <i>Methods and Protocols</i> , 2019, 2, 18.	2.0	18
54	<i>mcr-5</i> and a novel <i>mcr-5.2</i> variant in <i>Escherichia coli</i> isolates from food and food-producing animals, Germany, 2010 to 2017. <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 1433-1435.	3.0	50

#	ARTICLE	IF	CITATIONS
55	Multiplex PCR for detection of plasmid-mediated colistin resistance determinants, <i>mcr-1</i> , <i>mcr-2</i> , <i>mcr-3</i> , <i>mcr-4</i> and <i>mcr-5</i> for surveillance purposes. <i>Eurosurveillance</i> , 2018, 23, .	7.0	431
56	Complete Genome Sequence of a <i>bla</i> CTX-M-1 -Harboring <i>Escherichia coli</i> Isolate Recovered from Cattle in Germany. <i>Genome Announcements</i> , 2018, 6, .	0.8	6
57	Complete Draft Genome Sequence of an Extended-Spectrum β -Lactamase-Producing <i>Citrobacter freundii</i> Strain Recovered from the Intestine of a House Sparrow (<i>Passer domesticus</i>) in Germany, 2017. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
58	Complete Genome Sequence of a VIM-1-Producing <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar <i>Infantis</i> Isolate Derived from Minced Pork Meat. <i>Genome Announcements</i> , 2018, 6, .	0.8	11
59	Complete Genome Sequences of 10 <i>Yersinia pseudotuberculosis</i> Isolates Recovered from Wild Boars in Germany. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
60	<i>Yersinia pseudotuberculosis</i> Prevalence and Diversity in Wild Boars in Northeast Germany. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	17
61	Diversity of CTX-M-1-producing <i>E. coli</i> from German food samples and genetic diversity of the <i>bla</i> CTX-M-1 region on <i>Incl1</i> ST3 plasmids. <i>Veterinary Microbiology</i> , 2018, 221, 98-104.	1.9	54
62	Molecular Survey on Brucellosis in Rodents and Shrews - Natural Reservoirs of Novel <i>Brucella</i> Species in Germany?. <i>Transboundary and Emerging Diseases</i> , 2017, 64, 663-671.	3.0	6
63	Overview of validated alternative methods for the detection of foodborne bacterial pathogens. <i>Trends in Food Science and Technology</i> , 2017, 62, 113-118.	15.1	87
64	VIM-1-producing <i>Salmonella Infantis</i> isolated from swine and minced pork meat in Germany. <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 2131-2133.	3.0	45
65	<i>Brucella</i> spp. of amphibians comprise genomically diverse motile strains competent for replication in macrophages and survival in mammalian hosts. <i>Scientific Reports</i> , 2017, 7, 44420.	3.3	96
66	Identification of a novel transposon-associated phosphoethanolamine transferase gene, <i>mcr-5</i> , conferring colistin resistance in d-tartrate fermenting <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Paratyphi B</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017, 72, 3317-3324.	3.0	450
67	Complete Genome Sequence of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar <i>Paratyphi B</i> Sequence Type 28 Harboring <i>mcr-1</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	8
68	Complete Genome Sequence of the Temperate <i>Klebsiella pneumoniae</i> Phage KPP5665-2. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
69	Acquisition of virulence factors in livestock-associated MRSA: Lysogenic conversion of CC398 strains by virulence gene-containing phages. <i>Scientific Reports</i> , 2017, 7, 2004.	3.3	41
70	Differential detection of pathogenic <i>Yersinia</i> spp. by fluorescence in situ hybridization. <i>Food Microbiology</i> , 2017, 62, 39-45.	4.2	17
71	Turkey Meat as Source of CC9/CC398 Methicillin-Resistant <i>Staphylococcus aureus</i> in Humans?. <i>Clinical Infectious Diseases</i> , 2017, 64, 102-103.	5.8	14
72	Carbapenemase VCC-1-Producing <i>Vibrio cholerae</i> in Coastal Waters of Germany. <i>Emerging Infectious Diseases</i> , 2017, 23, 1735-1737.	4.3	52

#	ARTICLE	IF	CITATIONS
73	Molecular Tracing to Find Source of Protracted Invasive Listeriosis Outbreak, Southern Germany, 2012–2016. <i>Emerging Infectious Diseases</i> , 2017, 23, 1680-1683.	4.3	47
74	Genetic Diversity of Brucella Reference and Non-reference Phages and Its Impact on Brucella-Typing. <i>Frontiers in Microbiology</i> , 2017, 8, 408.	3.5	7
75	Prevalence, Host Range, and Comparative Genomic Analysis of Temperate Ochrobactrum Phages. <i>Frontiers in Microbiology</i> , 2017, 8, 1207.	3.5	31
76	Diversity of <i>Vibrio navarrensis</i> Revealed by Genomic Comparison: Veterinary Isolates Are Related to Strains Associated with Human Illness and Sewage Isolates While Seawater Strains Are More Distant. <i>Frontiers in Microbiology</i> , 2017, 8, 1717.	3.5	18
77	CTX-M-15-Producing <i>E. coli</i> Isolates from Food Products in Germany Are Mainly Associated with an IncF-Type Plasmid and Belong to Two Predominant Clonal <i>E. coli</i> Lineages. <i>Frontiers in Microbiology</i> , 2017, 8, 2318.	3.5	62
78	A multiplex real-time PCR for the detection and differentiation of Campylobacter phages. <i>PLoS ONE</i> , 2017, 12, e0190240.	2.5	21
79	Binding Specificities of the Telomere Phage λ KO2 Prophage Repressor CB and Lytic Repressor Cro. <i>Viruses</i> , 2016, 8, 213.	3.3	10
80	The Risk of Bacterial Infection After Tattooing. <i>Deutsches A&#x0308;rzteblatt International</i> , 2016, 113, 665-671.	0.9	41
81	Analysis of the First Temperate Broad Host Range Brucellaphage (BiPBO1) Isolated from <i>B. inopinata</i> . <i>Frontiers in Microbiology</i> , 2016, 7, 24.	3.5	29
82	The diverse genetic switch of enterobacterial and marine telomere phages. <i>Bacteriophage</i> , 2016, 6, 1-10.	1.9	6
83	Detection of foodborne bacterial zoonoses by fluorescence in situ hybridization. <i>Food Control</i> , 2016, 69, 297-305.	5.5	13
84	Rapid screening for antibiotic resistance elements on the RNA transcript, protein and enzymatic activity level. <i>Annals of Clinical Microbiology and Antimicrobials</i> , 2016, 15, 55.	3.8	6
85	Genome Sequence of the K139-Like Phage VcP032 Originating from the <i>Vibrio cholerae</i> O1 El Tor Ogawa Serotype. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
86	Rapid characterisation of <i>Klebsiella oxytoca</i> isolates from contaminated liquid hand soap using mass spectrometry, FTIR and Raman spectroscopy. <i>Faraday Discussions</i> , 2016, 187, 353-375.	3.2	29
87	<i>Brucella vulpis</i> sp. nov., isolated from mandibular lymph nodes of red foxes (<i>Vulpes vulpes</i>). <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2016, 66, 2090-2098.	1.7	155
88	The Molecular Switch of Telomere Phages: High Binding Specificity of the PY54 Cro Lytic Repressor to a Single Operator Site. <i>Viruses</i> , 2015, 7, 2771-2793.	3.3	7
89	Sampling and Homogenization Strategies Significantly Influence the Detection of Foodborne Pathogens in Meat. <i>BioMed Research International</i> , 2015, 2015, 1-8.	1.9	17
90	Primary Isolation Strain Determines Both Phage Type and Receptors Recognised by <i>Campylobacter jejuni</i> Bacteriophages. <i>PLoS ONE</i> , 2015, 10, e0116287.	2.5	58

#	ARTICLE	IF	CITATIONS
91	First Draft Genome Sequence of a Human <i>Coxiella burnetii</i> Isolate, Originating from the Largest Q Fever Outbreak Ever Reported, the Netherlands, 2007 to 2010. <i>Genome Announcements</i> , 2015, 3, .	0.8	8
92	Draft Genome Sequences of <i>Klebsiella oxytoca</i> Isolates Originating from a Highly Contaminated Liquid Hand Soap Product. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
93	<i>Campylobacter</i> group II phage CP21 is the prototype of a new subgroup revealing a distinct modular genome organization and host specificity. <i>BMC Genomics</i> , 2015, 16, 629.	2.8	16
94	Characterization of illegal food items and identification of foodborne pathogens brought into the European Union via two major German airports. <i>International Journal of Food Microbiology</i> , 2015, 209, 13-19.	4.7	37
95	FISHing for bacteria in food – A promising tool for the reliable detection of pathogenic bacteria?. <i>Food Microbiology</i> , 2015, 46, 395-407.	4.2	84
96	Development of transient phage resistance in <i>Campylobacter coli</i> against the group II phage CP84. <i>Berliner Und Munchener Tierarztliche Wochenschrift</i> , 2015, 128, 141-7.	0.7	0
97	Reduction of <i>Campylobacter jejuni</i> in Broiler Chicken by Successive Application of Group II and Group III Phages. <i>PLoS ONE</i> , 2014, 9, e114785.	2.5	80
98	<i>Leptospira</i> spp. in Rodents and Shrews in Germany. <i>International Journal of Environmental Research and Public Health</i> , 2014, 11, 7562-7574.	2.6	47
99	Complete Nucleotide Sequence of pVv01, a P1-Like Plasmid Prophage of <i>Vibrio vulnificus</i> . <i>Genome Announcements</i> , 2014, 2, .	0.8	7
100	Shiga Toxin 2A – Encoding Bacteriophages in Enteroaggregative <i>Escherichia coli</i> O104:H4 Strains. <i>Emerging Infectious Diseases</i> , 2014, 20, 1567-1568.	4.3	4
101	A suggested classification for two groups of <i>Campylobacter myoviruses</i> . <i>Archives of Virology</i> , 2014, 159, 181-190.	2.1	63
102	F1 and Tbilisi Are Closely Related Brucellaphages Exhibiting Some Distinct Nucleotide Variations Which Determine the Host Specificity. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
103	<i>Vibrio vulnificus</i> Phage PV94 Is Closely Related to Temperate Phages of <i>V. cholerae</i> and Other <i>Vibrio</i> Species. <i>PLoS ONE</i> , 2014, 9, e94707.	2.5	7
104	Shiga toxin-producing <i>Escherichia coli</i> strains from cattle as a source of the Stx2a bacteriophages present in enteroaggregative <i>Escherichia coli</i> O104:H4 strains. <i>International Journal of Medical Microbiology</i> , 2013, 303, 595-602.	3.6	34
105	Isolation and characterization of phages with lytic activity against methicillin-resistant <i>Staphylococcus aureus</i> strains belonging to clonal complex 398. <i>Archives of Virology</i> , 2013, 158, 2341-2350.	2.1	18
106	Post-harvest application of lytic bacteriophages for biocontrol of foodborne pathogens and spoilage bacteria. <i>Berliner Und Munchener Tierarztliche Wochenschrift</i> , 2013, 126, 357-69.	0.7	14
107	Spread of a Distinct Stx2-Encoding Phage Prototype among <i>Escherichia coli</i> O104:H4 Strains from Outbreaks in Germany, Norway, and Georgia. <i>Journal of Virology</i> , 2012, 86, 10444-10455.	3.4	39
108	The Complete Genome Sequence of Bacteriophage CP21 Reveals Modular Shuffling in <i>Campylobacter</i> Group II Phages. <i>Journal of Virology</i> , 2012, 86, 8896-8896.	3.4	13

#	ARTICLE	IF	CITATIONS
109	Control of <i>Campylobacter</i> spp. and <i>Yersinia enterocolitica</i> by virulent bacteriophages. <i>Journal of Molecular and Genetic Medicine: an International Journal of Biomedical Research</i> , 2012, 06, 273-8.	0.1	37
110	Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4: a New Challenge for Microbiology. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4065-4073.	3.1	169
111	The pYV virulence plasmids of <i>Yersinia pseudotuberculosis</i> and <i>Y. pseudotuberculosis</i> contain a conserved DNA region responsible for the mobilization by the self-transmissible plasmid pYE854. <i>Environmental Microbiology Reports</i> , 2012, 4, 433-438.	2.4	13
112	Simultaneous Identification of DNA and RNA Viruses Present in Pig Faeces Using Process-Controlled Deep Sequencing. <i>PLoS ONE</i> , 2012, 7, e34631.	2.5	77
113	Virulence and Resistance Determinants of German <i>Staphylococcus aureus</i> ST398 Isolates from Nonhuman Sources. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3052-3060.	3.1	190
114	Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) in Three Dairy Herds in Southwest Germany. <i>Zoonoses and Public Health</i> , 2011, 58, 252-261.	2.2	112
115	Factors associated with the occurrence of MRSA CC398 in herds of fattening pigs in Germany. <i>BMC Veterinary Research</i> , 2011, 7, 69.	1.9	64
116	<i>Campylobacter jejuni</i> Group III Phage CP81 Contains Many T4-Like Genes without Belonging to the T4-Type Phage Group: Implications for the Evolution of T4 Phages. <i>Journal of Virology</i> , 2011, 85, 8597-8605.	3.4	26
117	pSGI15, a small ColE-like qnrB19 plasmid of a <i>Salmonella enterica</i> serovar Typhimurium strain carrying <i>Salmonella</i> genomic island 1 (SGI1). <i>Journal of Antimicrobial Chemotherapy</i> , 2010, 65, 173-175.	3.0	28
118	High Heterogeneity within Methicillin-Resistant <i>Staphylococcus aureus</i> ST398 Isolates, Defined by Cfr9I Macrorestriction-Pulsed-Field Gel Electrophoresis Profiles and <i>spa</i> and SCC <i>mec</i> Types. <i>Applied and Environmental Microbiology</i> , 2010, 76, 652-658.	3.1	47
119	Livestock Associated Methicillin-Resistant <i>Staphylococcus aureus</i> (LaMRSA) Isolated from Lesions of Pigs at Necropsy in Northwest Germany Between 2004 and 2007. <i>Zoonoses and Public Health</i> , 2010, 57, e143-8.	2.2	40
120	The Linear Plasmid Prophage Vp58.5 of <i>Vibrio parahaemolyticus</i> Is Closely Related to the Integrating Phage VHML and Constitutes a New Incompatibility Group of Telomere Phages. <i>Journal of Virology</i> , 2009, 83, 9313-9320.	3.4	33
121	Prevalence of MRSA types in slaughter pigs in different German abattoirs. <i>Veterinary Record</i> , 2009, 165, 589-593.	0.3	64
122	Bacteriophage 2851 Is a Prototype Phage for Dissemination of the Shiga Toxin Variant Gene 2c in <i>Escherichia coli</i> O157:H7. <i>Infection and Immunity</i> , 2008, 76, 5466-5477.	2.2	64
123	Genetic and Functional Properties of the Self-Transmissible <i>Yersinia enterocolitica</i> Plasmid pYE854, Which Mobilizes the Virulence Plasmid pYV. <i>Journal of Bacteriology</i> , 2008, 190, 991-1010.	2.2	22
124	Interplay between the Temperate Phages PY54 and N15, Linear Plasmid Prophages with Covalently Closed Ends. <i>Journal of Bacteriology</i> , 2007, 189, 8366-8370.	2.2	17
125	Bacteriophages: New Tools for Safer Food?. <i>Journal Fur Verbraucherschutz Und Lebensmittelsicherheit</i> , 2007, 2, 138-143.	1.4	29
126	The <i>repA</i> Gene of the Linear <i>Yersinia enterocolitica</i> Prophage PY54 Functions as a Circular Minimal Replicon in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2005, 187, 3445-3454.	2.2	15

#	ARTICLE	IF	CITATIONS
127	Sequence Analysis of the Genome of the Temperate <i>Yersinia enterocolitica</i> Phage PY54. <i>Journal of Molecular Biology</i> , 2003, 331, 605-622.	4.2	66
128	Characterization of Two Conjugative <i>Yersinia</i> Plasmids Mobilizing pYV. , 2003, 529, 35-38.		6
129	Impact of <i>mcr-1</i> harbouring bacteria in clinical settings and the public health sector: how can we act against this novel threat?. <i>Journal of Public Health and Emergency</i> , 0, 1, 51-51.	4.4	2
130	Seroprevalence of <i>Yersinia</i> , Hepatitis E and <i>Trichinella</i> among migrant and nonmigrant populations in Berlin and Brandenburg (Germany). , 0, , .		0