Maite LJaime Muniesa

List of Publications by Year
in descending order

130 papers	6,444 citations	50566 48 h-index	87275 74 g-index
135 all docs	135 docs citations	135 times ranked	6278 citing authors

#	Article	IF	Citations
1	Modeling human pollution in water bodies using somatic coliphages and bacteriophages that infect Bacteroides thetaiotaomicron strain GA17. Journal of Environmental Management, 2022, 301, 113802.	3.8	1
2	Bacteriophages in sewage: abundance, roles, and applications. FEMS Microbes, 2022, 3, .	0.8	15
3	Essential Topics for the Regulatory Consideration of Phages as Clinically Valuable Therapeutic Agents: A Perspective from Spain. Microorganisms, 2022, 10, 717.	1.6	12
4	Antibiotic resistance in the viral fraction of dairy products and a nut-based milk. International Journal of Food Microbiology, 2022, 367, 109590.	2.1	7
5	Chicken liver is a potential reservoir of bacteriophages and phageâ€derived particles containing antibiotic resistance genes. Microbial Biotechnology, 2022, 15, 2464-2475.	2.0	4
6	Prevalence of bacterial genes in the phage fraction of food viromes. Food Research International, 2022, 156, 111342.	2.9	2
7	Isolation and Characterization of Shiga Toxin Bacteriophages. Methods in Molecular Biology, 2021, 2291, 119-144.	0.4	2
8	Bacteriophages immunomodulate the response of monocytes. Experimental Biology and Medicine, 2021, 246, 1263-1268.	1.1	10
9	Bacteriophages of Shiga Toxin-Producing Escherichia coli and Their Contribution to Pathogenicity. Pathogens, 2021, 10, 404.	1.2	44
10	Population genomics and antimicrobial resistance dynamics of Escherichia coli in wastewater and river environments. Communications Biology, 2021, 4, 457.	2.0	20
11	Editorial: Shiga Toxin-Converting Bacteriophages. Frontiers in Microbiology, 2021, 12, 680816.	1.5	2
12	Bacteriophages as Fecal Pollution Indicators. Viruses, 2021, 13, 1089.	1.5	21
13	Extensive antimicrobial resistance mobilization via multicopy plasmid encapsidation mediated by temperate phages. Journal of Antimicrobial Chemotherapy, 2020, 75, 3173-3180.	1.3	25
14	Investigation on the Evolution of Shiga Toxin-Converting Phages Based on Whole Genome Sequencing. Frontiers in Microbiology, 2020, 11, 1472.	1.5	13
15	F-specific coliphage detection by the Bluephage method. Water Research, 2020, 184, 116215.	5.3	4
16	Antibiotic Resistance Genes in Phage Particles from Antarctic and Mediterranean Seawater Ecosystems. Microorganisms, 2020, 8, 1293.	1.6	33
17	Analysis of a phase-variable restriction modification system of the human gut symbiont Bacteroides fragilis. Nucleic Acids Research, 2020, 48, 11040-11053.	6.5	10
18	Are Phages Parasites or Symbionts of Bacteria?. , 2020, , 143-162.		2

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19	Unravelling the consequences of the bacteriophages in human samples. Scientific Reports, 2020, 10, 6737.	1.6	24
20	Comparison of Commensal and Clinical Isolates for Diversity of Plasmids in Escherichia coli and Klebsiella pneumoniae. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	11
21	Bacteriophage Isolation and Characterization: Phages of Escherichia coli. Methods in Molecular Biology, 2020, 2075, 61-79.	0.4	9
22	Evaluation of New Components in Modified Scholtenâ€™s Medium for the Detection of Somatic Coliphages. Food and Environmental Virology, 2020, 12, 148-157.	1.5	3
23	Fast and easy methods for the detection of coliphages. Journal of Microbiological Methods, 2020, 173, 105940.	0.7	13
24	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	5.9	184
25	Infectious phage particles packaging antibiotic resistance genes found in meat products and chicken feces. Scientific Reports, 2019, 9, 13281.	1.6	67
26	Dynamics of crAssphage as a human source tracking marker in potentially faecally polluted environments. Water Research, 2019, 155, 233-244.	5.3	55
27	New approach for the simultaneous detection of somatic coliphages and F-specific RNA coliphages as indicators of fecal pollution. Science of the Total Environment, 2019, 655, 263-272.	3.9	11
28	Faecal phageome of healthy individuals: presence of antibiotic resistance genes and variations caused by ciprofloxacin treatment. Journal of Antimicrobial Chemotherapy, 2019, 74, 854-864.	1.3	24
29	Complete Genome Sequence ofEscherichia coliStrain WG5. Genome Announcements, 2018, 6, .	0.8	10
30	Phage particles harboring antibiotic resistance genes in fresh-cut vegetables and agricultural soil. Environment International, 2018, 115, 133-141.	4.8	84
31	Bluephage: A rapid method for the detection of somatic coliphages used as indicators of fecal pollution in water. Water Research, 2018, 128, 10-19.	5.3	29
32	Antibiotic resistance genes in phage particles isolated from human faeces and induced from clinical bacterial isolates. International Journal of Antimicrobial Agents, 2018, 51, 434-442.	1.1	46
33	Isolation of Bacteriophages of the Anaerobic Bacteria Bacteroides. Methods in Molecular Biology, 2018, 1693, 11-22.	0.4	4
34	Relevance of Bacteriophage 933W in the Development of Hemolytic Uremic Syndrome (HUS). Frontiers in Microbiology, 2018, 9, 3104.	1.5	14
35	Modulation of Enterohaemorrhagic Escherichia coli Survival and Virulence in the Human Gastrointestinal Tract. Microorganisms, 2018, 6, 115.	1.6	40
36	Closed Genome and Comparative Phylogenetic Analysis of the Clinical Multidrug Resistant Shigella sonnei Strain 866. Genome Biology and Evolution, 2018, 10, 2241-2247.	1.1	10

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37	Detection of Bacteriophage Particles Containing Antibiotic Resistance Genes in the Sputum of Cystic Fibrosis Patients. Frontiers in Microbiology, 2018, 9, 856.	1.5	40
38	Spread ofmcr-1-carrying Enterobacteriaceae in sewage water from Spain. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw533.	1.3	55
39	The occurrence of antibiotic resistance genes in a Mediterranean river and their persistence in the riverbed sediment. Environmental Pollution, 2017, 223, 384-394.	3.7	106
40	Beyond the canonical strategies of horizontal gene transfer in prokaryotes. Current Opinion in Microbiology, 2017, 38, 95-105.	2.3	58
41	Determination of crAssphage in water samples and applicability for tracking human faecal pollution. Microbial Biotechnology, 2017, 10, 1775-1780.	2.0	96
42	Contribution of cropland to the spread of Shiga toxin phages and the emergence of new Shiga toxin-producing strains. Scientific Reports, 2017, 7, 7796.	1.6	12
43	Is Genetic Mobilization Considered When Using Bacteriophages in Antimicrobial Therapy?. Antibiotics, 2017, 6, 32.	1.5	12
44	Phages in the Human Body. Frontiers in Microbiology, 2017, 8, 566.	1.5	86
45	Carbapenemase-producing enterobacteriaceae recovered from a Spanish river ecosystem. PLoS ONE, 2017, 12, e0175246.	1.1	58
46	Coliphages as Model Organisms in the Characterization and Management of Water Resources. Water (Switzerland), 2016, 8, 199.	1.2	76
47	Heterogeneity in phage induction enables the survival of the lysogenic population. Environmental Microbiology, 2016, 18, 957-969.	1.8	28
48	Short communication: Heat-resistant Escherichia coli as potential persistent reservoir of extended-spectrum Î²-lactamases and Shiga toxin-encoding phages in dairy. Journal of Dairy Science, 2016, 99, 8622-8632.	1.4	30
49	Tracking bacterial virulence: global modulators as indicators. Scientific Reports, 2016, 6, 25973.	1.6	12
50	Bacteriophages in clinical samples can interfere with microbiological diagnostic tools. Scientific Reports, 2016, 6, 33000.	1.6	86
51	Development of new hostâ€specific Bacteroides <scp>qPCR</scp>s for the identification of fecal contamination sources in water. MicrobiologyOpen, 2016, 5, 83-94.	1.2	30
52	Spread of bacterial genomes in packaged particles. Future Microbiology, 2016, 11, 171-173.	1.0	10
53	Persistence of naturally occurring antibiotic resistance genes in the bacteria and bacteriophage fractions of wastewater. Water Research, 2016, 95, 11-18.	5.3	129
54	Free <scp>S</scp>higa toxin 1â€encoding bacteriophages are less prevalent than <scp>S</scp>higa toxin 2 phages in extraintestinal environments. Environmental Microbiology, 2015, 17, 4790-4801.	1.8	22

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55	BaeSR, Involved in Envelope Stress Response, Protects against Lysogenic Conversion by Shiga Toxin 2-Encoding Phages. Infection and Immunity, 2015, 83, 1451-1457.	1.0	4
56	Predicting fecal sources in waters with diverse pollution loads using general and molecular host-specific indicators and applying machine learning methods. Journal of Environmental Management, 2015, 151, 317-325.	3.8	28
57	Transfer of antibiotic-resistance genes via phage-related mobile elements. Plasmid, 2015, 79, 1-7.	0.4	200
58	Improving Detection of Shiga Toxin-Producing Escherichia coli by Molecular Methods by Reducing the Interference of Free Shiga Toxin-Encoding Bacteriophages. Applied and Environmental Microbiology, 2015, 81, 415-421.	1.4	29
59	Implications of free Shiga toxin-converting bacteriophages occurring outside bacteria for the evolution and the detection of Shiga toxin-producing Escherichia coli. Frontiers in Cellular and Infection Microbiology, 2014, 4, 46.	1.8	46
60	Antibiotic Resistance Genes in the Bacteriophage DNA Fraction of Human Fecal Samples. Antimicrobial Agents and Chemotherapy, 2014, 58, 606-609.	1.4	105
61	Persistence of Infectious Shiga Toxin-Encoding Bacteriophages after Disinfection Treatments. Applied and Environmental Microbiology, 2014, 80, 2142-2149.	1.4	27
62	Bacteriophages infecting Bacteroides as a marker for microbial source tracking. Water Research, 2014, 55, 1-11.	5.3	47
63	Exploiting the explosion of information associated with whole genome sequencing to tackle Shiga toxin-producing Escherichia coli (STEC) in global food production systems. International Journal of Food Microbiology, 2014, 187, 57-72.	2.1	83
64	Identifying and analyzing bacteriophages in human fecal samples: what could we discover?. Future Microbiology, 2014, 9, 879-886.	1.0	7
65	Antibiotic resistance genes in bacterial and bacteriophage fractions of Tunisian and Spanish wastewaters as markers to compare the antibiotic resistance patterns in each population. Environment International, 2014, 73, 167-175.	4.8	76
66	Quinolone resistance genes (qnrA and qnrS) in bacteriophage particles from wastewater samples and the effect of inducing agents on packaged antibiotic resistance genes. Journal of Antimicrobial Chemotherapy, 2014, 69, 1265-1274.	1.3	92
67	Sludge As a Potential Important Source of Antibiotic Resistance Genes in Both the Bacterial and Bacteriophage Fractions. Environmental Science & Technology, 2014, 48, 7602-7611.	4.6	147
68	Potential impact of environmental bacteriophages in spreading antibiotic resistance genes. Future Microbiology, 2013, 8, 739-751.	1.0	91
69	Evolution of a Self-Inducible Cytolethal Distending Toxin Type V-Encoding Bacteriophage from Escherichia coli O157:H7 to Shigella sonnei. Journal of Virology, 2013, 87, 13665-13675.	1.5	18
70	Detection of quinolone-resistant Escherichia coli isolates belonging to clonal groups O25b:H4-B2-ST131 and O25b:H4-D-ST69 in raw sewage and river water in Barcelona, Spain. Journal of Antimicrobial Chemotherapy, 2013, 68, 758-765.	1.3	44
71	Shiga Toxin 2-Encoding Bacteriophages in Human Fecal Samples from Healthy Individuals. Applied and Environmental Microbiology, 2013, 79, 4862-4868.	1.4	50
72	Could bacteriophages transfer antibiotic resistance genes from environmental bacteria to human-body associated bacterial populations?. Mobile Genetic Elements, 2013, 3, e25847.	1.8	67

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73	Bacteriophage-driven emergence of novel pathogens. Future Virology, 2013, 8, 323-325.	0.9	3
74	Stability and Infectivity of Cytolethal Distending Toxin Type V Gene-Carrying Bacteriophages in a Water Mesocosm and under Different Inactivation Conditions. Applied and Environmental Microbiology, 2012, 78, 5818-5823.	1.4	18
75	Use of abundance ratios of somatic coliphages and bacteriophages of Bacteroides thetaiotaomicron GA17 for microbial source identification. Water Research, 2012, 46, 6410-6418.	5.3	44
76	New Molecular Quantitative PCR Assay for Detection of Host-Specific Bifidobacteriaceae Suitable for Microbial Source Tracking. Applied and Environmental Microbiology, 2012, 78, 5788-5795.	1.4	35
77	Characterizing RecA-Independent Induction of Shiga toxin2-Encoding Phages by EDTA Treatment. PLoS ONE, 2012, 7, e32393.	1.1	87
78	Shiga Toxin-Producing Escherichia coli O104:H4: a New Challenge for Microbiology. Applied and Environmental Microbiology, 2012, 78, 4065-4073.	1.4	169
79	Type III effector genes and other virulence factors of Shiga toxinâ€encoding Escherichia coli isolated from wastewater. Environmental Microbiology Reports, 2012, 4, 147-155.	1.0	12
80	Antibiotic Resistance Genes in the Bacteriophage DNA Fraction of Environmental Samples. PLoS ONE, 2011, 6, e17549.	1.1	275
81	Isolation of bacteriophage host strains of Bacteroides species suitable for tracking sources of animal faecal pollution in water. Environmental Microbiology, 2011, 13, 1622-1631.	1.8	32
82	Bacteriophages and genetic mobilization in sewage and faecally polluted environments. Microbial Biotechnology, 2011, 4, 725-734.	2.0	40
83	Quantification and Evaluation of Infectivity of Shiga Toxin-Encoding Bacteriophages in Beef and Salad. Applied and Environmental Microbiology, 2011, 77, 3536-3540.	1.4	28
84	Bacteriophages Carrying Antibiotic Resistance Genes in Fecal Waste from Cattle, Pigs, and Poultry. Antimicrobial Agents and Chemotherapy, 2011, 55, 4908-4911.	1.4	136
85	Bacteriophage-Encoding Cytolethal Distending Toxin Type V Gene Induced from Nonclinical Escherichia coli Isolates. Infection and Immunity, 2011, 79, 3262-3272.	1.0	29
86	Quantification of Shiga toxin 2â€encoding bacteriophages, by realâ€time PCR and correlation with phage infectivity. Journal of Applied Microbiology, 2010, 108, 1105-1114.	1.4	24
87	Quantification of Shiga Toxin-Converting Bacteriophages in Wastewater and in Fecal Samples by Real-Time Quantitative PCR. Applied and Environmental Microbiology, 2010, 76, 5693-5701.	1.4	58
88	Phage-Mediated Shiga Toxin 2 Gene Transfer in Food and Water. Applied and Environmental Microbiology, 2009, 75, 1764-1768.	1.4	55
89	Genotypic and Phenotypic Diversity among Induced, stx ₂ -Carrying Bacteriophages from Environmental Escherichia coli Strains. Applied and Environmental Microbiology, 2009, 75, 329-336.	1.4	52
90	Differential persistence of F-specific RNA phage subgroups hinders their use as single tracers for faecal source tracking in surface water. Water Research, 2009, 43, 1559-1564.	5.3	41

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91	The CI Repressors of Shiga Toxin-Converting Prophages Are Involved in Coinfection of Escherichia coli Strains, Which Causes a Down Regulation in the Production of Shiga Toxin 2. Journal of Bacteriology, 2008, 190, 4722-4735.	1.0	57
92	Conserved Stx2 Phages fromEscherichia coliO103:H25 Isolated from Patients Suffering from Hemolytic Uremic Syndrome. Foodborne Pathogens and Disease, 2008, 5, 801-810.	0.8	16
93	Insertion Site Occupancy by stx ₂ Bacteriophages Depends on the Locus Availability of the Host Strain Chromosome. Journal of Bacteriology, 2007, 189, 6645-6654.	1.0	80
94	The application of a recently isolated strain of Bacteroides (GB-124) to identify human sources of faecal pollution in a temperate river catchment. Water Research, 2007, 41, 3683-3690.	5.3	76
95	The contribution of induction of temperate phages to the numbers of free somatic coliphages in waters is not significant. FEMS Microbiology Letters, 2007, 270, 272-276.	0.7	11
96	Occurrence of Escherichia coli O157:H7 and Other Enterohemorrhagic Escherichia coli in the Environment. Environmental Science & Technology, 2006, 40, 7141-7149.	4.6	108
97	Use of the lambda Red recombinase system to produce recombinant prophages carrying antibiotic resistance genes. BMC Molecular Biology, 2006, 7, 31.	3.0	69
98	Newly identified bacteriophages carrying the stx2g Shiga toxin gene isolated from Escherichia coli strains in polluted waters. FEMS Microbiology Letters, 2006, 258, 127-135.	0.7	30
99	Extended-spectrum Â-lactamase-producing Enterobacteriaceae in different environments (humans,) Tj ETQq1 1 0.784314 rgBT /Overl	1.3	199
100	Active Genetic Elements Present in the Locus of Enterocyte Effacement in Escherichia coli O26 and Their Role in Mobility. Infection and Immunity, 2006, 74, 4190-4199.	1.0	10
101	Integrated Analysis of Established and Novel Microbial and Chemical Methods for Microbial Source Tracking. Applied and Environmental Microbiology, 2006, 72, 5915-5926.	1.4	145
102	Characterization of Shiga toxin-producingEscherichia coliisolated from aquatic environments. FEMS Microbiology Letters, 2005, 246, 55-65.	0.7	63
103	Method for Isolation of Bacteroides Bacteriophage Host Strains Suitable for Tracking Sources of Fecal Pollution in Water. Applied and Environmental Microbiology, 2005, 71, 5659-5662.	1.4	83
104	Bacteriophages May Bias Outcome of Bacterial Enrichment Cultures. Applied and Environmental Microbiology, 2005, 71, 4269-4275.	1.4	41
105	Abundance in Sewage of Bacteriophages Infecting <I>Escherichia coli O157:H7. , 2004, 268, 079-088.		20
106	Tracking the origin of faecal pollution in surface water: an ongoing project within the European Union research programme. Journal of Water and Health, 2004, 2, 249-260.	1.1	42
107	Bacteriophages and Diffusion of Î²-lactamase Genes. Emerging Infectious Diseases, 2004, 10, 1134-1137.	2.0	83
108	Diversity of stx 2 converting bacteriophages induced from Shiga-toxin-producing Escherichia coli strains isolated from cattle. Microbiology (United Kingdom), 2004, 150, 2959-2971.	0.7	135

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109	Prevalence of the stx2 Gene in Coliform Populations from Aquatic Environments. Applied and Environmental Microbiology, 2004, 70, 3535-3540.	1.4	43
110	Free Shiga toxin bacteriophages isolated from sewage showed diversity although the stx genes appeared conserved. Environmental Microbiology, 2004, 6, 716-725.	1.8	53
111	Factors influencing the replication of somatic coliphages in the water environment. Antonie Van Leeuwenhoek, 2004, 86, 65-76.	0.7	36
112	Tracking the origin of faecal pollution in surface water: an ongoing project within the European Union research programme. Journal of Water and Health, 2004, 2, 249-60.	1.1	12
113	Bacterial host strains that support replication of somatic coliphages. Antonie Van Leeuwenhoek, 2003, 83, 305-315.	0.7	37
114	Homogeneity of the Morphological Groups of Bacteriophages Infecting Bacteroides fragilis Strain HSP40 and Strain RYC2056. Current Microbiology, 2003, 46, 163-168.	1.0	14
115	Comparison of polyvinylidene fluoride and polyether sulfone membranes in filtering viral suspensions. Journal of Virological Methods, 2003, 109, 99-101.	1.0	32
116	Usefulness of different groups of bacteriophages as model micro-organisms for evaluating chlorination. Journal of Applied Microbiology, 2003, 95, 29-37.	1.4	60
117	Shiga Toxin 2-Converting Bacteriophages Associated with Clonal Variability in Escherichia coli O157:H7 Strains of Human Origin Isolated from a Single Outbreak. Infection and Immunity, 2003, 71, 4554-4562.	1.0	100
118	Survival of Bacterial Indicator Species and Bacteriophages after Thermal Treatment of Sludge and Sewage. Applied and Environmental Microbiology, 2003, 69, 1452-1456.	1.4	138
119	Detection, enumeration and isolation of strains carrying the stx2 gene from urban sewage. Water Science and Technology, 2003, 47, 109-116.	1.2	20
120	Optimisation of ISO 10705-1 on enumeration of F-specific bacteriophages. Journal of Virological Methods, 2002, 103, 129-136.	1.0	18
121	Removal and inactivation of indicator bacteriophages in fresh waters. Journal of Applied Microbiology, 2002, 92, 338-347.	1.4	102
122	Optimisation and standardisation of a method for detecting and enumerating bacteriophages infecting Bacteroides fragilis. Journal of Virological Methods, 2001, 93, 127-136.	1.0	28
123	Occurrence of phages infectingEscherichia coliO157:H7 carrying the Stx 2 gene in sewage from different countries. FEMS Microbiology Letters, 2000, 183, 197-200.	0.7	45
124	Characterization of a Shiga Toxin 2e-Converting Bacteriophage from an Escherichia coli Strain of Human Origin. Infection and Immunity, 2000, 68, 4850-4855.	1.0	100
125	Occurrence and numbers of bacteriophages and bacterial indicators in faeces of yellow-legged seagull (Larus cachinnans). Letters in Applied Microbiology, 1999, 29, 421-423.	1.0	7
126	Comparative Survival of Free Shiga Toxin 2-Encoding Phages and Escherichia coli Strains outside the Gut. Applied and Environmental Microbiology, 1999, 65, 5615-5618.	1.4	81

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127	Abundance in Sewage of Bacteriophages That InfectEscherichia coliO157:H7 and That Carry the Shiga Toxin 2 Gene. Applied and Environmental Microbiology, 1998, 64, 2443-2448.	1.4	109
128	Simple concentration method for bacteriophages of Bacteroides fragilis in drinking water. Journal of Virological Methods, 1995, 54, 121-130.	1.0	13
129	Occurrence of phages infecting Escherichia coli O157:H7 carrying the Stx 2 gene in sewage from different countries. , 0, .		4
130	General and host-associated bacteriophage indicators of faecal pollution. , 0, , .		7