

Matthew K Waldor

List of Publications by Year in descending order

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264
papers

26,647
citations

4370

86
h-index

8138

148
g-index

301
all docs

301
docs citations

301
times ranked

18833
citing authors

#	ARTICLE	IF	CITATIONS
1	Lysogenic Conversion by a Filamentous Phage Encoding Cholera Toxin. <i>Science</i> , 1996, 272, 1910-1914.	6.0	1,672
2	SOS response promotes horizontal dissemination of antibiotic resistance genes. <i>Nature</i> , 2004, 427, 72-74.	13.7	911
3	Origins of the <i>E. coli</i> Strain Causing an Outbreak of Hemolytic-Uremic Syndrome in Germany. <i>New England Journal of Medicine</i> , 2011, 365, 709-717.	13.9	778
4	The Origin of the Haitian Cholera Outbreak Strain. <i>New England Journal of Medicine</i> , 2011, 364, 33-42.	13.9	676
5	Integrative and conjugative elements: mosaic mobile genetic elements enabling dynamic lateral gene flow. <i>Nature Reviews Microbiology</i> , 2010, 8, 552-563.	13.6	674
6	<i>Vibrio</i> spp. infections. <i>Nature Reviews Disease Primers</i> , 2018, 4, 1-19.	18.1	572
7	Quinolone Antibiotics Induce Shiga Toxin-Encoding Bacteriophages, Toxin Production, and Death in Mice. <i>Journal of Infectious Diseases</i> , 2000, 181, 664-670.	1.9	530
8	D-Amino Acids Govern Stationary Phase Cell Wall Remodeling in Bacteria. <i>Science</i> , 2009, 325, 1552-1555.	6.0	519
9	Targeting QseC Signaling and Virulence for Antibiotic Development. <i>Science</i> , 2008, 321, 1078-1080.	6.0	452
10	Bacteriophage Control of Bacterial Virulence. <i>Infection and Immunity</i> , 2002, 70, 3985-3993.	1.0	419
11	Fucose sensing regulates bacterial intestinal colonization. <i>Nature</i> , 2012, 492, 113-117.	13.7	410
12	Shaping bacterial genomes with integrative and conjugative elements. <i>Research in Microbiology</i> , 2004, 155, 376-386.	1.0	402
13	A new type of conjugative transposon encodes resistance to sulfamethoxazole, trimethoprim, and streptomycin in <i>Vibrio cholerae</i> O139. <i>Journal of Bacteriology</i> , 1996, 178, 4157-4165.	1.0	365
14	Genome-wide mapping of methylated adenine residues in pathogenic <i>Escherichia coli</i> using single-molecule real-time sequencing. <i>Nature Biotechnology</i> , 2012, 30, 1232-1239.	9.4	365
15	Emerging knowledge of regulatory roles of d-amino acids in bacteria. <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 817-831.	2.4	311
16	Molecular Analysis of Antibiotic Resistance Gene Clusters in <i>Vibrio cholerae</i> O139 and O1 SXT Constins. <i>Antimicrobial Agents and Chemotherapy</i> , 2001, 45, 2991-3000.	1.4	300
17	Regulation and Temporal Expression Patterns of <i>Vibrio cholerae</i> Virulence Genes during Infection. <i>Cell</i> , 1999, 99, 625-634.	13.5	281
18	Distinct pathways for modification of the bacterial cell wall by non-canonical D-amino acids. <i>EMBO Journal</i> , 2011, 30, 3442-3453.	3.5	259

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19	Comparative ICE Genomics: Insights into the Evolution of the SXT/R391 Family of ICEs. <i>PLoS Genetics</i> , 2009, 5, e1000786.	1.5	247
20	Genomic and Functional Analyses of SXT, an Integrating Antibiotic Resistance Gene Transfer Element Derived from <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2002, 184, 4259-4269.	1.0	235
21	Role for a Phage Promoter in Shiga Toxin 2 Expression from a Pathogenic <i>Escherichia coli</i> Strain. <i>Journal of Bacteriology</i> , 2001, 183, 2081-2085.	1.0	234
22	Hfq is essential for <i>Vibrio cholerae</i> virulence and downregulates <i>ĳfE</i> expression. <i>Molecular Microbiology</i> , 2004, 53, 345-354.	1.2	232
23	Distribution of Centromere-Like <i><i>parS</i></i> Sites in Bacteria: Insights from Comparative Genomics. <i>Journal of Bacteriology</i> , 2007, 189, 8693-8703.	1.0	231
24	A dynamic, mitotic-like mechanism for bacterial chromosome segregation. <i>Genes and Development</i> , 2006, 20, 3269-3282.	2.7	227
25	Tn-Seq Analysis of <i>Vibrio cholerae</i> Intestinal Colonization Reveals a Role for T6SS-Mediated Antibacterial Activity in the Host. <i>Cell Host and Microbe</i> , 2013, 14, 652-663.	5.1	226
26	Bacteriophage control of Shiga toxin 1 production and release by <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2002, 44, 957-970.	1.2	212
27	Site-specific integration of the conjugal <i>Vibrio cholerae</i> SXT element into <i>prfC</i> . <i>Molecular Microbiology</i> , 1999, 32, 99-110.	1.2	209
28	The current ICE age: Biology and evolution of SXT-related integrating conjugative elements. <i>Plasmid</i> , 2006, 55, 173-183.	0.4	208
29	Phage regulatory circuits and virulence gene expression. <i>Current Opinion in Microbiology</i> , 2005, 8, 459-465.	2.3	201
30	The <i>Vibrio cholerae</i> O139 serogroup antigen includes an O-antigen capsule and lipopolysaccharide virulence determinants.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 11388-11392.	3.3	200
31	Regulation, replication, and integration functions of the <i>Vibrio cholerae</i> CTXĳ are encoded by region RS2. <i>Molecular Microbiology</i> , 1997, 24, 917-926.	1.2	200
32	Filamentous phages linked to virulence of <i>Vibrio cholerae</i> . <i>Current Opinion in Microbiology</i> , 2003, 6, 35-42.	2.3	194
33	High-Throughput, Kingdom-Wide Prediction and Annotation of Bacterial Non-Coding RNAs. <i>PLoS ONE</i> , 2008, 3, e3197.	1.1	192
34	A ToxinĳAntitoxin System Promotes the Maintenance of an Integrative Conjugative Element. <i>PLoS Genetics</i> , 2009, 5, e1000439.	1.5	191
35	RNA-Seq-Based Monitoring of Infection-Linked Changes in <i>Vibrio cholerae</i> Gene Expression. <i>Cell Host and Microbe</i> , 2011, 10, 165-174.	5.1	191
36	The design and analysis of transposon insertion sequencing experiments. <i>Nature Reviews Microbiology</i> , 2016, 14, 119-128.	13.6	180

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37	A hybrid approach for the automated finishing of bacterial genomes. <i>Nature Biotechnology</i> , 2012, 30, 701-707.	9.4	178
38	Filamentous phage integration requires the host recombinases XerC and XerD. <i>Nature</i> , 2002, 417, 656-659.	13.7	175
39	Identification of 17 <i>Pseudomonas aeruginosa</i> sRNAs and prediction of sRNA-encoding genes in 10 diverse pathogens using the bioinformatic tool sRNAPredict2. <i>Nucleic Acids Research</i> , 2006, 34, 3484-3493.	6.5	175
40	Identification of small RNAs in diverse bacterial species. <i>Current Opinion in Microbiology</i> , 2007, 10, 96-101.	2.3	173
41	Analysis of the Genome of the <i>Escherichia coli</i> O157:H7 2006 Spinach-Associated Outbreak Isolate Indicates Candidate Genes That May Enhance Virulence. <i>Infection and Immunity</i> , 2009, 77, 3713-3721.	1.0	163
42	Insights into <i>Vibrio cholerae</i> Intestinal Colonization from Monitoring Fluorescently Labeled Bacteria. <i>PLoS Pathogens</i> , 2014, 10, e1004405.	2.1	158
43	Distinct Replication Requirements for the Two <i>Vibrio cholerae</i> Chromosomes. <i>Cell</i> , 2003, 114, 521-530.	13.5	157
44	Emergence of a New Cholera Pandemic: Molecular Analysis of Virulence Determinants in <i>Vibrio cholerae</i> O139 and Development of a Live Vaccine Prototype. <i>Journal of Infectious Diseases</i> , 1994, 170, 278-283.	1.9	154
45	A multidomain hub anchors the chromosome segregation and chemotactic machinery to the bacterial pole. <i>Genes and Development</i> , 2012, 26, 2348-2360.	2.7	154
46	Interplay between microbial d-amino acids and host d-amino acid oxidase modifies murine mucosal defence and gut microbiota. <i>Nature Microbiology</i> , 2016, 1, 16125.	5.9	151
47	Critical Roles for <i>stx 2</i> , <i>eae</i> , and <i>tir</i> in Enterohemorrhagic <i>Escherichia coli</i> -Induced Diarrhea and Intestinal Inflammation in Infant Rabbits. <i>Infection and Immunity</i> , 2003, 71, 7129-7139.	1.0	149
48	The <i>Vibrio cholerae</i> ToxR-Regulated Porin OmpU Confers Resistance to Antimicrobial Peptides. <i>Infection and Immunity</i> , 2004, 72, 3577-3583.	1.0	148
49	Experimental discovery of sRNAs in <i>Vibrio cholerae</i> by direct cloning, 5S/tRNA depletion and parallel sequencing. <i>Nucleic Acids Research</i> , 2009, 37, e46-e46.	6.5	148
50	ARTIST: High-Resolution Genome-Wide Assessment of Fitness Using Transposon-Insertion Sequencing. <i>PLoS Genetics</i> , 2014, 10, e1004782.	1.5	148
51	ToxR regulates virulence gene expression in non-O1 strains of <i>Vibrio cholerae</i> that cause epidemic cholera. <i>Infection and Immunity</i> , 1994, 62, 72-78.	1.0	148
52	Inflammation and Disintegration of Intestinal Villi in an Experimental Model for <i>Vibrio parahaemolyticus</i> -Induced Diarrhea. <i>PLoS Pathogens</i> , 2012, 8, e1002593.	2.1	146
53	MicroReview: Divided genomes: negotiating the cell cycle in prokaryotes with multiple chromosomes. <i>Molecular Microbiology</i> , 2005, 56, 1129-1138.	1.2	139
54	Deciphering functional redundancy in the human microbiome. <i>Nature Communications</i> , 2020, 11, 6217.	5.8	139

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55	In Vivo Transduction with Shiga Toxin 1-Encoding Phage. <i>Infection and Immunity</i> , 1998, 66, 4496-4498.	1.0	136
56	Infectious CTX ϕ and the <i>Vibrio</i> Pathogenicity Island Prophage in <i>Vibrio mimicus</i> : Evidence for Recent Horizontal Transfer between <i>V. mimicus</i> and <i>V. cholerae</i> . <i>Infection and Immunity</i> , 2000, 68, 1507-1513.	1.0	130
57	Characterization of the Small Untranslated RNA RyhB and Its Regulon in <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2005, 187, 4005-4014.	1.0	126
58	Mapping the ecological networks of microbial communities. <i>Nature Communications</i> , 2017, 8, 2042.	5.8	125
59	Human Neutrophils and Their Products Induce Shiga Toxin Production by Enterohemorrhagic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2001, 69, 1934-1937.	1.0	121
60	Analysis of Bottlenecks in Experimental Models of Infection. <i>PLoS Pathogens</i> , 2015, 11, e1004823.	2.1	121
61	CTX ϕ immunity: Application in the development of cholera vaccines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 7035-7039.	3.3	117
62	CTX Prophages in Classical Biotype <i>Vibrio cholerae</i> : Functional Phage Genes but Dysfunctional Phage Genomes. <i>Journal of Bacteriology</i> , 2000, 182, 6992-6998.	1.0	116
63	High-resolution definition of the <i>Vibrio cholerae</i> essential gene set with hidden Markov model-based analyses of transposon-insertion sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, 9033-9048.	6.5	115
64	Where Next for Microbiome Research?. <i>PLoS Biology</i> , 2015, 13, e1002050.	2.6	115
65	Mobile Antibiotic Resistance Encoding Elements Promote Their Own Diversity. <i>PLoS Genetics</i> , 2009, 5, e1000775.	1.5	113
66	Mobilization of Plasmids and Chromosomal DNA Mediated by the SXT Element, a Constein Found in <i>Vibrio cholerae</i> O139. <i>Journal of Bacteriology</i> , 2000, 182, 2043-2047.	1.0	112
67	Entering the era of bacterial epigenomics with single molecule real time DNA sequencing. <i>Current Opinion in Microbiology</i> , 2013, 16, 192-198.	2.3	112
68	Convergence of the Secretory Pathways for Cholera Toxin and the Filamentous Phage, CTX. <i>Science</i> , 2000, 288, 333-335.	6.0	111
69	RNase E-dependent processing stabilizes MicX, a <i>Vibrio cholerae</i> sRNA. <i>Molecular Microbiology</i> , 2007, 65, 373-385.	1.2	109
70	A satellite phage-encoded antirepressor induces repressor aggregation and cholera toxin gene transfer. <i>EMBO Journal</i> , 2002, 21, 4240-4249.	3.5	108
71	Distinct segregation dynamics of the two <i>Vibrio cholerae</i> chromosomes. <i>Molecular Microbiology</i> , 2004, 55, 125-136.	1.2	106
72	CTX ϕ Infection of <i>Vibrio cholerae</i> Requires the tolQRA Gene Products. <i>Journal of Bacteriology</i> , 2000, 182, 1739-1747.	1.0	105

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73	Control of SXT Integration and Excision. <i>Journal of Bacteriology</i> , 2003, 185, 5045-5054.	1.0	105
74	Meeting Cholera's Challenge to Haiti and the World: A Joint Statement on Cholera Prevention and Care. <i>PLoS Neglected Tropical Diseases</i> , 2011, 5, e1145.	1.3	105
75	The <i>Vibrio cholerae</i> O139 Calcutta Bacteriophage CTX ϕ Is Infectious and Encodes a Novel Repressor. <i>Journal of Bacteriology</i> , 1999, 181, 6779-6787.	1.0	105
76	Antimicrobial peptides activate the <i>Vibrio cholerae</i> χ Regulon through an OmpU-dependent signalling pathway. <i>Molecular Microbiology</i> , 2007, 63, 848-58.	1.2	104
77	Transcription of the Toxin Genes Present within the Staphylococcal Phage ϕ Sa3ms Is Intimately Linked with the Phage's Life Cycle. <i>Journal of Bacteriology</i> , 2003, 185, 6841-6851.	1.0	102
78	sRNAPredict: an integrative computational approach to identify sRNAs in bacterial genomes. <i>Nucleic Acids Research</i> , 2005, 33, 4096-4105.	6.5	100
79	Sequence tag-based analysis of microbial population dynamics. <i>Nature Methods</i> , 2015, 12, 223-226.	9.0	100
80	Genetic analysis of <i>Vibrio parahaemolyticus</i> intestinal colonization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6283-6288.	3.3	100
81	Bacterial Adrenergic Sensors Regulate Virulence of Enteric Pathogens in the Gut. <i>MBio</i> , 2016, 7, .	1.8	100
82	Back to the Future: Studying Cholera Pathogenesis Using Infant Rabbits. <i>MBio</i> , 2010, 1, .	1.8	99
83	Bacteriophage biology and bacterial virulence. <i>Trends in Microbiology</i> , 1998, 6, 295-297.	3.5	96
84	Isogenic Lysogens of Diverse Shiga Toxin 2-Encoding Bacteriophages Produce Markedly Different Amounts of Shiga Toxin. <i>Infection and Immunity</i> , 1999, 67, 6710-6714.	1.0	96
85	<i>Vibrio cholerae</i> Intestinal Population Dynamics in the Suckling Mouse Model of Infection. <i>Infection and Immunity</i> , 1999, 67, 3733-3739.	1.0	96
86	A family of ParA-like ATPases promotes cell pole maturation by facilitating polar localization of chemotaxis proteins. <i>Genes and Development</i> , 2011, 25, 1544-1555.	2.7	95
87	LexA Cleavage Is Required for CTX Prophage Induction. <i>Molecular Cell</i> , 2005, 17, 291-300.	4.5	93
88	Formation of Chromosomal Tandem Arrays of the SXT Element and R391, Two Conjugative Chromosomally Integrating Elements That Share an Attachment Site. <i>Journal of Bacteriology</i> , 2001, 183, 1124-1132.	1.0	92
89	Comparison of SXT and R391, two conjugative integrating elements: definition of a genetic backbone for the mobilization of resistance determinants. <i>Cellular and Molecular Life Sciences</i> , 2002, 59, 2065-2070.	2.4	92
90	par genes and the pathology of chromosome loss in <i>Vibrio cholerae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 630-635.	3.3	92

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91	CTX ϕ and <i>Vibrio cholerae</i> : exploring a newly recognized type of phage-host cell relationship. <i>Molecular Microbiology</i> , 2005, 57, 347-356.	1.2	88
92	Characterization of a higBA Toxin-Antitoxin Locus in <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2007, 189, 491-500.	1.0	86
93	Type III Secretion Is Essential for the Rapidly Fatal Diarrheal Disease Caused by Non-O1, Non-O139 <i>Vibrio cholerae</i> . <i>MBio</i> , 2011, 2, e00106-11.	1.8	86
94	Molecular Analyses of a Putative CTX ϕ Precursor and Evidence for Independent Acquisition of Distinct CTX ϕ s by Toxigenic <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2000, 182, 5530-5538.	1.0	85
95	Single molecule-level detection and long read-based phasing of epigenetic variations in bacterial methylomes. <i>Nature Communications</i> , 2015, 6, 7438.	5.8	82
96	Peptidoglycan synthesis in <i>Mycobacterium tuberculosis</i> is organized into networks with varying drug susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13087-13092.	3.3	82
97	The Locus of Enterocyte Effacement-Encoded Effector Proteins All Promote Enterohemorrhagic <i>Escherichia coli</i> Pathogenicity in Infant Rabbits. <i>Infection and Immunity</i> , 2005, 73, 1466-1474.	1.0	80
98	<i>Vibrio cholerae</i> O139 specific gene sequences. <i>Lancet, The</i> , 1994, 343, 1366.	6.3	79
99	A cell wall damage response mediated by a sensor kinase/response regulator pair enables beta-lactam tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 404-409.	3.3	76
100	Comparison of Shiga Toxin Production by Hemolytic-Uremic Syndrome-Associated and Bovine-Associated Shiga Toxin-Producing <i>Escherichia coli</i> Isolates. <i>Applied and Environmental Microbiology</i> , 2003, 69, 1059-1066.	1.4	75
101	Diverse CTX ϕ s and evolution of new pathogenic <i>Vibrio cholerae</i> . <i>Lancet, The</i> , 1998, 352, 457-458.	6.3	72
102	Independent Control of Replication Initiation of the Two <i>Vibrio cholerae</i> Chromosomes by DnaA and RctB. <i>Journal of Bacteriology</i> , 2006, 188, 6419-6424.	1.0	72
103	Replication and integration of a <i>Vibrio cholerae</i> cryptic plasmid linked to the CTX prophage. <i>Molecular Microbiology</i> , 1998, 28, 1247-1254.	1.2	71
104	Hfq negatively regulates type III secretion in EHEC and several other pathogens. <i>Molecular Microbiology</i> , 2009, 74, 347-363.	1.2	70
105	A <i>Vibrio parahaemolyticus</i> T3SS Effector Mediates Pathogenesis by Independently Enabling Intestinal Colonization and Inhibiting TAK1 Activation. <i>Cell Reports</i> , 2013, 3, 1690-1702.	2.9	70
106	The RNA degradosome promotes tRNA quality control through clearance of hypomodified tRNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1394-1403.	3.3	69
107	CTX ϕ contains a hybrid genome derived from tandemly integrated elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 8572-8577.	3.3	68
108	pIII CTX, a Predicted CTX ϕ Minor Coat Protein, Can Expand the Host Range of Coliphage ϕ d To Include <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , 2003, 185, 1037-1044.	1.0	68

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109	Comparative Genomics of Recent Shiga Toxin-Producing <i>Escherichia coli</i> O104:H4: Short-Term Evolution of an Emerging Pathogen. <i>MBio</i> , 2013, 4, e00452-12.	1.8	68
110	Deciphering the landscape of host barriers to <i>Listeria monocytogenes</i> infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 6334-6339.	3.3	68
111	<i>Vibrio cholerae</i> ParE2 Poisons DNA Gyrase via a Mechanism Distinct from Other Gyrase Inhibitors. <i>Journal of Biological Chemistry</i> , 2010, 285, 40397-40408.	1.6	67
112	The Three <i>Vibrio cholerae</i> Chromosome II-Encoded ParE Toxins Degrade Chromosome I following Loss of Chromosome II. <i>Journal of Bacteriology</i> , 2011, 193, 611-619.	1.0	67
113	Classic reaction kinetics can explain complex patterns of antibiotic action. <i>Science Translational Medicine</i> , 2015, 7, 287ra73.	5.8	67
114	CRISPR/Cas9 Screens Reveal Requirements for Host Cell Sulfation and Fucosylation in Bacterial Type III Secretion System-Mediated Cytotoxicity. <i>Cell Host and Microbe</i> , 2016, 20, 226-237.	5.1	64
115	Evolutionary and functional analyses of variants of the toxin-coregulated pilus protein TcpA from toxigenic <i>Vibrio cholerae</i> non-O1/non-O139 serogroup isolates The GenBank accession numbers for the sequences reported in this paper are AY078355-AY078358. <i>Microbiology (United Kingdom)</i> , 2002, 148, 1655-1666.	0.7	63
116	Interactions between Inner Membrane Proteins in Donor and Recipient Cells Limit Conjugal DNA Transfer. <i>Developmental Cell</i> , 2005, 8, 963-970.	3.1	62
117	CRISPR Screen Reveals that EHEC's T3SS and Shiga Toxin Rely on Shared Host Factors for Infection. <i>MBio</i> , 2018, 9, .	1.8	62
118	SXT-Related Integrating Conjugative Element in New World <i>Vibrio cholerae</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 3054-3057.	1.4	61
119	Structural basis for the broad specificity of a new family of amino-acid racemases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 79-90.	2.5	61
120	Cell Separation in <i>Vibrio cholerae</i> Is Mediated by a Single Amidase Whose Action Is Modulated by Two Nonredundant Activators. <i>Journal of Bacteriology</i> , 2014, 196, 3937-3948.	1.0	61
121	Enterohemorrhagic <i>Escherichia coli</i> O157:H7 gal Mutants Are Sensitive to Bacteriophage P1 and Defective in Intestinal Colonization. <i>Infection and Immunity</i> , 2007, 75, 1661-1666.	1.0	60
122	An <i>Escherichia coli</i> O157-Specific Engineered Pyocin Prevents and Ameliorates Infection by <i>E. coli</i> O157:H7 in an Animal Model of Diarrheal Disease. <i>Antimicrobial Agents and Chemotherapy</i> , 2011, 55, 5469-5474.	1.4	60
123	Sunlight-Induced Propagation of the Lysogenic Phage Encoding Cholera Toxin. <i>Infection and Immunity</i> , 2000, 68, 4795-4801.	1.0	58
124	Genomic and Functional Analysis of ICE <i>Pda</i> Spa1, a Fish-Pathogen-Derived SXT-Related Integrating Conjugative Element That Can Mobilize a Virulence Plasmid. <i>Journal of Bacteriology</i> , 2008, 190, 3353-3361.	1.0	58
125	Horizontal Transfer of Shiga Toxin and Antibiotic Resistance Genes Among <i>Escherichia coli</i> Strains in House Fly (Diptera: Muscidae) Gut. <i>Journal of Medical Entomology</i> , 2006, 43, 288-295.	0.9	57
126	Type 2 Secretion Promotes Enterohemorrhagic <i>Escherichia coli</i> Adherence and Intestinal Colonization. <i>Infection and Immunity</i> , 2008, 76, 1858-1865.	1.0	57

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127	Formation of SXT Tandem Arrays and SXT-R391 Hybrids. <i>Journal of Bacteriology</i> , 2004, 186, 2636-2645.	1.0	56
128	ParA2, a <i>Vibrio cholerae</i> chromosome partitioning protein, forms left-handed helical filaments on DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4590-4595.	3.3	56
129	Substrate specificity of an elongation-specific peptidoglycan endopeptidase and its implications for cell wall architecture and growth of <i>Vibrio cholerae</i> . <i>Molecular Microbiology</i> , 2013, 89, 949-962.	1.2	56
130	Endopeptidase-Mediated Beta Lactam Tolerance. <i>PLoS Pathogens</i> , 2015, 11, e1004850.	2.1	56
131	Characterization of XerC- and XerD-dependent CTX phage integration in <i>Vibrio cholerae</i> . <i>Molecular Microbiology</i> , 2004, 54, 935-947.	1.2	55
132	Reactogenicity of live-attenuated <i>Vibrio cholerae</i> vaccines is dependent on flagellins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4359-4364.	3.3	55
133	A live vaccine rapidly protects against cholera in an infant rabbit model. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	55
134	ToxR-Independent Expression of Cholera Toxin from the Replicative Form of CTX ϕ . <i>Infection and Immunity</i> , 1998, 66, 394-397.	1.0	55
135	<i>Vibrio cholerae</i> Interactions with the Gastrointestinal Tract: Lessons from Animal Studies. <i>Current Topics in Microbiology and Immunology</i> , 2009, 337, 37-59.	0.7	54
136	Comparative tRNA sequencing and RNA mass spectrometry for surveying tRNA modifications. <i>Nature Chemical Biology</i> , 2020, 16, 964-972.	3.9	54
137	Synchronous replication initiation of the two <i>Vibrio cholerae</i> chromosomes. <i>Current Biology</i> , 2004, 14, R501-R502.	1.8	53
138	Distinct Centromere-Like parS Sites on the Two Chromosomes of <i>Vibrio</i> spp. <i>Journal of Bacteriology</i> , 2007, 189, 5314-5324.	1.0	53
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