

Maite Muniesa

List of Publications by Year in descending order

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92
papers

5,362
citations

61984

43
h-index

88630

70
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92
all docs

92
docs citations

92
times ranked

4943
citing authors

#	ARTICLE	IF	CITATIONS
1	Antibiotic Resistance Genes in the Bacteriophage DNA Fraction of Environmental Samples. PLoS ONE, 2011, 6, e17549.	2.5	275
2	Transfer of antibiotic-resistance genes via phage-related mobile elements. Plasmid, 2015, 79, 1-7.	1.4	200
3	Extended-spectrum β -lactamase-producing Enterobacteriaceae in different environments (humans, Tj ETQq1 1 0.784314 rgBT /Overl 3.0 199	3.0	199
4	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	13.3	184
5	Shiga Toxin-Producing Escherichia coli O104:H4: a New Challenge for Microbiology. Applied and Environmental Microbiology, 2012, 78, 4065-4073.	3.1	169
6	Sludge As a Potential Important Source of Antibiotic Resistance Genes in Both the Bacterial and Bacteriophage Fractions. Environmental Science & Technology, 2014, 48, 7602-7611.	10.0	147
7	Integrated Analysis of Established and Novel Microbial and Chemical Methods for Microbial Source Tracking. Applied and Environmental Microbiology, 2006, 72, 5915-5926.	3.1	145
8	Survival of Bacterial Indicator Species and Bacteriophages after Thermal Treatment of Sludge and Sewage. Applied and Environmental Microbiology, 2003, 69, 1452-1456.	3.1	138
9	Bacteriophages Carrying Antibiotic Resistance Genes in Fecal Waste from Cattle, Pigs, and Poultry. Antimicrobial Agents and Chemotherapy, 2011, 55, 4908-4911.	3.2	136
10	Diversity of stx 2 converting bacteriophages induced from Shiga-toxin-producing Escherichia coli strains isolated from cattle. Microbiology (United Kingdom), 2004, 150, 2959-2971.	1.8	135
11	Persistence of naturally occurring antibiotic resistance genes in the bacteria and bacteriophage fractions of wastewater. Water Research, 2016, 95, 11-18.	11.3	129
12	Abundance in Sewage of Bacteriophages That Infect Escherichia coli O157:H7 and That Carry the Shiga Toxin 2 Gene. Applied and Environmental Microbiology, 1998, 64, 2443-2448.	3.1	109
13	Occurrence of Escherichia coli O157:H7 and Other Enterohemorrhagic Escherichia coli in the Environment. Environmental Science & Technology, 2006, 40, 7141-7149.	10.0	108
14	The occurrence of antibiotic resistance genes in a Mediterranean river and their persistence in the riverbed sediment. Environmental Pollution, 2017, 223, 384-394.	7.5	106
15	Antibiotic Resistance Genes in the Bacteriophage DNA Fraction of Human Fecal Samples. Antimicrobial Agents and Chemotherapy, 2014, 58, 606-609.	3.2	105
16	Characterization of a Shiga Toxin 2e-Converting Bacteriophage from an Escherichia coli Strain of Human Origin. Infection and Immunity, 2000, 68, 4850-4855.	2.2	100
17	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.	2.2	100
18	Determination of crAssphage in water samples and applicability for tracking human faecal pollution. Microbial Biotechnology, 2017, 10, 1775-1780.	4.2	96

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19	Quinolone resistance genes (qnrA and qnrS) in bacteriophage particles from wastewater samples and the effect of inducing agents on packaged antibiotic resistance genes. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 1265-1274.	3.0	92
20	Potential impact of environmental bacteriophages in spreading antibiotic resistance genes. <i>Future Microbiology</i> , 2013, 8, 739-751.	2.0	91
21	Characterizing RecA-Independent Induction of Shiga toxin2-Encoding Phages by EDTA Treatment. <i>PLoS ONE</i> , 2012, 7, e32393.	2.5	87
22	Bacteriophages in clinical samples can interfere with microbiological diagnostic tools. <i>Scientific Reports</i> , 2016, 6, 33000.	3.3	86
23	Phages in the Human Body. <i>Frontiers in Microbiology</i> , 2017, 8, 566.	3.5	86
24	Phage particles harboring antibiotic resistance genes in fresh-cut vegetables and agricultural soil. <i>Environment International</i> , 2018, 115, 133-141.	10.0	84
25	Bacteriophages and Diffusion of β -lactamase Genes. <i>Emerging Infectious Diseases</i> , 2004, 10, 1134-1137.	4.3	83
26	Method for Isolation of Bacteroides Bacteriophage Host Strains Suitable for Tracking Sources of Fecal Pollution in Water. <i>Applied and Environmental Microbiology</i> , 2005, 71, 5659-5662.	3.1	83
27	Comparative Survival of Free Shiga Toxin 2-Encoding Phages and <i>Escherichia coli</i> Strains outside the Gut. <i>Applied and Environmental Microbiology</i> , 1999, 65, 5615-5618.	3.1	81
28	Insertion Site Occupancy by λ Bacteriophages Depends on the Locus Availability of the Host Strain Chromosome. <i>Journal of Bacteriology</i> , 2007, 189, 6645-6654.	2.2	80
29	The application of a recently isolated strain of Bacteroides (GB-124) to identify human sources of faecal pollution in a temperate river catchment. <i>Water Research</i> , 2007, 41, 3683-3690.	11.3	76
30	Antibiotic resistance genes in bacterial and bacteriophage fractions of Tunisian and Spanish wastewaters as markers to compare the antibiotic resistance patterns in each population. <i>Environment International</i> , 2014, 73, 167-175.	10.0	76
31	Coliphages as Model Organisms in the Characterization and Management of Water Resources. <i>Water (Switzerland)</i> , 2016, 8, 199.	2.7	76
32	Use of the lambda Red recombinase system to produce recombinant prophages carrying antibiotic resistance genes. <i>BMC Molecular Biology</i> , 2006, 7, 31.	3.0	69
33	Could bacteriophages transfer antibiotic resistance genes from environmental bacteria to human-body associated bacterial populations?. <i>Mobile Genetic Elements</i> , 2013, 3, e25847.	1.8	67
34	Infectious phage particles packaging antibiotic resistance genes found in meat products and chicken feces. <i>Scientific Reports</i> , 2019, 9, 13281.	3.3	67
35	Quantification of Shiga Toxin-Converting Bacteriophages in Wastewater and in Fecal Samples by Real-Time Quantitative PCR. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5693-5701.	3.1	58
36	Phage-Mediated Shiga Toxin 2 Gene Transfer in Food and Water. <i>Applied and Environmental Microbiology</i> , 2009, 75, 1764-1768.	3.1	55

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37	Genotypic and Phenotypic Diversity among Induced, <i>stx2</i> -Carrying Bacteriophages from Environmental <i>Escherichia coli</i> Strains. <i>Applied and Environmental Microbiology</i> , 2009, 75, 329-336.	3.1	52
38	Shiga Toxin 2-Encoding Bacteriophages in Human Fecal Samples from Healthy Individuals. <i>Applied and Environmental Microbiology</i> , 2013, 79, 4862-4868.	3.1	50
39	Bacteriophages infecting <i>Bacteroides</i> as a marker for microbial source tracking. <i>Water Research</i> , 2014, 55, 1-11.	11.3	47
40	Implications of free Shiga toxin-converting bacteriophages occurring outside bacteria for the evolution and the detection of Shiga toxin-producing <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 46.	3.9	46
41	Antibiotic resistance genes in phage particles isolated from human faeces and induced from clinical bacterial isolates. <i>International Journal of Antimicrobial Agents</i> , 2018, 51, 434-442.	2.5	46
42	Occurrence of phages infecting <i>Escherichia coli</i> O157:H7 carrying the <i>Stx 2</i> gene in sewage from different countries. <i>FEMS Microbiology Letters</i> , 2000, 183, 197-200.	1.8	45
43	Use of abundance ratios of somatic coliphages and bacteriophages of <i>Bacteroides thetaiotaomicron</i> GA17 for microbial source identification. <i>Water Research</i> , 2012, 46, 6410-6418.	11.3	44
44	Detection of quinolone-resistant <i>Escherichia coli</i> isolates belonging to clonal groups O25b:H4-B2-ST131 and O25b:H4-D-ST69 in raw sewage and river water in Barcelona, Spain. <i>Journal of Antimicrobial Chemotherapy</i> , 2013, 68, 758-765.	3.0	44
45	Bacteriophages of Shiga Toxin-Producing <i>Escherichia coli</i> and Their Contribution to Pathogenicity. <i>Pathogens</i> , 2021, 10, 404.	2.8	44
46	Prevalence of the <i>stx2</i> Gene in Coliform Populations from Aquatic Environments. <i>Applied and Environmental Microbiology</i> , 2004, 70, 3535-3540.	3.1	43
47	Tracking the origin of faecal pollution in surface water: an ongoing project within the European Union research programme. <i>Journal of Water and Health</i> , 2004, 2, 249-260.	2.6	42
48	Bacteriophages May Bias Outcome of Bacterial Enrichment Cultures. <i>Applied and Environmental Microbiology</i> , 2005, 71, 4269-4275.	3.1	41
49	Differential persistence of F-specific RNA phage subgroups hinders their use as single tracers for faecal source tracking in surface water. <i>Water Research</i> , 2009, 43, 1559-1564.	11.3	41
50	Bacteriophages and genetic mobilization in sewage and faecally polluted environments. <i>Microbial Biotechnology</i> , 2011, 4, 725-734.	4.2	40
51	Detection of Bacteriophage Particles Containing Antibiotic Resistance Genes in the Sputum of Cystic Fibrosis Patients. <i>Frontiers in Microbiology</i> , 2018, 9, 856.	3.5	40
52	Bacterial host strains that support replication of somatic coliphages. <i>Antonie Van Leeuwenhoek</i> , 2003, 83, 305-315.	1.7	37
53	New Molecular Quantitative PCR Assay for Detection of Host-Specific Bifidobacteriaceae Suitable for Microbial Source Tracking. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5788-5795.	3.1	35
54	Antibiotic Resistance Genes in Phage Particles from Antarctic and Mediterranean Seawater Ecosystems. <i>Microorganisms</i> , 2020, 8, 1293.	3.6	33

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55	Isolation of bacteriophage host strains of <i>Bacteroides</i> species suitable for tracking sources of animal faecal pollution in water. <i>Environmental Microbiology</i> , 2011, 13, 1622-1631.	3.8	32
56	Newly identified bacteriophages carrying the stx2g Shiga toxin gene isolated from <i>Escherichia coli</i> strains in polluted waters. <i>FEMS Microbiology Letters</i> , 2006, 258, 127-135.	1.8	30
57	Development of new host-specific <i>Bacteroides</i> qPCR for the identification of fecal contamination sources in water. <i>MicrobiologyOpen</i> , 2016, 5, 83-94.	3.0	30
58	Bacteriophage-Encoding Cytolethal Distending Toxin Type V Gene Induced from Nonclinical <i>Escherichia coli</i> Isolates. <i>Infection and Immunity</i> , 2011, 79, 3262-3272.	2.2	29
59	Improving Detection of Shiga Toxin-Producing <i>Escherichia coli</i> by Molecular Methods by Reducing the Interference of Free Shiga Toxin-Encoding Bacteriophages. <i>Applied and Environmental Microbiology</i> , 2015, 81, 415-421.	3.1	29
60	Optimisation and standardisation of a method for detecting and enumerating bacteriophages infecting <i>Bacteroides fragilis</i> . <i>Journal of Virological Methods</i> , 2001, 93, 127-136.	2.1	28
61	Quantification and Evaluation of Infectivity of Shiga Toxin-Encoding Bacteriophages in Beef and Salad. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3536-3540.	3.1	28
62	Predicting fecal sources in waters with diverse pollution loads using general and molecular host-specific indicators and applying machine learning methods. <i>Journal of Environmental Management</i> , 2015, 151, 317-325.	7.8	28
63	Heterogeneity in phage induction enables the survival of the lysogenic population. <i>Environmental Microbiology</i> , 2016, 18, 957-969.	3.8	28
64	Persistence of Infectious Shiga Toxin-Encoding Bacteriophages after Disinfection Treatments. <i>Applied and Environmental Microbiology</i> , 2014, 80, 2142-2149.	3.1	27
65	Extensive antimicrobial resistance mobilization via multicopy plasmid encapsidation mediated by temperate phages. <i>Journal of Antimicrobial Chemotherapy</i> , 2020, 75, 3173-3180.	3.0	25
66	Faecal phageome of healthy individuals: presence of antibiotic resistance genes and variations caused by ciprofloxacin treatment. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 854-864.	3.0	24
67	Unravelling the consequences of the bacteriophages in human samples. <i>Scientific Reports</i> , 2020, 10, 6737.	3.3	24
68	Free Shiga toxin encoding bacteriophages are less prevalent than Shiga toxin 2 phages in extraintestinal environments. <i>Environmental Microbiology</i> , 2015, 17, 4790-4801.	3.8	22
69	Bacteriophages as Fecal Pollution Indicators. <i>Viruses</i> , 2021, 13, 1089.	3.3	21
70	Abundance in Sewage of Bacteriophages Infecting <i>Escherichia coli</i> O157:H7. , 2004, 268, 079-088.		20
71	Stability and Infectivity of Cytolethal Distending Toxin Type V Gene-Carrying Bacteriophages in a Water Mesocosm and under Different Inactivation Conditions. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5818-5823.	3.1	18
72	Conserved Stx2 Phages from <i>Escherichia coli</i> O103:H25 Isolated from Patients Suffering from Hemolytic Uremic Syndrome. <i>Foodborne Pathogens and Disease</i> , 2008, 5, 801-810.	1.8	16

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73	Bacteriophages in sewage: abundance, roles, and applications. FEMS Microbes, 2022, 3, .	2.1	15
74	Investigation on the Evolution of Shiga Toxin-Converting Phages Based on Whole Genome Sequencing. Frontiers in Microbiology, 2020, 11, 1472.	3.5	13
75	Type III effector genes and other virulence factors of Shiga toxin-encoding <i>Escherichia coli</i> isolated from wastewater. Environmental Microbiology Reports, 2012, 4, 147-155.	2.4	12
76	Contribution of cropland to the spread of Shiga toxin phages and the emergence of new Shiga toxin-producing strains. Scientific Reports, 2017, 7, 7796.	3.3	12
77	Is Genetic Mobilization Considered When Using Bacteriophages in Antimicrobial Therapy?. Antibiotics, 2017, 6, 32.	3.7	12
78	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.	2.6	12
79	Essential Topics for the Regulatory Consideration of Phages as Clinically Valuable Therapeutic Agents: A Perspective from Spain. Microorganisms, 2022, 10, 717.	3.6	12
80	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.	1.8	11
81	Active Genetic Elements Present in the Locus of Enterocyte Effacement in <i>Escherichia coli</i> O26 and Their Role in Mobility. Infection and Immunity, 2006, 74, 4190-4199.	2.2	10
82	Spread of bacterial genomes in packaged particles. Future Microbiology, 2016, 11, 171-173.	2.0	10
83	Identifying and analyzing bacteriophages in human fecal samples: what could we discover?. Future Microbiology, 2014, 9, 879-886.	2.0	7
84	Antibiotic resistance in the viral fraction of dairy products and a nut-based milk. International Journal of Food Microbiology, 2022, 367, 109590.	4.7	7
85	BaeSR, Involved in Envelope Stress Response, Protects against Lysogenic Conversion by Shiga Toxin 2-Encoding Phages. Infection and Immunity, 2015, 83, 1451-1457.	2.2	4
86	Isolation of Bacteriophages of the Anaerobic Bacteria <i>Bacteroides</i> . Methods in Molecular Biology, 2018, 1693, 11-22.	0.9	4
87	Chicken liver is a potential reservoir of bacteriophages and phage-derived particles containing antibiotic resistance genes. Microbial Biotechnology, 2022, 15, 2464-2475.	4.2	4
88	Bacteriophage-driven emergence of novel pathogens. Future Virology, 2013, 8, 323-325.	1.8	3
89	Are Phages Parasites or Symbionts of Bacteria?. , 2020, , 143-162.		2
90	Isolation and Characterization of Shiga Toxin Bacteriophages. Methods in Molecular Biology, 2021, 2291, 119-144.	0.9	2

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91	Prevalence of bacterial genes in the phage fraction of food viromes. Food Research International, 2022, 156, 111342.	6.2	2
92	Modeling human pollution in water bodies using somatic coliphages and bacteriophages that infect Bacteroides thetaiotaomicron strain GA17. Journal of Environmental Management, 2022, 301, 113802.	7.8	1