

Rasko David

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

180
papers

13,536
citations

58
h-index

114
g-index

203
ext. papers

15,863
ext. citations

7.8
avg, IF

6.2
L-index

#	Paper	IF	Citations
180	Anti-virulence strategies to combat bacteria-mediated disease. <i>Nature Reviews Drug Discovery</i> , 2010 , 9, 117-28	64.1	854
179	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012 , 30, 693-700	44.5	758
178	Origins of the E. coli strain causing an outbreak of hemolytic-uremic syndrome in Germany. <i>New England Journal of Medicine</i> , 2011 , 365, 709-17	59.2	658
177	The pangenome structure of Escherichia coli: comparative genomic analysis of E. coli commensal and pathogenic isolates. <i>Journal of Bacteriology</i> , 2008 , 190, 6881-93	3.5	607
176	Patellamide A and C biosynthesis by a microcin-like pathway in Prochloron didemni, the cyanobacterial symbiont of Lissoclinum patella. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 7315-20	11.5	486
175	Major structural differences and novel potential virulence mechanisms from the genomes of multiple campylobacter species. <i>PLoS Biology</i> , 2005 , 3, e15	9.7	440
174	Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen Listeria monocytogenes reveal new insights into the core genome components of this species. <i>Nucleic Acids Research</i> , 2004 , 32, 2386-95	20.1	404
173	Targeting QseC signaling and virulence for antibiotic development. <i>Science</i> , 2008 , 321, 1078-80	33.3	382
172	Identification of anthrax toxin genes in a Bacillus cereus associated with an illness resembling inhalation anthrax. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 8449-54	11.5	377
171	Genomics of the Bacillus cereus group of organisms. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 303-29	15.1	362
170	Genome sequence of Silicibacter pomeroyi reveals adaptations to the marine environment. <i>Nature</i> , 2004 , 432, 910-3	50.4	345
169	Multiple antimicrobial resistance in plague: an emerging public health risk. <i>PLoS ONE</i> , 2007 , 2, e309	3.7	296
168	The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1. <i>Nucleic Acids Research</i> , 2004 , 32, 977-88	20.1	253
167	Skewed genomic variability in strains of the toxigenic bacterial pathogen, Clostridium perfringens. <i>Genome Research</i> , 2006 , 16, 1031-40	9.7	250
166	Molecular mechanisms of enterotoxigenic Escherichia coli infection. <i>Microbes and Infection</i> , 2010 , 12, 89-98	9.3	199
165	Visualization of comparative genomic analyses by BLAST score ratio. <i>BMC Bioinformatics</i> , 2005 , 6, 2	3.6	183
164	Defining genomic islands and uropathogen-specific genes in uropathogenic Escherichia coli. <i>Journal of Bacteriology</i> , 2007 , 189, 3532-46	3.5	175

163	Formation and composition of the Bacillus anthracis endospore. <i>Journal of Bacteriology</i> , 2004 , 186, 164-78	7.8	170
162	AB5075, a Highly Virulent Isolate of Acinetobacter baumannii, as a Model Strain for the Evaluation of Pathogenesis and Antimicrobial Treatments. <i>MBio</i> , 2014 , 5, e01076-14	7.8	168
161	Escherichia coli global gene expression in urine from women with urinary tract infection. <i>PLoS Pathogens</i> , 2010 , 6, e1001187	7.6	160
160	The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. <i>PeerJ</i> , 2014 , 2, e332	3.1	154
159	The QseC adrenergic signaling cascade in Enterohemorrhagic E. coli (EHEC). <i>PLoS Pathogens</i> , 2009 , 5, e1000553	7.6	150
158	Characterization of the complete zwittermicin A biosynthesis gene cluster from Bacillus cereus. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 1144-55	4.8	141
157	Host-specific induction of Escherichia coli fitness genes during human urinary tract infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 18327-32	11.5	136
156	Simultaneous expression of type 1 and type 2 Lewis blood group antigens by Helicobacter pylori lipopolysaccharides. Molecular mimicry between h. pylori lipopolysaccharides and human gastric epithelial cell surface glycoforms. <i>Journal of Biological Chemistry</i> , 1998 , 273, 11533-43	5.4	136
155	Identification of enterotoxigenic Escherichia coli (ETEC) clades with long-term global distribution. <i>Nature Genetics</i> , 2014 , 46, 1321-6	36.3	134
154	Complete genome sequence and comparative metabolic profiling of the prototypical enteroaggregative Escherichia coli strain 042. <i>PLoS ONE</i> , 2010 , 5, e8801	3.7	134
153	Genomic characterization of enteroaggregative Escherichia coli from children in Mali. <i>Journal of Infectious Diseases</i> , 2012 , 205, 431-44	7	131
152	Bacillus anthracis comparative genome analysis in support of the Amerithrax investigation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 5027-32	11.5	130
151	Antimicrobial resistance-conferring plasmids with similarity to virulence plasmids from avian pathogenic Escherichia coli strains in Salmonella enterica serovar Kentucky isolates from poultry. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5963-71	4.8	126
150	LPS remodeling is an evolved survival strategy for bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 8716-21	11.5	123
149	The human microbiome: from symbiosis to pathogenesis. <i>Annual Review of Medicine</i> , 2013 , 64, 145-63	17.4	122
148	Molecular genetic basis for the variable expression of Lewis Y antigen in Helicobacter pylori: analysis of the alpha (1,2) fucosyltransferase gene. <i>Molecular Microbiology</i> , 1999 , 31, 1265-74	4.1	122
147	Complete sequence analysis of novel plasmids from emetic and periodontal Bacillus cereus isolates reveals a common evolutionary history among the B. cereus-group plasmids, including Bacillus anthracis pXO1. <i>Journal of Bacteriology</i> , 2007 , 189, 52-64	3.5	114
146	The two-component system QseEF and the membrane protein QseG link adrenergic and stress sensing to bacterial pathogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 5889-94	11.5	112

145	Bacterial genome sequencing in the clinic: bioinformatic challenges and solutions. <i>Nature Reviews Genetics</i> , 2014 , 15, 49-55	30.1	109
144	A comparative genomic analysis of diverse clonal types of enterotoxigenic <i>Escherichia coli</i> reveals pathovar-specific conservation. <i>Infection and Immunity</i> , 2011 , 79, 950-60	3.7	106
143	Lewis antigens in <i>Helicobacter pylori</i> : biosynthesis and phase variation. <i>Molecular Microbiology</i> , 2000 , 36, 1187-96	4.1	106
142	Chemical sensing in mammalian host-bacterial commensal associations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 9831-6	11.5	100
141	Global effects of the cell-to-cell signaling molecules autoinducer-2, autoinducer-3, and epinephrine in a luxS mutant of enterohemorrhagic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2007 , 75, 4875-84	3.7	96
140	Enterotoxigenic <i>Escherichia coli</i> secretes a highly conserved mucin-degrading metalloprotease to effectively engage intestinal epithelial cells. <i>Infection and Immunity</i> , 2014 , 82, 509-21	3.7	94
139	The complete genome sequence of <i>Yersinia pseudotuberculosis</i> IP31758, the causative agent of Far East scarlet-like fever. <i>PLoS Genetics</i> , 2007 , 3, e142	6	88
138	Autotransporter genes pic and tsh are associated with <i>Escherichia coli</i> strains that cause acute pyelonephritis and are expressed during urinary tract infection. <i>Infection and Immunity</i> , 2004 , 72, 593-7	3.7	88
137	Lipopolysaccharide structures of <i>Helicobacter pylori</i> genomic strains 26695 and J99, mouse model H. pylori Sydney strain, H. pylori P466 carrying sialyl Lewis X, and H. pylori UA915 expressing Lewis B classification of H. pylori lipopolysaccharides into glyco-type families. <i>FEBS Journal</i> , 2000 , 267, 305-20		86
136	QseC inhibitors as an antivirulence approach for Gram-negative pathogens. <i>MBio</i> , 2014 , 5, e02165	7.8	85
135	Refining the pathovar paradigm via phylogenomics of the attaching and effacing <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 12810-5	11.5	84
134	The complete genome sequence of <i>Bacillus anthracis</i> Ames "Ancestor". <i>Journal of Bacteriology</i> , 2009 , 191, 445-6	3.5	81
133	Quantitative PCR for detection of <i>Shigella</i> improves ascertainment of <i>Shigella</i> burden in children with moderate-to-severe diarrhea in low-income countries. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 1740-6	9.7	78
132	Correction for Hughes et al., Chemical sensing in mammalian host-bacterial commensal associations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 12734-12734	11.5	78
131	Global Effects of the Cell-to-Cell Signaling Molecules Autoinducer-2, Autoinducer-3, and Epinephrine in a luxS Mutant of Enterohemorrhagic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2008 , 76, 1319-1319	3.7	78
130	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016 , 7, 12218	17.4	69
129	Cloning and characterization of the alpha(1,3/4) fucosyltransferase of <i>Helicobacter pylori</i> . <i>Journal of Biological Chemistry</i> , 2000 , 275, 4988-94	5.4	68
128	Transcriptome of swarming <i>Proteus mirabilis</i> . <i>Infection and Immunity</i> , 2010 , 78, 2834-45	3.7	67

127	Comparative genomics and stx phage characterization of LEE-negative Shiga toxin-producing <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2012 , 2, 133	5.9	66
126	Role of the K2 capsule in <i>Escherichia coli</i> urinary tract infection and serum resistance. <i>Journal of Infectious Diseases</i> , 2009 , 199, 1689-97	7	65
125	Hfq virulence regulation in enterohemorrhagic <i>Escherichia coli</i> O157:H7 strain 86-24. <i>Journal of Bacteriology</i> , 2011 , 193, 6843-51	3.5	65
124	Impact of oral typhoid vaccination on the human gut microbiota and correlations with s. Typhi-specific immunological responses. <i>PLoS ONE</i> , 2013 , 8, e62026	3.7	62
123	Native outer membrane proteins protect mice against pulmonary challenge with virulent type A <i>Francisella tularensis</i> . <i>Infection and Immunity</i> , 2008 , 76, 3664-71	3.7	60
122	Exploiting the explosion of information associated with whole genome sequencing to tackle Shiga toxin-producing <i>Escherichia coli</i> (STEC) in global food production systems. <i>International Journal of Food Microbiology</i> , 2014 , 187, 57-72	5.8	58
121	Genomic comparison of multi-drug resistant invasive and colonizing <i>Acinetobacter baumannii</i> isolated from diverse human body sites reveals genomic plasticity. <i>BMC Genomics</i> , 2011 , 12, 291	4.5	58
120	Defining the phylogenomics of <i>Shigella</i> species: a pathway to diagnostics. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 951-60	9.7	57
119	QseA and GrlR/GrlA regulation of the locus of enterocyte effacement genes in enterohemorrhagic <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2007 , 189, 5387-92	3.5	51
118	Transcriptional modulation of enterotoxigenic <i>Escherichia coli</i> virulence genes in response to epithelial cell interactions. <i>Infection and Immunity</i> , 2013 , 81, 259-70	3.7	50
117	Whole-genome assembly of <i>Klebsiella pneumoniae</i> coproducing NDM-1 and OXA-232 carbapenemases using single-molecule, real-time sequencing. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 5947-53	5.9	49
116	Genomic diversity of EPEC associated with clinical presentations of differing severity. <i>Nature Microbiology</i> , 2016 , 1, 15014	26.6	48
115	Conservation and immunogenicity of novel antigens in diverse isolates of enterotoxigenic <i>Escherichia coli</i> . <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003446	4.8	45
114	Sequencing <i>Bacillus anthracis</i> typing phages gamma and cherry reveals a common ancestry. <i>Journal of Bacteriology</i> , 2006 , 188, 3402-8	3.5	44
113	Differential response of the cynomolgus macaque gut microbiota to <i>Shigella</i> infection. <i>PLoS ONE</i> , 2013 , 8, e64212	3.7	43
112	Survival of the Fittest: How Bacterial Pathogens Utilize Bile To Enhance Infection. <i>Clinical Microbiology Reviews</i> , 2016 , 29, 819-36	34	43
111	<i>Shigella flexneri</i> effectors OspE1 and OspE2 mediate induced adherence to the colonic epithelium following bile salts exposure. <i>Molecular Microbiology</i> , 2012 , 85, 107-21	4.1	42
110	Metabolic analysis of <i>Moraxella catarrhalis</i> and the effect of selected in vitro growth conditions on global gene expression. <i>Infection and Immunity</i> , 2007 , 75, 4959-71	3.7	40

109	Structural modification of LPS in colistin-resistant, KPC-producing <i>Klebsiella pneumoniae</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 3035-3042	5.1	39
108	Locus of Adhesion and Autoaggregation (LAA), a pathogenicity island present in emerging Shiga Toxin-producing <i>Escherichia coli</i> strains. <i>Scientific Reports</i> , 2017 , 7, 7011	4.9	39
107	Analysis of <i>Shigella flexneri</i> Resistance, Biofilm Formation, and Transcriptional Profile in Response to Bile Salts. <i>Infection and Immunity</i> , 2017 , 85,	3.7	38
106	Blocking yersiniabactin import attenuates extraintestinal pathogenic <i>Escherichia coli</i> in cystitis and pyelonephritis and represents a novel target to prevent urinary tract infection. <i>Infection and Immunity</i> , 2015 , 83, 1443-50	3.7	38
105	Whole-genome sequences of <i>Bacillus subtilis</i> and close relatives. <i>Journal of Bacteriology</i> , 2012 , 194, 2378-9	3.9	38
104	Analysis of global transcriptional profiles of enterotoxigenic <i>Escherichia coli</i> isolate E24377A. <i>Infection and Immunity</i> , 2012 , 80, 1232-42	3.7	38
103	Colonization factors among enterotoxigenic <i>Escherichia coli</i> isolates from children with moderate-to-severe diarrhea and from matched controls in the Global Enteric Multicenter Study (GEMS). <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007037	4.8	35
102	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. <i>Genome Medicine</i> , 2015 , 7, 52	14.4	32
101	Genome sequences of four divergent multidrug-resistant <i>Acinetobacter baumannii</i> strains isolated from patients with sepsis or osteomyelitis. <i>Journal of Bacteriology</i> , 2012 , 194, 1619-20	3.5	32
100	Examination of the Enterotoxigenic <i>Escherichia coli</i> Population Structure during Human Infection. <i>MBio</i> , 2015 , 6, e00501	7.8	31
99	Investigating the Relatedness of Enteroinvasive <i>Escherichia coli</i> to Other <i>E. coli</i> and <i>Shigella</i> Isolates by Using Comparative Genomics. <i>Infection and Immunity</i> , 2016 , 84, 2362-2371	3.7	31
98	Phylomark, a tool to identify conserved phylogenetic markers from whole-genome alignments. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 4884-92	4.8	31
97	Genomic and Phenotypic Diversity among Ten Laboratory Isolates of PAO1. <i>Journal of Bacteriology</i> , 2019 , 201,	3.5	31
96	The LysR-type regulator QseA regulates both characterized and putative virulence genes in enterohaemorrhagic <i>Escherichia coli</i> O157:H7. <i>Molecular Microbiology</i> , 2010 , 76, 1306-21	4.1	30
95	A divergent <i>Pseudomonas aeruginosa</i> palmitoyltransferase essential for cystic fibrosis-specific lipid A. <i>Molecular Microbiology</i> , 2014 , 91, 158-74	4.1	29
94	Comparative genomics and transcriptomics of <i>Escherichia coli</i> isolates carrying virulence factors of both enteropathogenic and enterotoxigenic <i>E. coli</i> . <i>Scientific Reports</i> , 2017 , 7, 3513	4.9	27
93	Investigating the genome diversity of <i>B. cereus</i> and evolutionary aspects of <i>B. anthracis</i> emergence. <i>Genomics</i> , 2011 , 98, 26-39	4.3	27
92	Influence of Lewis antigen expression by <i>Helicobacter pylori</i> on bacterial internalization by gastric epithelial cells. <i>Infection and Immunity</i> , 2003 , 71, 2902-6	3.7	27

91	CadA negatively regulates Escherichia coli O157:H7 adherence and intestinal colonization. <i>Infection and Immunity</i> , 2008 , 76, 5072-81	3.7	26
90	Synthesis of mono- and di-fucosylated type I Lewis blood group antigens by Helicobacter pylori. <i>FEBS Journal</i> , 2000 , 267, 6059-66		26
89	Standardized metadata for human pathogen/vector genomic sequences. <i>PLoS ONE</i> , 2014 , 9, e99979	3.7	25
88	A transcriptome study of the QseEF two-component system and the QseG membrane protein in enterohaemorrhagic Escherichia coli O157 : H7. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 1167-1175	2.9	24
87	Patients with Acinetobacter baumannii bloodstream infections are colonized in the gastrointestinal tract with identical strains. <i>American Journal of Infection Control</i> , 2010 , 38, 751-3	3.8	24
86	Insights into the environmental reservoir of pathogenic Vibrio parahaemolyticus using comparative genomics. <i>Frontiers in Microbiology</i> , 2015 , 6, 204	5.7	23
85	Human Experimental Challenge With Enterotoxigenic Escherichia coli Elicits Immune Responses to Canonical and Novel Antigens Relevant to Vaccine Development. <i>Journal of Infectious Diseases</i> , 2018 , 218, 1436-1446	7	23
84	Comparative Genomics Provides Insight into the Diversity of the Attaching and Effacing Escherichia coli Virulence Plasmids. <i>Infection and Immunity</i> , 2015 , 83, 4103-17	3.7	22
83	Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. <i>Bioinformatics</i> , 2014 , 30, 3125-7	7.2	22
82	Comparative genomics of an Inca/C multidrug resistance plasmid from Escherichia coli and Klebsiella isolates from intensive care unit patients and the utility of whole-genome sequencing in health care settings. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 4814-25	5.9	21
81	Insights into enterotoxigenic Escherichia coli diversity in Bangladesh utilizing genomic epidemiology. <i>Scientific Reports</i> , 2017 , 7, 3402	4.9	20
80	EHEC Genomics: Past, Present, and Future. <i>Microbiology Spectrum</i> , 2014 , 2, EHEC-0020-2013	8.9	20
79	The role of genomics in the identification, prediction, and prevention of biological threats. <i>PLoS Biology</i> , 2009 , 7, e1000217	9.7	20
78	Cumulative acquisition of pathogenicity islands has shaped virulence potential and contributed to the emergence of LEE-negative Shiga toxin-producing Escherichia coli strains. <i>Emerging Microbes and Infections</i> , 2019 , 8, 486-502	18.9	19
77	RNA-Seq analysis of isolate- and growth phase-specific differences in the global transcriptomes of enteropathogenic Escherichia coli prototype isolates. <i>Frontiers in Microbiology</i> , 2015 , 6, 569	5.7	19
76	Diversity among bla-containing plasmids in Escherichia coli and other bacterial species isolated from the same patients. <i>Scientific Reports</i> , 2018 , 8, 10291	4.9	19
75	Characterization of Klebsiella sp. strain 10982, a colonizer of humans that contains novel antibiotic resistance alleles and exhibits genetic similarities to plant and clinical Klebsiella isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 1879-88	5.9	19
74	Draft genome sequences of the diarrheagenic Escherichia coli collection. <i>Journal of Bacteriology</i> , 2012 , 194, 3026-7	3.5	19

73	Use of Comparative Genomics To Characterize the Diversity of <i>Acinetobacter baumannii</i> Surveillance Isolates in a Health Care Institution. <i>Antimicrobial Agents and Chemotherapy</i> , 2016 , 60, 5933-41	5.9	19
72	Hybrid Shiga Toxin-Producing and Enterotoxigenic <i>Escherichia</i> sp. Cryptic Lineage 1 Strain 7v Harbors a Hybrid Plasmid. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 4309-4319	4.8	18
71	Enterotoxigenic <i>Escherichia coli</i> : Orchestrated host engagement. <i>Gut Microbes</i> , 2013 , 4, 392-6	8.8	18
70	A Novel Proteome Microarray Discriminates Targets of Human Antibody Reactivity following Oral Vaccination and Experimental Challenge. <i>MSphere</i> , 2018 , 3,	5	17
69	Bacterial Factors Associated with Lethal Outcome of Enteropathogenic <i>Escherichia coli</i> Infection: Genomic Case-Control Studies. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003791	4.8	16
68	H-NST induces LEE expression and the formation of attaching and effacing lesions in enterohemorrhagic <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2014 , 9, e86618	3.7	16
67	Draft Genome Sequence of the Methicillin-Resistant <i>Staphylococcus aureus</i> Isolate MRSA-M2. <i>Genome Announcements</i> , 2013 , 1,		16
66	Genome and Functional Characterization of Colonization Factor Antigen I- and CS6-Encoding Heat-Stable Enterotoxin-Only Enterotoxigenic Reveals Lineage and Geographic Variation. <i>MSystems</i> , 2019 , 4,	7.6	15
65	The AraC Negative Regulator family modulates the activity of histone-like proteins in pathogenic bacteria. <i>PLoS Pathogens</i> , 2017 , 13, e1006545	7.6	15
64	Host Adaptation Predisposes <i>Pseudomonas aeruginosa</i> to Type VI Secretion System-Mediated Predation by the <i>Burkholderia cepacia</i> Complex. <i>Cell Host and Microbe</i> , 2020 , 28, 534-547.e3	23.4	15
63	Interrogation of a live-attenuated enterotoxigenic vaccine highlights features unique to wild-type infection. <i>Npj Vaccines</i> , 2019 , 4, 37	9.5	14
62	Responses of the Human Gut Population to Pathogen and Antibiotic Disturbances. <i>MSystems</i> , 2018 , 3,	7.6	14
61	Outbreak caused by cad-negative Shiga toxin-producing <i>Escherichia coli</i> O111, Oklahoma. <i>Foodborne Pathogens and Disease</i> , 2010 , 7, 107-9	3.8	14
60	<i>Helicobacter pylori</i> from asymptomatic hosts expressing heptoglycan but lacking Lewis O-chains: Lewis blood-group O-chains may play a role in <i>Helicobacter pylori</i> induced pathology. <i>Biochemistry and Cell Biology</i> , 2001 , 79, 449-459	3.6	14
59	High frequency, spontaneous <i>motA</i> mutations in <i>Campylobacter jejuni</i> strain 81-176. <i>PLoS ONE</i> , 2014 , 9, e88043	3.7	14
58	Draft genome sequences of five recent human uropathogenic <i>Escherichia coli</i> isolates. <i>Pathogens and Disease</i> , 2013 , 69, 66-70	4.2	13
57	Draft genome sequence of <i>Vibrio fischeri</i> SR5, a strain isolated from the light organ of the Mediterranean squid <i>Sepiola robusta</i> . <i>Journal of Bacteriology</i> , 2012 , 194, 1639	3.5	13
56	Development of novel plasmid vectors and a promoter trap system in <i>Francisella tularensis</i> compatible with the pFLN10 based plasmids. <i>Plasmid</i> , 2007 , 58, 159-66	3.3	13

55	Diarrhea, bacteremia and multiorgan dysfunction due to an extraintestinal pathogenic <i>Escherichia coli</i> strain with enteropathogenic <i>E. coli</i> genes. <i>Pathogens and Disease</i> , 2015 , 73, ftv076	4.2	12
54	New family of tungstate-responsive transcriptional regulators in sulfate-reducing bacteria. <i>Journal of Bacteriology</i> , 2013 , 195, 4466-75	3.5	12
53	Redefining enteroaggregative <i>Escherichia coli</i> (EAEC): Genomic characterization of epidemiological EAEC strains. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008613	4.8	12
52	Temporal Variability of Diversity in the Gastrointestinal Tracts of Tanzanian Children with and without Exposure to Antibiotics. <i>MSphere</i> , 2018 , 3,	5	12
51	Chaperone-Usher Pili Loci of Colonization Factor-Negative Human Enterotoxigenic. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016 , 6, 200	5.9	11
50	Draft Genome Sequence of Biocontrol Agent <i>Bacillus cereus</i> UW85. <i>Genome Announcements</i> , 2016 , 4,		11
49	Conservation and global distribution of non-canonical antigens in Enterotoxigenic <i>Escherichia coli</i> . <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007825	4.8	11
48	Characterization of intracellular growth regulator <i>icgR</i> by utilizing transcriptomics to identify mediators of pathogenesis in <i>Shigella flexneri</i> . <i>Infection and Immunity</i> , 2013 , 81, 3068-76	3.7	10
47	The synthesis of <i>OspD3</i> (ShET2) in <i>Shigella flexneri</i> is independent of <i>OspC1</i> . <i>Gut Microbes</i> , 2016 , 7, 486-502		10
46	Adherence Factor Expression in -Like Conditions. <i>MSphere</i> , 2019 , 4,	5	10
45	Characterization of the pathogenome and phylogenomic classification of enteropathogenic <i>Escherichia coli</i> of the O157:non-H7 serotypes. <i>Pathogens and Disease</i> , 2015 , 73,	4.2	9
44	Genomic characterization of asymptomatic <i>Escherichia coli</i> isolated from the neobladder. <i>Microbiology (United Kingdom)</i> , 2011 , 157, 1088-1102	2.9	9
43	Functional and phylogenetic analysis of <i>ureD</i> in Shiga toxin-producing <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2011 , 193, 875-86	3.5	9
42	Targeted enrichment outperforms other enrichment techniques and enables more multi-species RNA-Seq analyses. <i>Scientific Reports</i> , 2018 , 8, 13377	4.9	9
41	Changes in microbiome during and after travellers' diarrhea: what we know and what we do not. <i>Journal of Travel Medicine</i> , 2017 , 24, S52-S56	12.9	8
40	Transcriptional Variation of Diverse Enteropathogenic Isolates under Virulence-Inducing Conditions. <i>MSystems</i> , 2017 , 2,	7.6	8
39	Genome Sequence of <i>Escherichia coli</i> O157:H7 Strain 2886-75, Associated with the First Reported Case of Human Infection in the United States. <i>Genome Announcements</i> , 2014 , 2,		8
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Redefining enteroaggregative *Escherichia coli* (EAEC): Genomic characterization of epidemiological EAEC strains **2020**, 14, e0008613