

# Matthew K Waldor

## List of Publications by Citations

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24,490  
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L-index

#	Paper	IF	Citations
271	Lysogenic conversion by a filamentous phage encoding cholera toxin. <i>Science</i> , <b>1996</b> , 272, 1910-4	33.3	1396
270	SOS response promotes horizontal dissemination of antibiotic resistance genes. <i>Nature</i> , <b>2004</b> , 427, 72-4	50.4	716
269	Origins of the E. coli strain causing an outbreak of hemolytic-uremic syndrome in Germany. <i>New England Journal of Medicine</i> , <b>2011</b> , 365, 709-17	59.2	658
268	The origin of the Haitian cholera outbreak strain. <i>New England Journal of Medicine</i> , <b>2011</b> , 364, 33-42	59.2	559
267	Integrative and conjugative elements: mosaic mobile genetic elements enabling dynamic lateral gene flow. <i>Nature Reviews Microbiology</i> , <b>2010</b> , 8, 552-63	22.2	518
266	Quinolone antibiotics induce Shiga toxin-encoding bacteriophages, toxin production, and death in mice. <i>Journal of Infectious Diseases</i> , <b>2000</b> , 181, 664-70	7	444
265	D-amino acids govern stationary phase cell wall remodeling in bacteria. <i>Science</i> , <b>2009</b> , 325, 1552-5	33.3	410
264	Targeting QseC signaling and virulence for antibiotic development. <i>Science</i> , <b>2008</b> , 321, 1078-80	33.3	382
263	Bacteriophage control of bacterial virulence. <i>Infection and Immunity</i> , <b>2002</b> , 70, 3985-93	3.7	353
262	Shaping bacterial genomes with integrative and conjugative elements. <i>Research in Microbiology</i> , <b>2004</b> , 155, 376-86	4	320
261	Fucose sensing regulates bacterial intestinal colonization. <i>Nature</i> , <b>2012</b> , 492, 113-7	50.4	312
260	A new type of conjugative transposon encodes resistance to sulfamethoxazole, trimethoprim, and streptomycin in <i>Vibrio cholerae</i> O139. <i>Journal of Bacteriology</i> , <b>1996</b> , 178, 4157-65	3.5	304
259	<i>Vibrio</i> spp. infections. <i>Nature Reviews Disease Primers</i> , <b>2018</b> , 4, 8	51.1	301
258	Regulation and temporal expression patterns of <i>Vibrio cholerae</i> virulence genes during infection. <i>Cell</i> , <b>1999</b> , 99, 625-34	56.2	260
257	Genome-wide mapping of methylated adenine residues in pathogenic <i>Escherichia coli</i> using single-molecule real-time sequencing. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 1232-9	44.5	256
256	Molecular analysis of antibiotic resistance gene clusters in <i>vibrio cholerae</i> O139 and O1 SXT constins. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2001</b> , 45, 2991-3000	5.9	245
255	Hfq is essential for <i>Vibrio cholerae</i> virulence and downregulates sigma expression. <i>Molecular Microbiology</i> , <b>2004</b> , 53, 345-54	4.1	215

254	Emerging knowledge of regulatory roles of D-amino acids in bacteria. <i>Cellular and Molecular Life Sciences</i> , <b>2011</b> , 68, 817-31	10.3	214
253	Role for a phage promoter in Shiga toxin 2 expression from a pathogenic <i>Escherichia coli</i> strain. <i>Journal of Bacteriology</i> , <b>2001</b> , 183, 2081-5	3.5	211
252	Genomic and functional analyses of SXT, an integrating antibiotic resistance gene transfer element derived from <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , <b>2002</b> , 184, 4259-69	3.5	206
251	A dynamic, mitotic-like mechanism for bacterial chromosome segregation. <i>Genes and Development</i> , <b>2006</b> , 20, 3269-82	12.6	203
250	Distinct pathways for modification of the bacterial cell wall by non-canonical D-amino acids. <i>EMBO Journal</i> , <b>2011</b> , 30, 3442-53	13	200
249	Comparative ICE genomics: insights into the evolution of the SXT/R391 family of ICEs. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000786	6	188
248	Site-specific integration of the conjugal <i>Vibrio cholerae</i> SXT element into <i>prfC</i> . <i>Molecular Microbiology</i> , <b>1999</b> , 32, 99-110	4.1	182
247	Bacteriophage control of Shiga toxin 1 production and release by <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , <b>2002</b> , 44, 957-70	4.1	180
246	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> , <b>2013</b> , 14, 652-63	23.4	171
245	Regulation, replication, and integration functions of the <i>Vibrio cholerae</i> CTXphi are encoded by region RS2. <i>Molecular Microbiology</i> , <b>1997</b> , 24, 917-26	4.1	171
244	Distribution of centromere-like <i>parS</i> sites in bacteria: insights from comparative genomics. <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 8693-703	3.5	167
243	RNA-Seq-based monitoring of infection-linked changes in <i>Vibrio cholerae</i> gene expression. <i>Cell Host and Microbe</i> , <b>2011</b> , 10, 165-74	23.4	166
242	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> , <b>1994</b> , 91, 11388-92	11.5	166
241	Phage regulatory circuits and virulence gene expression. <i>Current Opinion in Microbiology</i> , <b>2005</b> , 8, 459-65	7.9	165
240	The current ICE age: biology and evolution of SXT-related integrating conjugative elements. <i>Plasmid</i> , <b>2006</b> , 55, 173-83	3.3	164
239	A toxin-antitoxin system promotes the maintenance of an integrative conjugative element. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000439	6	160
238	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> , <b>2006</b> , 34, 3484-93	20.1	159
237	Filamentous phages linked to virulence of <i>Vibrio cholerae</i> . <i>Current Opinion in Microbiology</i> , <b>2003</b> , 6, 35-42	7.9	158

- 236 A hybrid approach for the automated finishing of bacterial genomes. *Nature Biotechnology*, **2012**, 30, 701-707 44.5 157
- 235 High-throughput, kingdom-wide prediction and annotation of bacterial non-coding RNAs. *PLoS ONE*, **2008**, 3, e3197 3.7 151
- 234 Filamentous phage integration requires the host recombinases XerC and XerD. *Nature*, **2002**, 417, 656-9 50.4 150
- 233 Experimental discovery of sRNAs in *Vibrio cholerae* by direct cloning, 5S/tRNA depletion and parallel sequencing. *Nucleic Acids Research*, **2009**, 37, e46 20.1 141
- 232 Distinct replication requirements for the two *Vibrio cholerae* chromosomes. *Cell*, **2003**, 114, 521-30 56.2 140
- 231 Identification of small RNAs in diverse bacterial species. *Current Opinion in Microbiology*, **2007**, 10, 96-101 7.9 136
- 230 Critical roles for stx2, eae, and tir in enterohemorrhagic *Escherichia coli*-induced diarrhea and intestinal inflammation in infant rabbits. *Infection and Immunity*, **2003**, 71, 7129-39 3.7 133
- 229 The design and analysis of transposon insertion sequencing experiments. *Nature Reviews Microbiology*, **2016**, 14, 119-28 22.2 126
- 228 Emergence of a new cholera pandemic: molecular analysis of virulence determinants in *Vibrio cholerae* O139 and development of a live vaccine prototype. *Journal of Infectious Diseases*, **1994**, 170, 278-83 7 124
- 227 Analysis of the genome of the *Escherichia coli* O157:H7 2006 spinach-associated outbreak isolate indicates candidate genes that may enhance virulence. *Infection and Immunity*, **2009**, 77, 3713-21 3.7 122
- 226 Divided genomes: negotiating the cell cycle in prokaryotes with multiple chromosomes. *Molecular Microbiology*, **2005**, 56, 1129-38 4.1 121
- 225 In vivo transduction with shiga toxin 1-encoding phage. *Infection and Immunity*, **1998**, 66, 4496-8 3.7 121
- 224 A multidomain hub anchors the chromosome segregation and chemotactic machinery to the bacterial pole. *Genes and Development*, **2012**, 26, 2348-60 12.6 118
- 223 The *Vibrio cholerae* ToxR-regulated porin OmpU confers resistance to antimicrobial peptides. *Infection and Immunity*, **2004**, 72, 3577-83 3.7 117
- 222 Insights into *Vibrio cholerae* intestinal colonization from monitoring fluorescently labeled bacteria. *PLoS Pathogens*, **2014**, 10, e1004405 7.6 116
- 221 Infectious CTXPhi and the vibrio pathogenicity island prophage in *Vibrio mimicus*: evidence for recent horizontal transfer between *V. mimicus* and *V. cholerae*. *Infection and Immunity*, **2000**, 68, 1507-13 3.7 116
- 220 Human neutrophils and their products induce Shiga toxin production by enterohemorrhagic *Escherichia coli*. *Infection and Immunity*, **2001**, 69, 1934-7 3.7 113
- 219 Inflammation and disintegration of intestinal villi in an experimental model for *Vibrio parahaemolyticus*-induced diarrhea. *PLoS Pathogens*, **2012**, 8, e1002593 7.6 110

218	Characterization of the small untranslated RNA RyhB and its regulon in <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , <b>2005</b> , 187, 4005-14	3.5	109
217	CTXphi immunity: application in the development of cholera vaccines. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1998</b> , 95, 7035-9	11.5	109
216	CTX prophages in classical biotype <i>Vibrio cholerae</i> : functional phage genes but dysfunctional phage genomes. <i>Journal of Bacteriology</i> , <b>2000</b> , 182, 6992-8	3.5	106
215	ToxR regulates virulence gene expression in non-O1 strains of <i>Vibrio cholerae</i> that cause epidemic cholera. <i>Infection and Immunity</i> , <b>1994</b> , 62, 72-8	3.7	106
214	ARTIST: high-resolution genome-wide assessment of fitness using transposon-insertion sequencing. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004782	6	101
213	The <i>Vibrio cholerae</i> O139 Calcutta bacteriophage CTXphi is infectious and encodes a novel repressor. <i>Journal of Bacteriology</i> , <b>1999</b> , 181, 6779-87	3.5	100
212	Mobilization of plasmids and chromosomal DNA mediated by the SXT element, a constin found in <i>Vibrio cholerae</i> O139. <i>Journal of Bacteriology</i> , <b>2000</b> , 182, 2043-7	3.5	99
211	Control of SXT integration and excision. <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 5045-54	3.5	98
210	Where next for microbiome research?. <i>PLoS Biology</i> , <b>2015</b> , 13, e1002050	9.7	97
209	A satellite phage-encoded antirepressor induces repressor aggregation and cholera toxin gene transfer. <i>EMBO Journal</i> , <b>2002</b> , 21, 4240-9	13	95
208	Distinct segregation dynamics of the two <i>Vibrio cholerae</i> chromosomes. <i>Molecular Microbiology</i> , <b>2005</b> , 55, 125-36	4.1	94
207	Convergence of the secretory pathways for cholera toxin and the filamentous phage, CTXphi. <i>Science</i> , <b>2000</b> , 288, 333-5	33.3	93
206	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> , <b>2013</b> , 41, 9033-48	20.1	92
205	Transcription of the toxin genes present within the Staphylococcal phage phiSa3ms is intimately linked with the phage's life cycle. <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 6841-51	3.5	89
204	CTXphi infection of <i>Vibrio cholerae</i> requires the tolQRA gene products. <i>Journal of Bacteriology</i> , <b>2000</b> , 182, 1739-47	3.5	88
203	Interplay between microbial d-amino acids and host d-amino acid oxidase modifies murine mucosal defence and gut microbiota. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16125	26.6	87
202	Entering the era of bacterial epigenomics with single molecule real time DNA sequencing. <i>Current Opinion in Microbiology</i> , <b>2013</b> , 16, 192-8	7.9	87
201	Back to the future: studying cholera pathogenesis using infant rabbits. <i>MBio</i> , <b>2010</b> , 1,	7.8	87

200	sRNAPredict: an integrative computational approach to identify sRNAs in bacterial genomes. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 4096-105	20.1	87
199	<i>Vibrio cholerae</i> intestinal population dynamics in the suckling mouse model of infection. <i>Infection and Immunity</i> , <b>1999</b> , 67, 3733-9	3.7	86
198	LexA cleavage is required for CTX prophage induction. <i>Molecular Cell</i> , <b>2005</b> , 17, 291-300	17.6	85
197	Mobile antibiotic resistance encoding elements promote their own diversity. <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000775	8.4	
196	Antimicrobial peptides activate the <i>Vibrio cholerae</i> sigmaE regulon through an OmpU-dependent signalling pathway. <i>Molecular Microbiology</i> , <b>2007</b> , 63, 848-58	4.1	80
195	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> , <b>2001</b> , 183, 1124-32	3.5	80
194	Characterization of a higBA toxin-antitoxin locus in <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 491-500	3.5	78
193	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> , <b>2002</b> , 59, 2065-70	10.3	78
192	Mapping the ecological networks of microbial communities. <i>Nature Communications</i> , <b>2017</b> , 8, 2042	17.4	77
191	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> , <b>2007</b> , 104, 630-5	11.5	76
190	Molecular analyses of a putative CTXphi precursor and evidence for independent acquisition of distinct CTX(phi)s by toxigenic <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , <b>2000</b> , 182, 5530-8	3.5	76
189	RNase E-dependent processing stabilizes MicX, a <i>Vibrio cholerae</i> sRNA. <i>Molecular Microbiology</i> , <b>2007</b> , 65, 373-85	4.1	74
188	A family of ParA-like ATPases promotes cell pole maturation by facilitating polar localization of chemotaxis proteins. <i>Genes and Development</i> , <b>2011</b> , 25, 1544-55	12.6	73
187	Analysis of Bottlenecks in Experimental Models of Infection. <i>PLoS Pathogens</i> , <b>2015</b> , 11, e1004823	7.6	72
186	Bacteriophage biology and bacterial virulence. <i>Trends in Microbiology</i> , <b>1998</b> , 6, 295-7	12.4	71
185	The locus of enterocyte effacement-encoded effector proteins all promote enterohemorrhagic <i>Escherichia coli</i> pathogenicity in infant rabbits. <i>Infection and Immunity</i> , <b>2005</b> , 73, 1466-74	3.7	71
184	Isogenic lysogens of diverse shiga toxin 2-encoding bacteriophages produce markedly different amounts of shiga toxin. <i>Infection and Immunity</i> , <b>1999</b> , 67, 6710-4	3.7	71
183	Sequence tag-based analysis of microbial population dynamics. <i>Nature Methods</i> , <b>2015</b> , 12, 223-6, 3 p following 226	21.6	70

182	Meeting cholera's challenge to Haiti and the world: a joint statement on cholera prevention and care. <i>PLoS Neglected Tropical Diseases</i> , <b>2011</b> , 5, e1145	4.8	69
181	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> , <b>2003</b> , 69, 1059-66	4.8	69
180	Hfq negatively regulates type III secretion in EHEC and several other pathogens. <i>Molecular Microbiology</i> , <b>2009</b> , 74, 347-63	4.1	65
179	Replication and integration of a <i>Vibrio cholerae</i> cryptic plasmid linked to the CTX prophage. <i>Molecular Microbiology</i> , <b>1998</b> , 28, 1247-54	4.1	65
178	Single molecule-level detection and long read-based phasing of epigenetic variations in bacterial methylomes. <i>Nature Communications</i> , <b>2015</b> , 6, 7438	17.4	64
177	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> , <b>2015</b> , 112, 13087-92	11.5	64
176	<i>Vibrio cholerae</i> O139 specific gene sequences. <i>Lancet, The</i> , <b>1994</b> , 343, 1366	4.0	64
175	CTXphi and <i>Vibrio cholerae</i> : exploring a newly recognized type of phage-host cell relationship. <i>Molecular Microbiology</i> , <b>2005</b> , 57, 347-56	4.1	63
174	Diverse CTXphis and evolution of new pathogenic <i>Vibrio cholerae</i> . <i>Lancet, The</i> , <b>1998</b> , 352, 457-8	4.0	62
173	Independent control of replication initiation of the two <i>Vibrio cholerae</i> chromosomes by DnaA and RctB. <i>Journal of Bacteriology</i> , <b>2006</b> , 188, 6419-24	3.5	61
172	CTXphi contains a hybrid genome derived from tandemly integrated elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2000</b> , 97, 8572-7	11.5	61
171	Genetic analysis of <i>Vibrio parahaemolyticus</i> intestinal colonization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 6283-8	11.5	61
170	Bacterial Adrenergic Sensors Regulate Virulence of Enteric Pathogens in the Gut. <i>MBio</i> , <b>2016</b> , 7,	7.8	60
169	Comparative genomics of recent Shiga toxin-producing <i>Escherichia coli</i> O104:H4: short-term evolution of an emerging pathogen. <i>MBio</i> , <b>2013</b> , 4, e00452-12	7.8	59
168	SXT-related integrating conjugative element in New World <i>Vibrio cholerae</i> . <i>Applied and Environmental Microbiology</i> , <b>2006</b> , 72, 3054-7	4.8	56
167	Genomic and functional analysis of ICEPdaSpa1, a fish-pathogen-derived SXT-related integrating conjugative element that can mobilize a virulence plasmid. <i>Journal of Bacteriology</i> , <b>2008</b> , 190, 3353-61	3.5	54
166	pIICTX, a predicted CTXphi minor coat protein, can expand the host range of coliphage fd to include <i>Vibrio cholerae</i> . <i>Journal of Bacteriology</i> , <b>2003</b> , 185, 1037-44	3.5	54
165	Sunlight-induced propagation of the lysogenic phage encoding cholera toxin. <i>Infection and Immunity</i> , <b>2000</b> , 68, 4795-801	3.7	54



164	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. <i>Microbiology (United Kingdom)</i> , <b>2002</b> , 148, 1655-1666	2.9	54
163	A <i>Vibrio parahaemolyticus</i> T3SS effector mediates pathogenesis by independently enabling intestinal colonization and inhibiting TAK1 activation. <i>Cell Reports</i> , <b>2013</b> , 3, 1690-702	10.6	53
162	<i>Vibrio cholerae</i> ParE2 poisons DNA gyrase via a mechanism distinct from other gyrase inhibitors. <i>Journal of Biological Chemistry</i> , <b>2010</b> , 285, 40397-408	5.4	53
161	Type III secretion is essential for the rapidly fatal diarrheal disease caused by non-O1, non-O139 <i>Vibrio cholerae</i> . <i>MBio</i> , <b>2011</b> , 2, e00106-11	7.8	53
160	Classic reaction kinetics can explain complex patterns of antibiotic action. <i>Science Translational Medicine</i> , <b>2015</b> , 7, 287ra73	17.5	51
159	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> , <b>2011</b> , 55, 5469-74	5.9	50
158	Type 2 secretion promotes enterohemorrhagic <i>Escherichia coli</i> adherence and intestinal colonization. <i>Infection and Immunity</i> , <b>2008</b> , 76, 1858-65	3.7	50
157	Interactions between inner membrane proteins in donor and recipient cells limit conjugal DNA transfer. <i>Developmental Cell</i> , <b>2005</b> , 8, 963-70	10.2	50
156	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> , <b>2006</b> , 43, 288-295	2.2	50
155	Enterohemorrhagic <i>Escherichia coli</i> O157:H7 gal mutants are sensitive to bacteriophage P1 and defective in intestinal colonization. <i>Infection and Immunity</i> , <b>2007</b> , 75, 1661-6	3.7	49
154	Characterization of XerC- and XerD-dependent CTX phage integration in <i>Vibrio cholerae</i> . <i>Molecular Microbiology</i> , <b>2004</b> , 54, 935-47	4.1	48
153	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> , <b>2014</b> , 196, 3937-48	3.5	46
152	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> , <b>2010</b> , 107, 4359-64	11.5	46
151	Formation of SXT tandem arrays and SXT-R391 hybrids. <i>Journal of Bacteriology</i> , <b>2004</b> , 186, 2636-45	3.5	46
150	Synchronous replication initiation of the two <i>Vibrio cholerae</i> chromosomes. <i>Current Biology</i> , <b>2004</b> , 14, R501-2	6.3	46
149	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> , <b>2016</b> , 20, 226-37	23.4	45
148	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> , <b>2010</b> , 107, 4590-5	11.5	45
147	Deciphering the landscape of host barriers to infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 6334-6339	11.5	44



146	The three vibrio cholerae chromosome II-encoded ParE toxins degrade chromosome I following loss of chromosome II. <i>Journal of Bacteriology</i> , <b>2011</b> , 193, 611-9	3.5	44
145	Distinct centromere-like parS sites on the two chromosomes of <i>Vibrio</i> spp. <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 5314-24	3.5	44
144	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> , <b>2016</b> , 113, 404-9	11.5	43
143	<i>Vibrio cholerae</i> interactions with the gastrointestinal tract: lessons from animal studies. <i>Current Topics in Microbiology and Immunology</i> , <b>2009</b> , 337, 37-59	3.3	43
142	Cholera: molecular basis for emergence and pathogenesis. <i>FEMS Immunology and Medical Microbiology</i> , <b>1997</b> , 18, 241-8		42
141	Identification of operators and promoters that control SXT conjugative transfer. <i>Journal of Bacteriology</i> , <b>2004</b> , 186, 5945-9	3.5	42
140	Structural basis for the broad specificity of a new family of amino-acid racemases. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2014</b> , 70, 79-90		40
139	The CTXphi repressor RstR binds DNA cooperatively to form tetrameric repressor-operator complexes. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 2640-7	5.4	40
138	ToxR-independent expression of cholera toxin from the replicative form of CTXphi. <i>Infection and Immunity</i> , <b>1998</b> , 66, 394-7	3.7	40
137	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> , <b>2013</b> , 89, 949-62	4.1	39
136	EspFU, a type III-translocated effector of actin assembly, fosters epithelial association and late-stage intestinal colonization by <i>E. coli</i> O157:H7. <i>Cellular Microbiology</i> , <b>2008</b> , 10, 836-47	3.9	39
135	The SXT/R391 family of integrative conjugative elements is composed of two exclusion groups. <i>Journal of Bacteriology</i> , <b>2007</b> , 189, 3302-5	3.5	39
134	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> , <b>2019</b> , 116, 1394-1403	11.5	39
133	Differential requirement for PBP1a and PBP1b in in vivo and in vitro fitness of <i>Vibrio cholerae</i> . <i>Infection and Immunity</i> , <b>2014</b> , 82, 2115-24	3.7	38
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13	Contribution of Phages to Group A <i>Streptococcus</i> Genetic Diversity and Pathogenesis319-P4		1
12	Virulence-Linked Bacteriophages of Pathogenic <i>Vibrios</i> 187-205		1
11	Functional remodeling of lysosomes by type I interferon modifies host defense		1
10	Surveying the landscape of tRNA modifications by combining tRNA sequencing and RNA mass spectrometry		1
9	Modulation of peptidoglycan synthesis by recycled cell wall tetrapeptides		1
8	Use of Phages in Therapy and Bacterial Detection430-440		1
7	Refined quantification of infection bottlenecks and pathogen dissemination with STAMPR		1
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- 2 A Genome-Scale Antibiotic Screen in *Serratia marcescens* Identifies YdgH as a Conserved Modifier of Cephalosporin and Detergent Susceptibility. *Antimicrobial Agents and Chemotherapy*, **2021**, 65, e0078621 <sup>5.0</sup>
- 1 Genomic and Phenotypic Insights for Toxigenic Clinical *Vibrio cholerae* O141.. *Emerging Infectious Diseases*, **2022**, 28, 617-624 10.2