

# HervÃ© Tettelin

## List of Publications by Year in descending order

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65  
papers

8,319  
citations

126907

33  
h-index

123424

61  
g-index

70  
all docs

70  
docs citations

70  
times ranked

9155  
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	The microbial pan-genome. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 589-594.	3.3	1,151
3	Comparative genomics: the bacterial pan-genome. <i>Current Opinion in Microbiology</i> , 2008, 11, 472-477.	5.1	868
4	Ten years of pan-genome analyses. <i>Current Opinion in Microbiology</i> , 2015, 23, 148-154.	5.1	498
5	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
6	Structure and dynamics of the pan-genome of <i>Streptococcus pneumoniae</i> and closely related species. <i>Genome Biology</i> , 2010, 11, R107.	8.8	321
7	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
8	<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
9	Pyrosequencing-based comparative genome analysis of the nosocomial pathogen <i>Enterococcus faecium</i> and identification of a large transferable pathogenicity island. <i>BMC Genomics</i> , 2010, 11, 239.	2.8	190
10	Parallel Evolution of <i>Streptococcus pneumoniae</i> and <i>Streptococcus mitis</i> to Pathogenic and Mutualistic Lifestyles. <i>MBio</i> , 2014, 5, e01490-14.	4.1	159
11	Comparative genomics of the genus <i>Bifidobacterium</i> . <i>Microbiology (United Kingdom)</i> , 2010, 156, 3243-3254.	1.8	116
12	Essential Genes in the Core Genome of the Human Pathogen <i>Streptococcus pyogenes</i> . <i>Scientific Reports</i> , 2015, 5, 9838.	3.3	114
13	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
14	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
15	<i>Streptococcus pneumoniae</i> in Biofilms Are Unable to Cause Invasive Disease Due to Altered Virulence Determinant Production. <i>PLoS ONE</i> , 2011, 6, e28738.	2.5	99
16	Genome-Wide Identification of Genes Required for Fitness of Group A <i>Streptococcus</i> in Human Blood. <i>Infection and Immunity</i> , 2013, 81, 862-875.	2.2	98
17	Extensive genomic diversity of closely related <i>Wolbachia</i> strains. <i>Microbiology (United Kingdom)</i> , 2009, 155, 2211-2222.	1.8	87
18	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

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19	The two-component response regulator LiaR regulates cell wall stress responses, pili expression and virulence in group B Streptococcus. <i>Microbiology (United Kingdom)</i> , 2013, 159, 1521-1534.	1.8	74
20	Molecular epidemiology and genomics of group A Streptococcus. <i>Infection, Genetics and Evolution</i> , 2015, 33, 393-418.	2.3	65
21	<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
22	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
23	<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
24	Using Sybil for interactive comparative genomics of microbes on the web. <i>Bioinformatics</i> , 2012, 28, 160-166.	4.1	53
25	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
26	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
27	Sugar-Coated Killer: Serotype 3 Pneumococcal Disease. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 613287.	3.9	48
28	Genome flexibility in <i>Neisseria meningitidis</i> . <i>Vaccine</i> , 2009, 27, B103-B111.	3.8	47
29	Genome-wide discovery of novel M1T1 group A streptococcal determinants important for fitness and virulence during soft-tissue infection. <i>PLoS Pathogens</i> , 2017, 13, e1006584.	4.7	42
30	Whole-Genome Association Study on Tissue Tropism Phenotypes in Group A Streptococcus. <i>Journal of Bacteriology</i> , 2011, 193, 6651-6663.	2.2	41
31	The essential genome of <i>Streptococcus agalactiae</i> . <i>BMC Genomics</i> , 2016, 17, 406.	2.8	41
32	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
33	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
34	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
35	Improving pan-genome annotation using whole genome multiple alignment. <i>BMC Bioinformatics</i> , 2011, 12, 272.	2.6	38
36	Standardized Metadata for Human Pathogen/Vector Genomic Sequences. <i>PLoS ONE</i> , 2014, 9, e99979.	2.5	34

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37	The Streptococcus agalactiae Stringent Response Enhances Virulence and Persistence in Human Blood. Infection and Immunity, 2018, 86, .	2.2	31
38	Genomic Analysis Reveals the Molecular Basis for Capsule Loss in the Group B Streptococcus Population. PLoS ONE, 2015, 10, e0125985.	2.5	29
39	Whole-Exome Sequencing Identifies the 6q12-q16 Linkage Region and a Candidate Gene, <i>TTK</i>, for Pulmonary Nontuberculous Mycobacterial Disease. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 1599-1604.	5.6	28
40	Towards a universal group B Streptococcus vaccine using multistrain genome analysis. Expert Review of Vaccines, 2006, 5, 687-694.	4.4	27
41	Identification of novel cps locus polymorphisms in nontypable group B Streptococcus. Journal of Medical Microbiology, 2006, 55, 775-783.	1.8	24
42	Genomic Insights into the Emerging Human Pathogen Mycobacterium massiliense. Journal of Bacteriology, 2012, 194, 5450-5450.	2.2	22
43	Complete Genome Sequence of Streptococcus agalactiae CNCTC 10/84, a Hypervirulent Sequence Type 26 Strain. Genome Announcements, 2014, 2, .	0.8	22
44	In-silico prediction and deep-DNA sequencing validation indicate phase variation in 115 Neisseria meningitidis genes. BMC Genomics, 2016, 17, 843.	2.8	22
45	Bacterial Genome Sequencing. Methods in Molecular Biology, 2009, 551, 231-247.	0.9	19
46	ReVac: a reverse vaccinology computational pipeline for prioritization of prokaryotic protein vaccine candidates. BMC Genomics, 2019, 20, 981.	2.8	18
47	Use of a novel antigen expressing system to study the Salmonella enterica serovar Typhi protein recognition by T cells. PLoS Neglected Tropical Diseases, 2017, 11, e0005912.	3.0	16
48	Changes in IgA Protease Expression Are Conferred by Changes in Genomes during Persistent Infection by Nontypeable Haemophilus influenzae in Chronic Obstructive Pulmonary Disease. Infection and Immunity, 2018, 86, .	2.2	15
49	Persistence of Moraxella catarrhalis in Chronic Obstructive Pulmonary Disease and Regulation of the Hag/MID Adhesin. Journal of Infectious Diseases, 2019, 219, 1448-1455.	4.0	14
50	Comparative Genomics of Streptococcus Pneumoniae: Intrastrain Diversity and Genome Plasticity. , 2014, , 15-29.		12
51	Transcriptional organization of pneumococcal psrP-secY2A2 and impact of GtfA and GtfB deletion on PsrP-associated virulence properties. Microbes and Infection, 2017, 19, 323-333.	1.9	12
52	Genome-Wide fitness analysis of group B Streptococcus in human amniotic fluid reveals a transcription factor that controls multiple virulence traits. PLoS Pathogens, 2021, 17, e1009116.	4.7	11
53	The Pangenome: A Data-Driven Discovery in Biology. , 2020, , 3-20.		11
54	The Malaria Genome Sequencing Project. Expert Reviews in Molecular Medicine, 1998, 1, 1-9.	3.9	8

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55	Differential functional patterns of memory CD4+ and CD8+ T-cells from volunteers immunized with Ty21a typhoid vaccine observed using a recombinant Escherichia coli system expressing S. Typhi proteins. <i>Vaccine</i> , 2020, 38, 258-270.	3.8	7
56	Anatomical Site-Specific Carbohydrate Availability Impacts <i>Streptococcus pneumoniae</i> Virulence and Fitness during Colonization and Disease. <i>Infection and Immunity</i> , 2022, 90, IAI0045121.	2.2	7
57	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
58	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
59	Tissue specific diversification, virulence and immune response to <i>Mycobacterium bovis</i> BCG in a patient with an IFN- $\gamma$ R1 deficiency. <i>Virulence</i> , 2020, 11, 1656-1673.	4.4	5
60	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
61	Genomics, Genetic Variation, and Regions of Differences. , 2015, , 81-107.		2
62	Complete Genome Sequences of <i>Mycobacterium kansasii</i> Strains Isolated from Rhesus Macaques. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
63	Complete Genome Sequence of <i>Neisseria musculi</i> Using Illumina and PacBio Sequencing. <i>Microbiology Resource Announcements</i> , 2021, 10, e0045221.	0.6	2
64	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
65	Whole-Genome Sequences of Bacteremia Isolates of <i>Bordetella holmesii</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	0