

Sean C Daugherty

List of Publications by Year in descending order

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37
papers

11,676
citations

186265
28
h-index

315739
38
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38
all docs

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docs citations

38
times ranked

14562
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Analysis of Genome of Ehrlichia sp. HF, a Model Bacterium to Study Fatal Human Ehrlichiosis. BMC Genomics, 2021, 22, 11.	2.8	21
2	Tissue specific diversification, virulence and immune response to <i>Mycobacterium bovis</i> BCG in a patient with an IFN- β R1 deficiency. Virulence, 2020, 11, 1656-1673.	4.4	5
3	The Streptococcus agalactiae Stringent Response Enhances Virulence and Persistence in Human Blood. Infection and Immunity, 2018, 86, .	2.2	31
4	Analysis of complete genome sequence and major surface antigens of <i>Neorickettsia helminthoeca</i> , causative agent of salmon poisoning disease. Microbial Biotechnology, 2017, 10, 933-957.	4.2	11
5	Comparative genomics and transcriptomics of Escherichia coli isolates carrying virulence factors of both enteropathogenic and enterotoxigenic E. coli. Scientific Reports, 2017, 7, 3513.	3.3	45
6	Transcriptional Variation of Diverse Enteropathogenic Escherichia coli Isolates under Virulence-Inducing Conditions. MSystems, 2017, 2, .	3.8	12
7	Streptococcus pneumoniae in the heart subvert the host response through biofilm-mediated resident macrophage killing. PLoS Pathogens, 2017, 13, e1006582.	4.7	62
8	Use of Comparative Genomics To Characterize the Diversity of Acinetobacter baumannii Surveillance Isolates in a Health Care Institution. Antimicrobial Agents and Chemotherapy, 2016, 60, 5933-5941.	3.2	28
9	Neuraminidase A-Exposed Galactose Promotes Streptococcus pneumoniae Biofilm Formation during Colonization. Infection and Immunity, 2016, 84, 2922-2932.	2.2	61
10	RNA-Seq analysis of isolate- and growth phase-specific differences in the global transcriptomes of enteropathogenic Escherichia coli prototype isolates. Frontiers in Microbiology, 2015, 6, 569.	3.5	32
11	Transcriptional Attenuation Controls Macrolide Inducible Efflux and Resistance in Streptococcus pneumoniae and in Other Gram-Positive Bacteria Containing mef/mel(msr(D)) Elements. PLoS ONE, 2015, 10, e0116254.	2.5	41
12	Complete Genome Sequence of Streptococcus agalactiae CNCTC 10/84, a Hypervirulent Sequence Type 26 Strain. Genome Announcements, 2014, 2, .	0.8	22
13	High-level Relatedness among <i>Mycobacterium abscessus</i> subsp. <i>massiliense</i> Strains from Widely Separated Outbreaks. Emerging Infectious Diseases, 2014, 20, 364-371.	4.3	108
14	Genomic Insights into the Emerging Human Pathogen Mycobacterium massiliense. Journal of Bacteriology, 2012, 194, 5450-5450.	2.2	22
15	Whole Genome Sequencing to Investigate the Emergence of Clonal Complex 23 Neisseria meningitidis Serogroup Y Disease in the United States. PLoS ONE, 2012, 7, e35699.	2.5	26
16	An Enterotoxin-Bearing Pathogenicity Island in Staphylococcus epidermidis. Journal of Bacteriology, 2011, 193, 1854-1862.	2.2	54
17	<i>Neisseria meningitidis</i> is structured in clades associated with restriction modification systems that modulate homologous recombination. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4494-4499.	7.1	198
18	Three Genomes from the Phylum Acidobacteria Provide Insight into the Lifestyles of These Microorganisms in Soils. Applied and Environmental Microbiology, 2009, 75, 2046-2056.	3.1	804

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19	Secrets of Soil Survival Revealed by the Genome Sequence of <i>Arthrobacter aurescens</i> TC1. <i>PLoS Genetics</i> , 2006, 2, e214.	3.5	213
20	Genome sequence of <i>Synechococcus</i> CC9311: Insights into adaptation to a coastal environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13555-13559.	7.1	230
21	Comparative Genomics of Emerging Human Ehrlichiosis Agents. <i>PLoS Genetics</i> , 2006, 2, e21.	3.5	423
22	Comparative Genomic Evidence for a Close Relationship between the Dimorphic Prosthecate Bacteria <i>Hyphomonas neptunium</i> and <i>Caulobacter crescentus</i> . <i>Journal of Bacteriology</i> , 2006, 188, 6841-6850.	2.2	57
23	Metabolic Complementarity and Genomics of the Dual Bacterial Symbiosis of Sharpshooters. <i>PLoS Biology</i> , 2006, 4, e188.	5.6	391
24	Life in Hot Carbon Monoxide: The Complete Genome Sequence of <i>Carboxydotherrmus hydrogenoformans</i> Z-2901. <i>PLoS Genetics</i> , 2005, 1, e65.	3.5	226
25	Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. <i>Nature Biotechnology</i> , 2005, 23, 873-878.	17.5	615
26	Whole-Genome Sequence Analysis of <i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A Reveals Divergence among Pathovars in Genes Involved in Virulence and Transposition. <i>Journal of Bacteriology</i> , 2005, 187, 6488-6498.	2.2	301
27	The psychrophilic lifestyle as revealed by the genome sequence of <i>Colwellia psychrerythraea</i> 34H through genomic and proteomic analyses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10913-10918.	7.1	529
28	Genome analysis of multiple pathogenic isolates of <i>Streptococcus agalactiae</i> : Implications for the microbial "pan-genome". <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13950-13955.	7.1	2,161
29	Insights on Evolution of Virulence and Resistance from the Complete Genome Analysis of an Early Methicillin-Resistant <i>Staphylococcus aureus</i> Strain and a Biofilm-Producing Methicillin-Resistant <i>Staphylococcus epidermidis</i> Strain. <i>Journal of Bacteriology</i> , 2005, 187, 2426-2438.	2.2	940
30	Major Structural Differences and Novel Potential Virulence Mechanisms from the Genomes of Multiple <i>Campylobacter</i> Species. <i>PLoS Biology</i> , 2005, 3, e15.	5.6	483
31	Phylogenomics of the Reproductive Parasite <i>Wolbachia pipientis</i> wMel: A Streamlined Genome Overrun by Mobile Genetic Elements. <i>PLoS Biology</i> , 2004, 2, e69.	5.6	713
32	The genome sequence of the anaerobic, sulfate-reducing bacterium <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Nature Biotechnology</i> , 2004, 22, 554-559.	17.5	559
33	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004, 432, 910-913.	27.8	415
34	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.	14.5	460
35	Complete genome sequence of the Q-fever pathogen <i>Coxiella burnetii</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 5455-5460.	7.1	506
36	The <i>Brucella suis</i> genome reveals fundamental similarities between animal and plant pathogens and symbionts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 13148-13153.	7.1	422

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37	Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V<i>Streptococcus agalactiae</i>. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12391-12396.	7.1	447