

Rasko David

List of Publications by Year in Descending Order

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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	Pathogenomic analyses of Shigella isolates inform factors limiting shigellosis prevention and control across LMICs.. <i>Nature Microbiology</i> , 2022 ,	26.6	3
179	Comparative Genomics Identifies Features Associated with Methicillin-Resistant Staphylococcus aureus (MRSA) Transmission in Hospital Settings.. <i>MSphere</i> , 2022 , e0011622	5	0
178	Comparison of long read sequencing technologies in interrogating bacteria and fly genomes. <i>G3: Genes, Genomes, Genetics</i> , 2021 ,	3.2	4
177	Best practices on the differential expression analysis of multi-species RNA-seq. <i>Genome Biology</i> , 2021 , 22, 121	18.3	6
176	Contribution of Noncanonical Antigens to Virulence and Adaptive Immunity in Human Infection with Enterotoxigenic E. coli. <i>Infection and Immunity</i> , 2021 , 89,	3.7	2
175	Draft Genome Sequences of Two Enteroinvasive Escherichia coli Strains Representative of Major Enteroinvasive Clades. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0031921	1.3	
174	Comparative Genomics of Atypical Enteropathogenic Escherichia coli from Kittens and Children Identifies Bacterial Factors Associated with Virulence in Kittens. <i>Infection and Immunity</i> , 2021 , 89,	3.7	1
173	FADU: a Quantification Tool for Prokaryotic Transcriptomic Analyses. <i>MSystems</i> , 2021 , 6,	7.6	2
172	Evaluation of a high-throughput, cost-effective Illumina library preparation kit. <i>Scientific Reports</i> , 2021 , 11, 15925	4.9	0
171	Genome Sequences of Four Shigella boydii Strains Representative of the Major S. boydii Clades. <i>Microbiology Resource Announcements</i> , 2020 , 9,	1.3	1
170	Comparative genomic analysis provides insight into the phylogeny and virulence of atypical enteropathogenic Escherichia coli strains from Brazil. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008373	4.8	3
169	Host Adaptation Predisposes Pseudomonas aeruginosa to Type VI Secretion System-Mediated Predation by the Burkholderia cepacia Complex. <i>Cell Host and Microbe</i> , 2020 , 28, 534-547.e3	23.4	15
168	Redefining enteroaggregative Escherichia coli (EAEC): Genomic characterization of epidemiological EAEC strains. <i>PLoS Neglected Tropical Diseases</i> , 2020 , 14, e0008613	4.8	12
167	Redefining enteroaggregative Escherichia coli (EAEC): Genomic characterization of epidemiological EAEC strains 2020 , 14, e0008613		
166	Redefining enteroaggregative Escherichia coli (EAEC): Genomic characterization of epidemiological EAEC strains 2020 , 14, e0008613		
165	Redefining enteroaggregative Escherichia coli (EAEC): Genomic characterization of epidemiological EAEC strains 2020 , 14, e0008613		
164	Redefining enteroaggregative Escherichia coli (EAEC): Genomic characterization of epidemiological EAEC strains 2020 , 14, e0008613		

163	Interrogation of a live-attenuated enterotoxigenic vaccine highlights features unique to wild-type infection. <i>Npj Vaccines</i> , 2019 , 4, 37	9.5	14
162	Genetic changes associated with the temporal shift in invasive non-typhoidal Salmonella serovars in Bamako Mali. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007297	4.8	1
161	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
160	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
159	The Complete Genome of the Atypical Enteropathogenic Escherichia coli Archetype Isolate E110019 Highlights a Role for Plasmids in Dissemination of the Type III Secreted Effector EspT. <i>Infection and Immunity</i> , 2019 , 87,	3.7	2
158	Examination of 388 Staphylococcus aureus Isolates from Intensive Care Unit Patients. <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	1
157	Adherence Factor Expression in -Like Conditions. <i>MSphere</i> , 2019 , 4,	5	10
156	Comparative genomic analysis and molecular examination of the diversity of enterotoxigenic Escherichia coli isolates from Chile. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007828	4.8	7
155	Conservation and global distribution of non-canonical antigens in Enterotoxigenic Escherichia coli. <i>PLoS Neglected Tropical Diseases</i> , 2019 , 13, e0007825	4.8	11
154	Colonization factors among enterotoxigenic Escherichia coli 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
153	Genomic and Phenotypic Diversity among Ten Laboratory Isolates of PAO1. <i>Journal of Bacteriology</i> , 2019 , 201,	3.5	31
152	Phosphotyrosine-Mediated Regulation of Enterohemorrhagic Virulence. <i>MBio</i> , 2018 , 9,	7.8	4
151	Responses of the Human Gut Population to Pathogen and Antibiotic Disturbances. <i>MSystems</i> , 2018 , 3,	7.6	14
150	A Novel Proteome Microarray Discriminates Targets of Human Antibody Reactivity following Oral Vaccination and Experimental Challenge. <i>MSphere</i> , 2018 , 3,	5	17
149	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
148	Temporal Variability of Diversity in the Gastrointestinal Tracts of Tanzanian Children with and without Exposure to Antibiotics. <i>MSphere</i> , 2018 , 3,	5	12
147	Improving Our Understanding of Serovar Paratyphi B through the Engineering and Testing of a Live Attenuated Vaccine Strain. <i>MSphere</i> , 2018 , 3,	5	5
146	Draft Genome Sequences of -Containing Enterobacter aerogenes, Citrobacter freundii, and Citrobacter koseri Strains. <i>Genome Announcements</i> , 2018 , 6,		1

145	Coli Surface Antigen 26 Acts as an Adherence Determinant of Enterotoxigenic and Is Cross-Recognized by Anti-CS20 Antibodies. <i>Frontiers in Microbiology</i> , 2018 , 9, 2463	5.7	3
144	Targeted enrichment outperforms other enrichment techniques and enables more multi-species RNA-Seq analyses. <i>Scientific Reports</i> , 2018 , 8, 13377	4.9	9
143	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
142	Changes in microbiome during and after travellersRdiarrhea: what we know and what we do not. <i>Journal of Travel Medicine</i> , 2017 , 24, S52-S56	12.9	8
141	Insights into enterotoxigenic Escherichia coli diversity in Bangladesh utilizing genomic epidemiology. <i>Scientific Reports</i> , 2017 , 7, 3402	4.9	20
140	Analysis of Shigella flexneri Resistance, Biofilm Formation, and Transcriptional Profile in Response to Bile Salts. <i>Infection and Immunity</i> , 2017 , 85,	3.7	38
139	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
138	Structural modification of LPS in colistin-resistant, KPC-producing Klebsiella pneumoniae. <i>Journal of Antimicrobial Chemotherapy</i> , 2017 , 72, 3035-3042	5.1	39
137	Comparative genomics and transcriptomics of Escherichia coli isolates carrying virulence factors of both enteropathogenic and enterotoxigenic E. coli. <i>Scientific Reports</i> , 2017 , 7, 3513	4.9	27
136	Locus of Adhesion and Autoaggregation (LAA), a pathogenicity island present in emerging Shiga Toxin-producing Escherichia coli strains. <i>Scientific Reports</i> , 2017 , 7, 7011	4.9	39
135	Transcriptional Variation of Diverse Enteropathogenic Isolates under Virulence-Inducing Conditions. <i>MSystems</i> , 2017 , 2,	7.6	8
134	Characterization of a Large Antibiotic Resistance Plasmid Found in Enteropathogenic Escherichia coli Strain B171 and Its Relatedness to Plasmids of Diverse E. coli and Shigella Strains. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	7
133	Aligner optimization increases accuracy and decreases compute times in multi-species sequence data. <i>Microbial Genomics</i> , 2017 , 3, e000122	4.4	8
132	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016 , 7, 12218	17.4	69
131	Genomic diversity of EPEC associated with clinical presentations of differing severity. <i>Nature Microbiology</i> , 2016 , 1, 15014	26.6	48
130	Investigating the Relatedness of Enteroinvasive Escherichia coli to Other E. coli and Shigella Isolates by Using Comparative Genomics. <i>Infection and Immunity</i> , 2016 , 84, 2362-2371	3.7	31
129	Hybrid Shiga Toxin-Producing and Enterotoxigenic Escherichia sp. Cryptic Lineage 1 Strain 7v Harbors a Hybrid Plasmid. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 4309-4319	4.8	18
128	Chaperone-Usher Pili Loci of Colonization Factor-Negative Human Enterotoxigenic. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016 , 6, 200	5.9	11

127	Draft Genome Sequence of Biocontrol Agent <i>Bacillus cereus</i> UW85. <i>Genome Announcements</i> , 2016 , 4,		11
126	Overcoming Enterotoxigenic <i>Escherichia coli</i> Pathogen Diversity: Translational Molecular Approaches to Inform Vaccine Design. <i>Methods in Molecular Biology</i> , 2016 , 1403, 363-83	1.4	5
125	Genome diversity of <i>Shigella boydii</i> . <i>Pathogens and Disease</i> , 2016 , 74, ftw027	4.2	8
124	The synthesis of OspD3 (ShET2) in <i>Shigella flexneri</i> is independent of OspC1. <i>Gut Microbes</i> , 2016 , 7, 486-502		10
123	Survival of the Fittest: How Bacterial Pathogens Utilize Bile To Enhance Infection. <i>Clinical Microbiology Reviews</i> , 2016 , 29, 819-36	34	43
122	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
121	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
120	RNA-Seq analysis of isolate- and growth phase-specific differences in the global transcriptomes of enteropathogenic <i>Escherichia coli</i> prototype isolates. <i>Frontiers in Microbiology</i> , 2015 , 6, 569	5.7	19
119	Comparative Genomics Provides Insight into the Diversity of the Attaching and Effacing <i>Escherichia coli</i> Virulence Plasmids. <i>Infection and Immunity</i> , 2015 , 83, 4103-17	3.7	22
118	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
117	Examination of the Enterotoxigenic <i>Escherichia coli</i> Population Structure during Human Infection. <i>MBio</i> , 2015 , 6, e00501	7.8	31
116	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
115	Insights into the environmental reservoir of pathogenic <i>Vibrio parahaemolyticus</i> using comparative genomics. <i>Frontiers in Microbiology</i> , 2015 , 6, 204	5.7	23
114	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
113	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
112	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
111	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
110	Bacterial genome sequencing in the clinic: bioinformatic challenges and solutions. <i>Nature Reviews Genetics</i> , 2014 , 15, 49-55	30.1	109

109	Identification of enterotoxigenic <i>Escherichia coli</i> (ETEC) clades with long-term global distribution. <i>Nature Genetics</i> , 2014 , 46, 1321-6	36.3	134
108	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
107	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
106	Comparative genomics of an IncA/C multidrug resistance plasmid from <i>Escherichia coli</i> and <i>Klebsiella</i> 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
105	Characterization of <i>Klebsiella</i> sp. strain 10982, a colonizer of humans that contains novel antibiotic resistance alleles and exhibits genetic similarities to plant and clinical <i>Klebsiella</i> isolates. <i>Antimicrobial Agents and Chemotherapy</i> , 2014 , 58, 1879-88	5.9	19
104	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
103	EHEC Genomics: Past, Present, and Future. <i>Microbiology Spectrum</i> , 2014 , 2, EHEC-0020-2013	8.9	20
102	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
101	Standardized metadata for human pathogen/vector genomic sequences. <i>PLoS ONE</i> , 2014 , 9, e99979	3.7	25
100	Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. <i>Bioinformatics</i> , 2014 , 30, 3125-7	7.2	22
99	QseC inhibitors as an antivirulence approach for Gram-negative pathogens. <i>MBio</i> , 2014 , 5, e02165	7.8	85
98	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
97	AB5075, a Highly Virulent Isolate of <i>Acinetobacter baumannii</i> , as a Model Strain for the Evaluation of Pathogenesis and Antimicrobial Treatments. <i>MBio</i> , 2014 , 5, e01076-14	7.8	168
96	Host-specific induction of <i>Escherichia coli</i> 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
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	High frequency, spontaneous motA mutations in <i>Campylobacter jejuni</i> strain 81-176. <i>PLoS ONE</i> , 2014 , 9, e88043	3.7	14
93	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
92	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

91	The human microbiome: from symbiosis to pathogenesis. <i>Annual Review of Medicine</i> , 2013 , 64, 145-63	17.4	122
90	Comparative genomics of pathogenic <i>Escherichia coli</i> 2013 , 21-43		4
89	Draft Genome Sequence of the Methicillin-Resistant <i>Staphylococcus aureus</i> Isolate MRSA-M2. <i>Genome Announcements</i> , 2013 , 1,		16
88	Draft Genome Sequences of Three O157 Enteropathogenic <i>Escherichia coli</i> Isolates. <i>Genome Announcements</i> , 2013 , 1,		5
87	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
86	In vitro evolution of an archetypal enteropathogenic <i>Escherichia coli</i> strain. <i>Journal of Bacteriology</i> , 2013 , 195, 4476-83	3.5	8
85	Enterotoxigenic <i>Escherichia coli</i> : Orchestrated host engagement. <i>Gut Microbes</i> , 2013 , 4, 392-6	8.8	18
84	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
83	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
82	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
81	New family of tungstate-responsive transcriptional regulators in sulfate-reducing bacteria. <i>Journal of Bacteriology</i> , 2013 , 195, 4466-75	3.5	12
80	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
79	Differential response of the cynomolgus macaque gut microbiota to <i>Shigella</i> infection. <i>PLoS ONE</i> , 2013 , 8, e64212	3.7	43
78	<i>Shigella flexneri</i> effectors <i>OspE1</i> and <i>OspE2</i> mediate induced adherence to the colonic epithelium following bile salts exposure. <i>Molecular Microbiology</i> , 2012 , 85, 107-21	4.1	42
77	Whole-genome sequences of <i>Bacillus subtilis</i> and close relatives. <i>Journal of Bacteriology</i> , 2012 , 194, 2378-9		38
76	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
75	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
74	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

73	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012 , 30, 693-700	44.5	758
72	Genomic characterization of enteroaggregative <i>Escherichia coli</i> from children in Mali. <i>Journal of Infectious Diseases</i> , 2012 , 205, 431-44	7	131
71	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
70	Draft genome sequences of the diarrheagenic <i>Escherichia coli</i> collection. <i>Journal of Bacteriology</i> , 2012 , 194, 3026-7	3.5	19
69	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
68	Correction for Li et al., 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, 13877-13877	11.5	2
67	Genome sequence of <i>Klebsiella oxytoca</i> 11492-1, a nosocomial isolate possessing a FOX-5 AmpC β -lactamase. <i>Journal of Bacteriology</i> , 2012 , 194, 3028-9	3.5	7
66	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
65	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, 709-17	59.2	658
64	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
63	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
62	Genomic characterization of asymptomatic <i>Escherichia coli</i> isolated from the neobladder. <i>Microbiology (United Kingdom)</i> , 2011 , 157, 1088-1102	2.9	9
61	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
60	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
59	Functional and phylogenetic analysis of ureD in Shiga toxin-producing <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2011 , 193, 875-86	3.5	9
58	<i>Bacillus anthracis</i> 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
57	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
56	Anti-virulence strategies to combat bacteria-mediated disease. <i>Nature Reviews Drug Discovery</i> , 2010 , 9, 117-28	64.1	854

55	Complete genome sequence and comparative metabolic profiling of the prototypical enteroaggregative <i>Escherichia coli</i> strain 042. <i>PLoS ONE</i> , 2010 , 5, e8801	3.7	134
54	Transcriptome of swarming <i>Proteus mirabilis</i> . <i>Infection and Immunity</i> , 2010 , 78, 2834-45	3.7	67
53	A transcriptome study of the QseEF two-component system and the QseG membrane protein in enterohaemorrhagic <i>Escherichia coli</i> O157 : H7. <i>Microbiology (United Kingdom)</i> , 2010 , 156, 1167-1175	2.9	24
52	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
51	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
50	<i>Escherichia coli</i> global gene expression in urine from women with urinary tract infection. <i>PLoS Pathogens</i> , 2010 , 6, e1001187	7.6	160
49	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
48	Patients with <i>Acinetobacter baumannii</i> 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
47	<i>Bacillus anthracis</i> Plasmids: Species Definition or Niche Adaptation? 2010 , 89-106		
46	Molecular mechanisms of enterotoxigenic <i>Escherichia coli</i> infection. <i>Microbes and Infection</i> , 2010 , 12, 89-98	9.3	199
45	Antimicrobial resistance-conferring plasmids with similarity to virulence plasmids from avian pathogenic <i>Escherichia coli</i> strains in <i>Salmonella enterica</i> serovar Kentucky isolates from poultry. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5963-71	4.8	126
44	Characterization of the complete zwittermicin A biosynthesis gene cluster from <i>Bacillus cereus</i> . <i>Applied and Environmental Microbiology</i> , 2009 , 75, 1144-55	4.8	141
43	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
42	The QseC adrenergic signaling cascade in Enterohemorrhagic <i>E. coli</i> (EHEC). <i>PLoS Pathogens</i> , 2009 , 5, e1000553	7.6	150
41	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
40	The complete genome sequence of <i>Bacillus anthracis</i> Ames "Ancestor". <i>Journal of Bacteriology</i> , 2009 , 191, 445-6	3.5	81
39	The role of genomics in the identification, prediction, and prevention of biological threats. <i>PLoS Biology</i> , 2009 , 7, e1000217	9.7	20
38	Novel approaches to bacterial infection therapy by interfering with cell-to-cell signaling. <i>Current Protocols in Microbiology</i> , 2009 , Chapter 17, Unit17.3	7.1	3

37	The pangenome structure of <i>Escherichia coli</i> : comparative genomic analysis of <i>E. coli</i> commensal and pathogenic isolates. <i>Journal of Bacteriology</i> , 2008 , 190, 6881-93	3.5	607
36	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
35	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
34	Targeting QseC signaling and virulence for antibiotic development. <i>Science</i> , 2008 , 321, 1078-80	33.3	382
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