

Garry Sa Myers

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

5,620
citations

159358

30
h-index

189595

50
g-index

51
all docs

51
docs citations

51
times ranked

7101
citing authors

#	ARTICLE	IF	CITATIONS
1	Role of Mobile DNA in the Evolution of Vancomycin-Resistant <i>Enterococcus faecalis</i> . <i>Science</i> , 2003, 299, 2071-2074.	6.0	849
2	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
3	Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. <i>Nature Biotechnology</i> , 2005, 23, 873-878.	9.4	615
4	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
5	Genome sequence of <i>Chlamydomonas reinhardtii</i> (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae. <i>Nucleic Acids Research</i> , 2003, 31, 2134-2147.	6.5	266
6	Comparison of the genome of the oral pathogen <i>Treponema denticola</i> with other spirochete genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 5646-5651.	3.3	251
7	Visualization of comparative genomic analyses by BLAST score ratio. <i>BMC Bioinformatics</i> , 2005, 6, 2.	1.2	238
8	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.	3.3	230
9	Genome Sequence of the Cellulolytic Gliding Bacterium <i>Cytophaga hutchinsonii</i> . <i>Applied and Environmental Microbiology</i> , 2007, 73, 3536-3546.	1.4	208
10	Unity in Variety--The Pan-Genome of the Chlamydiae. <i>Molecular Biology and Evolution</i> , 2011, 28, 3253-3270.	3.5	184
11	Type III secretion in <i>Chlamydia</i> . <i>Trends in Microbiology</i> , 2007, 15, 241-251.	3.5	154
12	Evidence for the existence of two new members of the family Chlamydiaceae and proposal of <i>Chlamydia avium</i> sp. nov. and <i>Chlamydia gallinacea</i> sp. nov.. <i>Systematic and Applied Microbiology</i> , 2014, 37, 79-88.	1.2	154
13	Simultaneous Transcriptional Profiling of Bacteria and Their Host Cells. <i>PLoS ONE</i> , 2013, 8, e80597.	1.1	125
14	Divergence without difference: phylogenetics and taxonomy of <i>Chlamydia</i> resolved. <i>FEMS Immunology and Medical Microbiology</i> , 2009, 55, 115-119.	2.7	118
15	Genome Degradation in <i>Brucella ovis</i> Corresponds with Narrowing of Its Host Range and Tissue Tropism. <i>PLoS ONE</i> , 2009, 4, e5519.	1.1	110
16	Evidence that Human <i>Chlamydia pneumoniae</i> Was Zoonotically Acquired. <i>Journal of Bacteriology</i> , 2009, 191, 7225-7233.	1.0	105
17	Predicting Phenotype and Emerging Strains among <i>Chlamydia trachomatis</i> Infections. <i>Emerging Infectious Diseases</i> , 2009, 15, 1385-1394.	2.0	87
18	Isolation of a New <i>Chlamydia</i> species from the Feral Sacred Ibis (<i>Threskiornis aethiopicus</i>): <i>Chlamydia ibidis</i> . <i>PLoS ONE</i> , 2013, 8, e74823.	1.1	82

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19	Strain and Virulence Diversity in the Mouse Pathogen <i>Chlamydia muridarum</i> . <i>Infection and Immunity</i> , 2009, 77, 3284-3293.	1.0	70
20	Genome sequence and identification of candidate vaccine antigens from the animal pathogen <i>Dichelobacter nodosus</i> . <i>Nature Biotechnology</i> , 2007, 25, 569-575.	9.4	66
21	Full Genome Sequences of All Nine <i>Chlamydia psittaci</i> Genotype Reference Strains. <i>Journal of Bacteriology</i> , 2012, 194, 6930-6931.	1.0	41
22	Circleator: flexible circular visualization of genome-associated data with BioPerl and SVG. <i>Bioinformatics</i> , 2014, 30, 3125-3127.	1.8	41
23	Early MicroRNA Expression Profile as a Prognostic Biomarker for the Development of Pelvic Inflammatory Disease in a Mouse Model of Chlamydial Genital Infection. <i>MBio</i> , 2014, 5, e01241-14.	1.8	40
24	Genome sequencing and comparative analysis of three <i>Chlamydia pecorum</i> strains associated with different pathogenic outcomes. <i>BMC Genomics</i> , 2014, 15, 23.	1.2	39
25	<i>Chlamydia pneumoniae</i> Is Genetically Diverse in Animals and Appears to Have Crossed the Host Barrier to Humans on (At Least) Two Occasions. <i>PLoS Pathogens</i> , 2010, 6, e1000903.	2.1	38
26	Preliminary phylogenetic identification of virulent <i>Chlamydophila pecorum</i> strains. <i>Infection, Genetics and Evolution</i> , 2008, 8, 764-771.	1.0	36
27	Genome Sequence of the Obligate Intracellular Animal Pathogen <i>Chlamydia pecorum</i> E58. <i>Journal of Bacteriology</i> , 2011, 193, 3690-3690.	1.0	36
28	High resolution typing of <i>Chlamydophila psittaci</i> by multilocus VNTR analysis (MLVA). <i>Infection, Genetics and Evolution</i> , 2008, 8, 171-181.	1.0	35
29	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	1.1	34
30	Comparative genomics of koala, cattle and sheep strains of <i>Chlamydia pecorum</i> . <i>BMC Genomics</i> , 2014, 15, 667.	1.2	33
31	Comparison of koala LPCoLN and human strains of <i>Chlamydia pneumoniae</i> highlights extended genetic diversity in the species. <i>BMC Genomics</i> , 2010, 11, 442.	1.2	31
32	Regulation of Type IV Fimbrial Biogenesis in <i>Dichelobacter nodosus</i> . <i>Journal of Bacteriology</i> , 2006, 188, 4801-4811.	1.0	28
33	Genome Sequences of the Zoonotic Pathogens <i>Chlamydia psittaci</i> 6BC and Cal10. <i>Journal of Bacteriology</i> , 2011, 193, 4039-4040.	1.0	26
34	Genomic profiling of <i>Escherichia coli</i> isolates from bacteraemia patients: a 3-year cohort study of isolates collected at a Sydney teaching hospital. <i>Microbial Genomics</i> , 2020, 6, .	1.0	25
35	Genomic Analysis of an Attenuated <i>Chlamydia abortus</i> Live Vaccine Strain Reveals Defects in Central Metabolism and Surface Proteins. <i>Infection and Immunity</i> , 2009, 77, 4161-4167.	1.0	24
36	Comparative genomic analysis of human <i>Chlamydia pneumoniae</i> isolates from respiratory, brain and cardiac tissues. <i>Genomics</i> , 2015, 106, 373-383.	1.3	23

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37	Genus-optimized strategy for the identification of chlamydial type III secretion substrates. <i>Pathogens and Disease</i> , 2013, 69, 213-222.	0.8	21
38	Identification of a <i>Dichelobacter nodosus</i> Ferric Uptake Regulator and Determination of Its Regulatory Targets. <i>Journal of Bacteriology</i> , 2005, 187, 366-375.	1.0	18
39	Genome Sequence of <i>Chlamydia suis</i> MD56, Isolated from the Conjunctiva of a Weaned Piglet. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
40	Identification and characterisation of coding tandem repeat variants in <i>incA</i> gene of <i>Chlamydomphila pecorum</i> . <i>Veterinary Research</i> , 2008, 39, 56.	1.1	15
41	Genetic Variation <i>In Vitro</i> and <i>In Vivo</i> of an Attenuated Lassa Vaccine Candidate. <i>Journal of Virology</i> , 2014, 88, 3058-3066.	1.5	12
42	Phylogenomics of two ST1 antibiotic-susceptible non-clinical <i>Acinetobacter baumannii</i> strains reveals multiple lineages and complex evolutionary history in global clone 1. <i>Microbial Genomics</i> , 2021, 7, .	1.0	11
43	Genomic Plasticity of the <i>rrn-nqrF</i> Intergenic Segment in the Chlamydiaceae. <i>Journal of Bacteriology</i> , 2007, 189, 2128-2132.	1.0	7
44	Dual RNA-Seq of <i>Chlamydia</i> and Host Cells. <i>Methods in Molecular Biology</i> , 2019, 2042, 123-135.	0.4	7
45	Cloning, expression, and purification of <i>Brucella suis</i> outer membrane proteins. <i>Protein Expression and Purification</i> , 2005, 40, 134-141.	0.6	6
46	Chromatin accessibility dynamics of <i>Chlamydia</i> -infected epithelial cells. <i>Epigenetics and Chromatin</i> , 2020, 13, 45.	1.8	6
47	A high efficiency cloning and expression system for proteomic analysis. <i>Proteomics</i> , 2006, 6, 4038-4046.	1.3	5
48	Phylogenetic analysis of human <i>Chlamydia pneumoniae</i> strains reveals a distinct Australian indigenous clade that predates European exploration of the continent. <i>BMC Genomics</i> , 2015, 16, 1094.	1.2	5
49	Expression of two novel proteins in <i>Chlamydia trachomatis</i> during natural infection. <i>Microbial Pathogenesis</i> , 2000, 29, 63-72.	1.3	4
50	Non-pathogenic bacteria take center stage: a lesson in contrasts. <i>Trends in Microbiology</i> , 2004, 12, 303-305.	3.5	1