

Rasko David

List of Publications by Year in descending order

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189
papers

17,013
citations

20759

60
h-index

16127

124
g-index

203
all docs

203
docs citations

203
times ranked

18456
citing authors

#	ARTICLE	IF	CITATIONS
1	Anti-virulence strategies to combat bacteria-mediated disease. <i>Nature Reviews Drug Discovery</i> , 2010, 9, 117-128.	21.5	1,098
2	Hybrid error correction and de novo assembly of single-molecule sequencing reads. <i>Nature Biotechnology</i> , 2012, 30, 693-700.	9.4	946
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 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, 6881-6893.	1.0	763
5	Patellamide A and C biosynthesis by a microcin-like pathway in <i>Prochloron didemni</i> , the cyanobacterial symbiont of <i>Lissoclinum patella</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 7315-7320.	3.3	553
6	Major Structural Differences and Novel Potential Virulence Mechanisms from the Genomes of Multiple <i>Campylobacter</i> Species. <i>PLoS Biology</i> , 2005, 3, e15.	2.6	483
7	Whole genome comparisons of serotype 4b and 1/2a strains of the food-borne pathogen <i>Listeria monocytogenes</i> reveal new insights into the core genome components of this species. <i>Nucleic Acids Research</i> , 2004, 32, 2386-2395.	6.5	460
8	Identification of anthrax toxin genes in a <i>Bacillus cereus</i> associated with an illness resembling inhalation anthrax. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 8449-8454.	3.3	457
9	Targeting QseC Signaling and Virulence for Antibiotic Development. <i>Science</i> , 2008, 321, 1078-1080.	6.0	452
10	Genomics of the group of organisms. <i>FEMS Microbiology Reviews</i> , 2005, 29, 303-329.	3.9	421
11	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004, 432, 910-913.	13.7	415
12	Multiple Antimicrobial Resistance in Plague: An Emerging Public Health Risk. <i>PLoS ONE</i> , 2007, 2, e309.	1.1	344
13	Skewed genomic variability in strains of the toxigenic bacterial pathogen, <i>Clostridium perfringens</i> . <i>Genome Research</i> , 2006, 16, 1031-1040.	2.4	281
14	The genome sequence of <i>Bacillus cereus</i> ATCC 10987 reveals metabolic adaptations and a large plasmid related to <i>Bacillus anthracis</i> pXO1. <i>Nucleic Acids Research</i> , 2004, 32, 977-988.	6.5	273
15	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.	0.9	265
16	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.	1.8	258
17	Molecular mechanisms of enterotoxigenic <i>Escherichia coli</i> infection. <i>Microbes and Infection</i> , 2010, 12, 89-98.	1.0	248
18	Visualization of comparative genomic analyses by BLAST score ratio. <i>BMC Bioinformatics</i> , 2005, 6, 2.	1.2	238

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19	Defining Genomic Islands and Uropathogen-Specific Genes in Uropathogenic <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2007, 189, 3532-3546.	1.0	234
20	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, 18327-18332.	3.3	215
21	<i>Escherichia coli</i> Global Gene Expression in Urine from Women with Urinary Tract Infection. <i>PLoS Pathogens</i> , 2010, 6, e1001187.	2.1	203
22	Identification of enterotoxigenic <i>Escherichia coli</i> (ETEC) clades with long-term global distribution. <i>Nature Genetics</i> , 2014, 46, 1321-1326.	9.4	192
23	The QseC Adrenergic Signaling Cascade in Enterohemorrhagic <i>E. coli</i> (EHEC). <i>PLoS Pathogens</i> , 2009, 5, e1000553.	2.1	191
24	Formation and Composition of the <i>Bacillus anthracis</i> Endospore. <i>Journal of Bacteriology</i> , 2004, 186, 164-178.	1.0	187
25	The Human Microbiome: From Symbiosis to Pathogenesis. <i>Annual Review of Medicine</i> , 2013, 64, 145-163.	5.0	175
26	Genomic Characterization of Enteroaggregative <i>Escherichia coli</i> From Children in Mali. <i>Journal of Infectious Diseases</i> , 2012, 205, 431-444.	1.9	169
27	Characterization of the Complete Zwittermicin A Biosynthesis Gene Cluster from <i>Bacillus cereus</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 1144-1155.	1.4	168
28	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, 8716-8721.	3.3	167
29	Complete Genome Sequence and Comparative Metabolic Profiling of the Prototypical Enteroaggregative <i>Escherichia coli</i> Strain 042. <i>PLoS ONE</i> , 2010, 5, e8801.	1.1	165
30	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, 5963-5971.	1.4	160
31	Simultaneous Expression of Type 1 and Type 2 Lewis Blood Group Antigens by <i>Helicobacter pylori</i> Lipopolysaccharides. <i>Journal of Biological Chemistry</i> , 1998, 273, 11533-11543.	1.6	157
32	<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, 5027-5032.	3.3	152
33	Bacterial genome sequencing in the clinic: bioinformatic challenges and solutions. <i>Nature Reviews Genetics</i> , 2014, 15, 49-55.	7.7	141
34	Complete Sequence Analysis of Novel Plasmids from Emetic and Periodontal <i>Bacillus cereus</i> Isolates Reveals a Common Evolutionary History among the <i>B. cereus</i> -Group Plasmids, Including <i>Bacillus anthracis</i> pXO1. <i>Journal of Bacteriology</i> , 2007, 189, 52-64.	1.0	140
35	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, 5889-5894.	3.3	137
36	Molecular genetic basis for the variable expression of Lewis Y antigen in <i>Helicobacter pylori</i> : analysis of the alpha(1,2) fucosyltransferase gene. <i>Molecular Microbiology</i> , 1999, 31, 1265-1274.	1.2	130

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37	Lewis antigens in <i>Helicobacter pylori</i> : biosynthesis and phase variation. <i>Molecular Microbiology</i> , 2002, 36, 1187-1196.	1.2	129
38	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, 950-960.	1.0	122
39	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, 9831-9836.	3.3	121
40	QseC Inhibitors as an Antivirulence Approach for Gram-Negative Pathogens. <i>MBio</i> , 2014, 5, e02165.	1.8	110
41	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, 509-521.	1.0	109
42	Global Effects of the Cell-to-Cell Signaling Molecules Autoinducer-2, Autoinducer-3, and Epinephrine in a <i>luxS</i> Mutant of Enterohemorrhagic <i>Escherichia coli</i> . <i>Infection and Immunity</i> , 2007, 75, 4875-4884.	1.0	107
43	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, 12810-12815.	3.3	103
44	An integrated genomic and transcriptomic survey of mucormycosis-causing fungi. <i>Nature Communications</i> , 2016, 7, 12218.	5.8	103
45	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.	1.5	99
46	Lipopolysaccharide structures of <i>Helicobacter pylori</i> genomic strains 26695 and J99, mouse model <i>H. pylori</i> Sydney strain, <i>H. pylori</i> P466 carrying sialyl Lewis X, and <i>H. pylori</i> UA915 expressing Lewis B. <i>FEBS Journal</i> , 2000, 267, 305-320.	0.2	97
47	Autotransporter Genes <i>pic</i> and <i>tsh</i> 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, 593-597.	1.0	97
48	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, 1740-1746.	1.8	96
49	The Complete Genome Sequence of <i>Bacillus anthracis</i> Ames Ancestor. <i>Journal of Bacteriology</i> , 2009, 191, 445-446.	1.0	88
50	Survival of the Fittest: How Bacterial Pathogens Utilize Bile To Enhance Infection. <i>Clinical Microbiology Reviews</i> , 2016, 29, 819-836.	5.7	88
51	Comparative Genomics and <i>stx</i> Phage Characterization of LEE-Negative Shiga Toxin-Producing <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 133.	1.8	84
52	Transcriptome of Swarming <i>Proteus mirabilis</i> . <i>Infection and Immunity</i> , 2010, 78, 2834-2845.	1.0	83
53	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.	2.1	83
54	Defining the Phylogenomics of <i>Shigella</i> Species: a Pathway to Diagnostics. <i>Journal of Clinical Microbiology</i> , 2015, 53, 951-960.	1.8	82

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55	Impact of Oral Typhoid Vaccination on the Human Gut Microbiota and Correlations with S. Typhi-Specific Immunological Responses. PLoS ONE, 2013, 8, e62026.	1.1	82
56	Cloning and Characterization of the $\beta(1,3/4)$ Fucosyltransferase of Helicobacter pylori. Journal of Biological Chemistry, 2000, 275, 4988-4994.	1.6	81
57	Genomic comparison of multi-drug resistant invasive and colonizing Acinetobacter baumannii isolated from diverse human body sites reveals genomic plasticity. BMC Genomics, 2011, 12, 291.	1.2	80
58	Role of the K2 Capsule in <i>Escherichia coli</i> Urinary Tract Infection and Serum Resistance. Journal of Infectious Diseases, 2009, 199, 1689-1697.	1.9	78
59	Native Outer Membrane Proteins Protect Mice against Pulmonary Challenge with Virulent Type A Francisella tularensis. Infection and Immunity, 2008, 76, 3664-3671.	1.0	72
60	Hfq Virulence Regulation in Enterohemorrhagic Escherichia coli O157:H7 Strain 86-24. Journal of Bacteriology, 2011, 193, 6843-6851.	1.0	71
61	Locus of Adhesion and Autoaggregation (LAA), a pathogenicity island present in emerging Shiga Toxin-producing Escherichia coli strains. Scientific Reports, 2017, 7, 7011.	1.6	69
62	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). PLoS Neglected Tropical Diseases, 2019, 13, e0007037.	1.3	68
63	Genomic diversity of EPEC associated with clinical presentations of differing severity. Nature Microbiology, 2016, 1, 15014.	5.9	66
64	Analysis of Shigella flexneri Resistance, Biofilm Formation, and Transcriptional Profile in Response to Bile Salts. Infection and Immunity, 2017, 85, .	1.0	65
65	Transcriptional Modulation of Enterotoxigenic Escherichia coli Virulence Genes in Response to Epithelial Cell Interactions. Infection and Immunity, 2013, 81, 259-270.	1.0	61
66	Whole-Genome Assembly of Klebsiella pneumoniae Coproducing NDM-1 and OXA-232 Carbapenemases Using Single-Molecule, Real-Time Sequencing. Antimicrobial Agents and Chemotherapy, 2014, 58, 5947-5953.	1.4	61
67	Conservation and Immunogenicity of Novel Antigens in Diverse Isolates of Enterotoxigenic Escherichia coli. PLoS Neglected Tropical Diseases, 2015, 9, e0003446.	1.3	60
68	Structural modification of LPS in colistin-resistant, KPC-producing Klebsiella pneumoniae. Journal of Antimicrobial Chemotherapy, 2017, 72, 3035-3042.	1.3	59
69	Genomic and Phenotypic Diversity among Ten Laboratory Isolates of <i>Pseudomonas aeruginosa</i> PAO1. Journal of Bacteriology, 2019, 201, .	1.0	56
70	QseA and GrlR/GrlA Regulation of the Locus of Enterocyte Effacement Genes in Enterohemorrhagic Escherichia coli. Journal of Bacteriology, 2007, 189, 5387-5392.	1.0	55
71	<i>Shigella flexneri</i> effectors OspE1 and OspE2 mediate induced adherence to the colonic epithelium following bile salts exposure. Molecular Microbiology, 2012, 85, 107-121.	1.2	53
72	Whole-Genome Sequences of Bacillus subtilis and Close Relatives. Journal of Bacteriology, 2012, 194, 2378-2379.	1.0	52

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73	Differential Response of the Cynomolgus Macaque Gut Microbiota to Shigella Infection. PLoS ONE, 2013, 8, e64212.	1.1	52
74	Best practices on the differential expression analysis of multi-species RNA-seq. Genome Biology, 2021, 22, 121.	3.8	51
75	EHEC Genomics: Past, Present, and Future. Microbiology Spectrum, 2014, 2, EHEC-0020-2013.	1.2	50
76	Sequencing Bacillus anthracis Typing Phages Gamma and Cherry Reveals a Common Ancestry. Journal of Bacteriology, 2006, 188, 3402-3408.	1.0	49
77	Metabolic Analysis of Moraxella catarrhalis and the Effect of Selected In Vitro Growth Conditions on Global Gene Expression. Infection and Immunity, 2007, 75, 4959-4971.	1.0	48
78	Blocking Yersiniabactin Import Attenuates Extraintestinal Pathogenic Escherichia coli in Cystitis and Pyelonephritis and Represents a Novel Target To Prevent Urinary Tract Infection. Infection and Immunity, 2015, 83, 1443-1450.	1.0	48
79	Genome Sequences of Four Divergent Multidrug-Resistant Acinetobacter baumannii Strains Isolated from Patients with Sepsis or Osteomyelitis. Journal of Bacteriology, 2012, 194, 1619-1620.	1.0	45
80	Comparative genomics and transcriptomics of Escherichia coli isolates carrying virulence factors of both enteropathogenic and enterotoxigenic E. coli. Scientific Reports, 2017, 7, 3513.	1.6	45
81	Analysis of Global Transcriptional Profiles of Enterotoxigenic Escherichia coli Isolate E24377A. Infection and Immunity, 2012, 80, 1232-1242.	1.0	43
82	A divergent <i>Pseudomonas aeruginosa</i> palmitoyltransferase essential for cystic fibrosis-specific lipid A. Molecular Microbiology, 2014, 91, 158-174.	1.2	42
83	Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. Bioinformatics, 2014, 30, 3125-3127.	1.8	41
84	Human Experimental Challenge With Enterotoxigenic Escherichia coli Elicits Immune Responses to Canonical and Novel Antigens Relevant to Vaccine Development. Journal of Infectious Diseases, 2018, 218, 1436-1446.	1.9	40
85	Phylomark, a Tool To Identify Conserved Phylogenetic Markers from Whole-Genome Alignments. Applied and Environmental Microbiology, 2012, 78, 4884-4892.	1.4	39
86	Examination of the Enterotoxigenic Escherichia coli Population Structure during Human Infection. MBio, 2015, 6, e00501.	1.8	39
87	Investigating the Relatedness of Enteroinvasive Escherichia coli to Other E. coli and Shigella Isolates by Using Comparative Genomics. Infection and Immunity, 2016, 84, 2362-2371.	1.0	39
88	Cumulative acquisition of pathogenicity islands has shaped virulence potential and contributed to the emergence of LEE-negative Shiga toxin-producing Escherichia coli strains. Emerging Microbes and Infections, 2019, 8, 486-502.	3.0	39
89	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. Genome Medicine, 2015, 7, 52.	3.6	38
90	The LysR-type regulator QseA regulates both characterized and putative virulence genes in enterohaemorrhagic Escherichia coli O157:H7. Molecular Microbiology, 2010, 76, 1306-1321.	1.2	34

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91	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. PLoS ONE, 2014, 9, e99979.	1.1	34
92	Host Adaptation Predisposes <i>Pseudomonas aeruginosa</i> to Type VI Secretion System-Mediated Predation by the <i>Burkholderia cepacia</i> Complex. Cell Host and Microbe, 2020, 28, 534-547.e3.	5.1	34
93	Redefining enteroaggregative <i>Escherichia coli</i> (EAEC): Genomic characterization of epidemiological EAEC strains. PLoS Neglected Tropical Diseases, 2020, 14, e0008613.	1.3	34
94	Insights into enterotoxigenic <i>Escherichia coli</i> diversity in Bangladesh utilizing genomic epidemiology. Scientific Reports, 2017, 7, 3402.	1.6	33
95	Diversity among blaKPC-containing plasmids in <i>Escherichia coli</i> and other bacterial species isolated from the same patients. Scientific Reports, 2018, 8, 10291.	1.6	33
96	Synthesis of mono- and di-fucosylated type I Lewis blood group antigens by <i>Helicobacter pylori</i> . FEBS Journal, 2000, 267, 6059-6066.	0.2	32
97	RNA-Seq analysis of isolate- and growth phase-specific differences in the global transcriptomes of enteropathogenic <i>Escherichia coli</i> prototype isolates. Frontiers in Microbiology, 2015, 6, 569.	1.5	32
98	Patients with <i>Acinetobacter baumannii</i> bloodstream infections are colonized in the gastrointestinal tract with identical strains. American Journal of Infection Control, 2010, 38, 751-753.	1.1	31
99	Influence of Lewis Antigen Expression by <i>Helicobacter pylori</i> on Bacterial Internalization by Gastric Epithelial Cells. Infection and Immunity, 2003, 71, 2902-2906.	1.0	30
100	Investigating the genome diversity of <i>B. cereus</i> and evolutionary aspects of <i>B. anthracis</i> emergence. Genomics, 2011, 98, 26-39.	1.3	30
101	Insights into the environmental reservoir of pathogenic <i>Vibrio parahaemolyticus</i> using comparative genomics. Frontiers in Microbiology, 2015, 6, 204.	1.5	30
102	Hybrid Shiga Toxin-Producing and Enterotoxigenic <i>Escherichia</i> sp. Cryptic Lineage 1 Strain 7v Harbors a Hybrid Plasmid. Applied and Environmental Microbiology, 2016, 82, 4309-4319.	1.4	30
103	CadA Negatively Regulates <i>Escherichia coli</i> O157:H7 Adherence and Intestinal Colonization. Infection and Immunity, 2008, 76, 5072-5081.	1.0	29
104	Use of Comparative Genomics To Characterize the Diversity of <i>Acinetobacter baumannii</i> Surveillance Isolates in a Health Care Institution. Antimicrobial Agents and Chemotherapy, 2016, 60, 5933-5941.	1.4	28
105	The AraC Negative Regulator family modulates the activity of histone-like proteins in pathogenic bacteria. PLoS Pathogens, 2017, 13, e1006545.	2.1	28
106	Responses of the Human Gut <i>Escherichia coli</i> Population to Pathogen and Antibiotic Disturbances. MSystems, 2018, 3, .	1.7	27
107	A Novel <i>Shigella</i> Proteome Microarray Discriminates Targets of Human Antibody Reactivity following Oral Vaccination and Experimental Challenge. MSphere, 2018, 3, .	1.3	27
108	Conservation and global distribution of non-canonical antigens in Enterotoxigenic <i>Escherichia coli</i> . PLoS Neglected Tropical Diseases, 2019, 13, e0007825.	1.3	27

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109	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.	0.7	26
110	Interrogation of a live-attenuated enterotoxigenic <i>Escherichia coli</i> vaccine highlights features unique to wild-type infection. <i>Npj Vaccines</i> , 2019, 4, 37.	2.9	26
111	Comparison of long-read sequencing technologies in interrogating bacteria and fly genomes. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	26
112	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, .	0.8	25
113	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, .	0.8	25
114	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, 4103-4117.	1.0	25
115	Genome and Functional Characterization of Colonization Factor Antigen I- and CS6-Encoding Heat-Stable Enterotoxin-Only Enterotoxigenic <i>Escherichia coli</i> Reveals Lineage and Geographic Variation. <i>MSystems</i> , 2019, 4, .	1.7	25
116	The Role of Genomics in the Identification, Prediction, and Prevention of Biological Threats. <i>PLoS Biology</i> , 2009, 7, e1000217.	2.6	23
117	Enterotoxigenic <i>Escherichia coli</i> . <i>Gut Microbes</i> , 2013, 4, 392-396.	4.3	23
118	Temporal Variability of <i>Escherichia coli</i> Diversity in the Gastrointestinal Tracts of Tanzanian Children with and without Exposure to Antibiotics. <i>MSphere</i> , 2018, 3, .	1.3	23
119	Pathogenomic analyses of <i>Shigella</i> isolates inform factors limiting shigellosis prevention and control across LMICs. <i>Nature Microbiology</i> , 2022, 7, 251-261.	5.9	23
120	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, 4814-4825.	1.4	22
121	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.	1.3	21
122	<i>Shigella flexneri</i> Adherence Factor Expression in <i>In Vivo</i> -Like Conditions. <i>MSphere</i> , 2019, 4, .	1.3	21
123	<i>Clostridium difficile</i> healthcare-associated epidemics. <i>Nature Genetics</i> , 2013, 45, 6-7.	9.4	20
124	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, 1879-1888.	1.4	20
125	Draft Genome Sequences of the Diarrheagenic <i>Escherichia coli</i> Collection. <i>Journal of Bacteriology</i> , 2012, 194, 3026-3027.	1.0	19
126	Draft Genome Sequence of Biocontrol Agent <i>Bacillus cereus</i> UW85. <i>Genome Announcements</i> , 2016, 4, .	0.8	19

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127	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, 159-166.	0.4	18
128	Draft Genome Sequence of the Methicillin-Resistant <i>Staphylococcus aureus</i> Isolate MRSA-M2. <i>Genome Announcements</i> , 2013, 1, .	0.8	18
129	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.	1.1	18
130	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.	0.8	17
131	Targeted enrichment outperforms other enrichment techniques and enables more multi-species RNA-Seq analyses. <i>Scientific Reports</i> , 2018, 8, 13377.	1.6	17
132	Comparative genomic analysis and molecular examination of the diversity of enterotoxigenic <i>Escherichia coli</i> isolates from Chile. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007828.	1.3	17
133	High Frequency, Spontaneous <i>motA</i> Mutations in <i>Campylobacter jejuni</i> Strain 81-176. <i>PLoS ONE</i> , 2014, 9, e88043.	1.1	17
134	New Family of Tungstate-Responsive Transcriptional Regulators in Sulfate-Reducing Bacteria. <i>Journal of Bacteriology</i> , 2013, 195, 4466-4475.	1.0	16
135	Genome diversity of <i>Shigella boydii</i> . <i>Pathogens and Disease</i> , 2016, 74, ftw027.	0.8	16
136	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, 1639-1639.	1.0	15
137	Chaperone-Usher Pili Loci of Colonization Factor-Negative Human Enterotoxigenic <i>Escherichia coli</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 200.	1.8	15
138	Contribution of Noncanonical Antigens to Virulence and Adaptive Immunity in Human Infection with Enterotoxigenic <i>E. coli</i> . <i>Infection and Immunity</i> , 2021, 89, .	1.0	15
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