

Mark Eppinger

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,869
citations

361413

20
h-index

477307

29
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all docs

30
docs citations

30
times ranked

2531
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathogenomes and variations in Shiga toxin production among geographically distinct clones of <i>Escherichia coli</i> O113:H21. <i>Microbial Genomics</i> , 2022, 8, .	2.0	4
2	Genetic and Virulence Profiles of Enterotoxigenic <i>Escherichia coli</i> (EAEC) Isolated From Deployed Military Personnel (DMP) With Travelers' Diarrhea. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 200.	3.9	15
3	Pathogenomes of Atypical Non-shigatoxigenic <i>Escherichia coli</i> NSF/SF O157:H7/NM: Comprehensive Phylogenomic Analysis Using Closed Genomes. <i>Frontiers in Microbiology</i> , 2020, 11, 619.	3.5	11
4	Genomic features of colistin resistant <i>Escherichia coli</i> ST69 strain harboring <i>mcr-1</i> on IncHI2 plasmid from raw milk cheese in Egypt. <i>Infection, Genetics and Evolution</i> , 2019, 73, 126-131.	2.3	50
5	Closed Genome Sequence of <i>Escherichia coli</i> K-12 Group Strain C600. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	21
6	Closed Genome and Comparative Phylogenetic Analysis of the Clinical Multidrug Resistant <i>Shigella sonnei</i> Strain 866. <i>Genome Biology and Evolution</i> , 2018, 10, 2241-2247.	2.5	10
7	<i>Acinetobacter baumannii</i> Gastrointestinal Colonization Is Facilitated by Secretory IgA Which Is Reductively Dissociated by Bacterial Thioredoxin A. <i>MBio</i> , 2018, 9, .	4.1	21
8	Closed Genome Sequence of <i>Vibrio cholerae</i> O1 El Tor Inaba Strain A1552. <i>Genome Announcements</i> , 2018, 6, .	0.8	35
9	Identification of a mouse <i>Lactobacillus johnsonii</i> strain with deconjugase activity against the FXR antagonist T-12-MCA. <i>PLoS ONE</i> , 2017, 12, e0183564.	2.5	28
10	Whole Genome Sequencing for Genomics-Guided Investigations of <i>Escherichia coli</i> O157:H7 Outbreaks. <i>Frontiers in Microbiology</i> , 2016, 7, 985.	3.5	70
11	Genome Sequences of Five Clinical Isolates of <i>Klebsiella pneumoniae</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	7
12	Phylogenetic Diversity of <i>Vibrio cholerae</i> Associated with Endemic Cholera in Mexico from 1991 to 2008. <i>MBio</i> , 2016, 7, e02160.	4.1	24
13	<i>Escherichia coli</i> O157:H7 strains harbor at least three distinct sequence types of Shiga toxin 2a-converting phages. <i>BMC Genomics</i> , 2015, 16, 733.	2.8	47
14	Public Health Investigation of Two Outbreaks of Shiga Toxin-Producing <i>Escherichia coli</i> O157 Associated with Consumption of Watercress. <i>Applied and Environmental Microbiology</i> , 2015, 81, 3946-3952.	3.1	68
15	Future perspectives, applications and challenges of genomic epidemiology studies for food-borne pathogens: A case study of Enterohemorrhagic <i>Escherichia coli</i> (EHEC) of the O157:H7 serotype. <i>Gut Microbes</i> , 2015, 6, 194-201.	9.8	53
16	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, .	2.0	25
17	Genome Sequence of <i>Bacillus thuringiensis</i> Strain Btm27, an Egyptian Isolate Highly Toxic to Cotton Leafworm. <i>Genome Announcements</i> , 2015, 3, .	0.8	2
18	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	2.5	34

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19	Genomic Epidemiology of the Haitian Cholera Outbreak: a Single Introduction Followed by Rapid, Extensive, and Continued Spread Characterized the Onset of the Epidemic. <i>MBio</i> , 2014, 5, e01721.	4.1	112
20	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.	4.7	83
21	EHEC Genomics: Past, Present, and Future. <i>Microbiology Spectrum</i> , 2014, 2, EHEC-0020-2013.	3.0	50
22	Whole-Genome Draft Sequences of 26 Enterohemorrhagic <i>Escherichia coli</i> O157:H7 Strains. <i>Genome Announcements</i> , 2013, 1, e0013412.	0.8	31
23	Novel Plasmids and Resistance Phenotypes in <i>Yersinia pestis</i> : Unique Plasmid Inventory of Strain Java 9 Mediates High Levels of Arsenic Resistance. <i>PLoS ONE</i> , 2012, 7, e32911.	2.5	16
24	Genome Signatures of <i>Escherichia coli</i> O157:H7 Isolates from the Bovine Host Reservoir. <i>Applied and Environmental Microbiology</i> , 2011, 77, 2916-2925.	3.1	54
25	Genome Sequences of the Biotechnologically Important <i>Bacillus megaterium</i> Strains QM B1551 and DSM319. <i>Journal of Bacteriology</i> , 2011, 193, 4199-4213.	2.2	155
26	Genomic anatomy of <i>Escherichia coli</i> O157:H7 outbreaks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20142-20147.	7.1	206
27	<i>Yersinia pestis</i> genome sequencing identifies patterns of global phylogenetic diversity. <i>Nature Genetics</i> , 2010, 42, 1140-1143.	21.4	504
28	Genome Sequence of the Deep-Rooted <i>Yersinia pestis</i> Strain Angola Reveals New Insights into the Evolution and Pangenome of the Plague Bacterium. <i>Journal of Bacteriology</i> , 2010, 192, 1685-1699.	2.2	117
29	Draft Genome Sequences of <i>Yersinia pestis</i> Isolates from Natural Foci of Endemic Plague in China. <i>Journal of Bacteriology</i> , 2009, 191, 7628-7629.	2.2	16
30	Enterohemorrhagic <i>Escherichia coli</i> Genomics: Past, Present, and Future. , 0, , 55-71.		0