

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
g-index

38
all docs

38
docs citations

38
times ranked

14562
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	Three Genomes from the Phylum <i>Acidobacteria</i> Provide Insight into the Lifestyles of These Microorganisms in Soils. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2046-2056.	3.1	804
4	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
5	Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. <i>Nature Biotechnology</i> , 2005, 23, 873-878.	17.5	615
6	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
7	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
8	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
9	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
10	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
11	Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V <i>Streptococcus agalactiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12391-12396.	7.1	447
12	Comparative Genomics of Emerging Human Ehrlichiosis Agents. <i>PLoS Genetics</i> , 2006, 2, e21.	3.5	423
13	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
14	Genome sequence of <i>Silicibacter pomeroyi</i> reveals adaptations to the marine environment. <i>Nature</i> , 2004, 432, 910-913.	27.8	415
15	Metabolic Complementarity and Genomics of the Dual Bacterial Symbiosis of Sharpshooters. <i>PLoS Biology</i> , 2006, 4, e188.	5.6	391
16	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
17	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
18	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

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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	<i>Neisseria meningitidis</i> is structured in clades associated with restriction modification systems that modulate homologous recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4494-4499.	7.1	198
21	High-level Relatedness among <i>Mycobacterium abscessus</i> subsp. <i>massiliense</i> Strains from Widely Separated Outbreaks. <i>Emerging Infectious Diseases</i> , 2014, 20, 364-371.	4.3	108
22	<i>Streptococcus pneumoniae</i> in the heart subvert the host response through biofilm-mediated resident macrophage killing. <i>PLoS Pathogens</i> , 2017, 13, e1006582.	4.7	62
23	Neuraminidase A-Exposed Galactose Promotes <i>Streptococcus pneumoniae</i> Biofilm Formation during Colonization. <i>Infection and Immunity</i> , 2016, 84, 2922-2932.	2.2	61
24	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
25	An Enterotoxin-Bearing Pathogenicity Island in <i>Staphylococcus epidermidis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 1854-1862.	2.2	54
26	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.	3.3	45
27	Transcriptional Attenuation Controls Macrolide Inducible Efflux and Resistance in <i>Streptococcus pneumoniae</i> and in Other Gram-Positive Bacteria Containing <i>mef/mel(msr(D))</i> Elements. <i>PLoS ONE</i> , 2015, 10, e0116254.	2.5	41
28	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.	3.5	32
29	The <i>Streptococcus agalactiae</i> Stringent Response Enhances Virulence and Persistence in Human Blood. <i>Infection and Immunity</i> , 2018, 86, .	2.2	31
30	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, 5933-5941.	3.2	28
31	Whole Genome Sequencing to Investigate the Emergence of Clonal Complex 23 <i>Neisseria meningitidis</i> Serogroup Y Disease in the United States. <i>PLoS ONE</i> , 2012, 7, e35699.	2.5	26
32	Genomic Insights into the Emerging Human Pathogen <i>Mycobacterium massiliense</i> . <i>Journal of Bacteriology</i> , 2012, 194, 5450-5450.	2.2	22
33	Complete Genome Sequence of <i>Streptococcus agalactiae</i> CNCTC 10/84, a Hypervirulent Sequence Type 26 Strain. <i>Genome Announcements</i> , 2014, 2, .	0.8	22
34	Comparative Analysis of Genome of <i>Ehrlichia</i> sp. HF, a Model Bacterium to Study Fatal Human Ehrlichiosis. <i>BMC Genomics</i> , 2021, 22, 11.	2.8	21
35	Transcriptional Variation of Diverse Enteropathogenic <i>Escherichia coli</i> Isolates under Virulence-Inducing Conditions. <i>MSystems</i> , 2017, 2, .	3.8	12
36	Analysis of complete genome sequence and major surface antigens of <i>Neorickettsia helminthoeca</i> , causative agent of salmon poisoning disease. <i>Microbial Biotechnology</i> , 2017, 10, 933-957.	4.2	11

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37	Tissue specific diversification, virulence and immune response to <i>Mycobacterium bovis</i> BCG in a patient with an IFN- γ R1 deficiency. <i>Virulence</i> , 2020, 11, 1656-1673.	4.4	5