

HervÃ© Tettelin

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

8,319
citations

126907

33
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123424

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70
docs citations

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times ranked

9155
citing authors

#	ARTICLE	IF	CITATIONS
1	Anatomical Site-Specific Carbohydrate Availability Impacts <i>Streptococcus pneumoniae</i> Virulence and Fitness during Colonization and Disease. <i>Infection and Immunity</i> , 2022, 90, IA10045121.	2.2	7
2	Induction of Susceptibility to Disseminated Infection with IgA1 Protease-Producing Encapsulated Pathogens <i>Streptococcus pneumoniae</i> , <i>Haemophilus influenzae</i> Type b, and <i>Neisseria meningitidis</i> . <i>MBio</i> , 2022, , e0055022.	4.1	1
3	COVID-19 vaccine design using reverse and structural vaccinology, ontology-based literature mining and machine learning. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	4
4	Genome-Wide fitness analysis of group B <i>Streptococcus</i> in human amniotic fluid reveals a transcription factor that controls multiple virulence traits. <i>PLoS Pathogens</i> , 2021, 17, e1009116.	4.7	11
5	Analysis of DnaK Expression from a Strain of <i>Mycoplasma fermentans</i> in Infected HCT116 Human Colon Carcinoma Cells. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3885.	4.1	6
6	Complete Genome Sequence of <i>Neisseria musculi</i> Using Illumina and PacBio Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, e0045221.	0.6	2
7	B Cells Control Mucosal-Associated Invariant T Cell Responses to <i>Salmonella enterica</i> Serovar Typhi Infection Through the CD85j HLA-G Receptor. <i>Frontiers in Immunology</i> , 2021, 12, 728685.	4.8	6
8	Differential functional patterns of memory CD4+ and CD8+ T-cells from volunteers immunized with Ty21a typhoid vaccine observed using a recombinant <i>Escherichia coli</i> system expressing <i>S. Typhi</i> proteins. <i>Vaccine</i> , 2020, 38, 258-270.	3.8	7
9	Sugar-Coated Killer: Serotype 3 Pneumococcal Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 613287.	3.9	48
10	The Pangenome: A Data-Driven Discovery in Biology. , 2020, , 3-20.		11
11	An in vivo atlas of host-“pathogen transcriptomes during <i>Streptococcus pneumoniae</i> colonization and disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 33507-33518.	7.1	40
12	Tissue specific diversification, virulence and immune response to <i>Mycobacterium bovis</i> BCG in a patient with an IFN- β R1 deficiency. <i>Virulence</i> , 2020, 11, 1656-1673.	4.4	5
13	Identification of Virulence-Associated Properties by Comparative Genome Analysis of <i>Streptococcus pneumoniae</i> , <i>S. pseudopneumoniae</i> , <i>S. mitis</i> , Three <i>S. oralis</i> Subspecies, and <i>S. infantis</i> . <i>MBio</i> , 2019, 10, .	4.1	39
14	ReVac: a reverse vaccinology computational pipeline for prioritization of prokaryotic protein vaccine candidates. <i>BMC Genomics</i> , 2019, 20, 981.	2.8	18
15	Persistence of <i>Moraxella catarrhalis</i> in Chronic Obstructive Pulmonary Disease and Regulation of the Hag/MID Adhesin. <i>Journal of Infectious Diseases</i> , 2019, 219, 1448-1455.	4.0	14
16	<i>Haemophilus influenzae</i> genome evolution during persistence in the human airways in chronic obstructive pulmonary disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3256-E3265.	7.1	57
17	The <i>Streptococcus agalactiae</i> Stringent Response Enhances Virulence and Persistence in Human Blood. <i>Infection and Immunity</i> , 2018, 86, .	2.2	31
18	Changes in IgA Protease Expression Are Conferred by Changes in Genomes during Persistent Infection by Nontypeable <i>Haemophilus influenzae</i> in Chronic Obstructive Pulmonary Disease. <i>Infection and Immunity</i> , 2018, 86, .	2.2	15

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19	Transcriptional organization of pneumococcal psrP-secY2A2 and impact of GtfA and GtfB deletion on PsrP-associated virulence properties. <i>Microbes and Infection</i> , 2017, 19, 323-333.	1.9	12
20	Complete Genome Sequences of <i>Mycobacterium kansasii</i> Strains Isolated from Rhesus Macaques. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
21	Whole-Exome Sequencing Identifies the 6q12-q16 Linkage Region and a Candidate Gene, <i>TTK</i> , for Pulmonary Nontuberculous Mycobacterial Disease. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2017, 196, 1599-1604.	5.6	28
22	Whole-Genome Sequences of Bacteremia Isolates of <i>Bordetella holmesii</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	0
23	Use of a novel antigen expressing system to study the <i>Salmonella enterica</i> serovar Typhi protein recognition by T cells. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005912.	3.0	16
24	<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
25	Genome-wide discovery of novel MIT1 group A streptococcal determinants important for fitness and virulence during soft-tissue infection. <i>PLoS Pathogens</i> , 2017, 13, e1006584.	4.7	42
26	In-silico prediction and deep-DNA sequencing validation indicate phase variation in 115 <i>Neisseria meningitidis</i> genes. <i>BMC Genomics</i> , 2016, 17, 843.	2.8	22
27	Capsular Polysaccharide Expression in Commensal <i>Streptococcus</i> Species: Genetic and Antigenic Similarities to <i>Streptococcus pneumoniae</i> . <i>MBio</i> , 2016, 7, .	4.1	87
28	The essential genome of <i>Streptococcus agalactiae</i> . <i>BMC Genomics</i> , 2016, 17, 406.	2.8	41
29	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
30	Genome stability of <i>Propionibacterium acnes</i> : a comprehensive study of indels and homopolymeric tracts. <i>Scientific Reports</i> , 2016, 6, 20662.	3.3	49
31	Essential Genes in the Core Genome of the Human Pathogen <i>Streptococcus pyogenes</i> . <i>Scientific Reports</i> , 2015, 5, 9838.	3.3	114
32	Genomics, Genetic Variation, and Regions of Differences. , 2015, , 81-107.		2
33	Clonal Diversification and Changes in Lipid Traits and Colony Morphology in <i>Mycobacterium abscessus</i> Clinical Isolates. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3438-3447.	3.9	48
34	Molecular epidemiology and genomics of group A <i>Streptococcus</i> . <i>Infection, Genetics and Evolution</i> , 2015, 33, 393-418.	2.3	65
35	Ten years of pan-genome analyses. <i>Current Opinion in Microbiology</i> , 2015, 23, 148-154.	5.1	498
36	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

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37	Genomic Analysis Reveals the Molecular Basis for Capsule Loss in the Group B Streptococcus Population. PLoS ONE, 2015, 10, e0125985.	2.5	29
38	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. PLoS ONE, 2014, 9, e99979.	2.5	34
39	Comparative Genomics of Streptococcus Pneumoniae: Intrastrain Diversity and Genome Plasticity. , 2014, , 15-29.		12
40	Complete Genome Sequence of Streptococcus agalactiae CNCTC 10/84, a Hypervirulent Sequence Type 26 Strain. Genome Announcements, 2014, 2, .	0.8	22
41	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
42	Parallel Evolution of Streptococcus pneumoniae and Streptococcus mitis to Pathogenic and Mutualistic Lifestyles. MBio, 2014, 5, e01490-14.	4.1	159
43	Genome-Wide Identification of Genes Required for Fitness of Group A Streptococcus in Human Blood. Infection and Immunity, 2013, 81, 862-875.	2.2	98
44	The two-component response regulator LiaR regulates cell wall stress responses, pili expression and virulence in group B Streptococcus. Microbiology (United Kingdom), 2013, 159, 1521-1534.	1.8	74
45	Genomic Insights into the Emerging Human Pathogen Mycobacterium massiliense. Journal of Bacteriology, 2012, 194, 5450-5450.	2.2	22
46	Using Sybil for interactive comparative genomics of microbes on the web. Bioinformatics, 2012, 28, 160-166.	4.1	53
47	Improving pan-genome annotation using whole genome multiple alignment. BMC Bioinformatics, 2011, 12, 272.	2.6	38
48	Whole-Genome Association Study on Tissue Tropism Phenotypes in Group A Streptococcus. Journal of Bacteriology, 2011, 193, 6651-6663.	2.2	41
49	<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
50	Streptococcus pneumoniae in Biofilms Are Unable to Cause Invasive Disease Due to Altered Virulence Determinant Production. PLoS ONE, 2011, 6, e28738.	2.5	99
51	Pyrosequencing-based comparative genome analysis of the nosocomial pathogen Enterococcus faecium and identification of a large transferable pathogenicity island. BMC Genomics, 2010, 11, 239.	2.8	190
52	Comparative genomics of the genus Bifidobacterium. Microbiology (United Kingdom), 2010, 156, 3243-3254.	1.8	116
53	Structure and dynamics of the pan-genome of Streptococcus pneumoniae and closely related species. Genome Biology, 2010, 11, R107.	8.8	321
54	Extensive genomic diversity of closely related Wolbachia strains. Microbiology (United Kingdom), 2009, 155, 2211-2222.	1.8	87

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55	Genome flexibility in <i>Neisseria meningitidis</i> . <i>Vaccine</i> , 2009, 27, B103-B111.	3.8	47
56	Bacterial Genome Sequencing. <i>Methods in Molecular Biology</i> , 2009, 551, 231-247.	0.9	19
57	Comparative genomics: the bacterial pan-genome. <i>Current Opinion in Microbiology</i> , 2008, 11, 472-477.	5.1	868
58	Towards a universal group B <i>Streptococcus</i> vaccine using multistrain genome analysis. <i>Expert Review of Vaccines</i> , 2006, 5, 687-694.	4.4	27
59	Comparative genomics of <i>Neisseria meningitidis</i> : core genome, islands of horizontal transfer and pathogen-specific genes. <i>Microbiology (United Kingdom)</i> , 2006, 152, 3733-3749.	1.8	102
60	Identification of novel <i>cps</i> locus polymorphisms in nontypable group B <i>Streptococcus</i> . <i>Journal of Medical Microbiology</i> , 2006, 55, 775-783.	1.8	24
61	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
62	The microbial pan-genome. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 589-594.	3.3	1,151
63	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
64	Repeat-associated phase variable genes in the complete genome sequence of <i>Neisseria meningitidis</i> strain MC58. <i>Molecular Microbiology</i> , 2000, 37, 207-215.	2.5	231
65	The Malaria Genome Sequencing Project. <i>Expert Reviews in Molecular Medicine</i> , 1998, 1, 1-9.	3.9	8