

Leonor Sanchez-Bus

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

47
papers

1,256
citations

18
h-index

35
g-index

54
ext. papers

1,841
ext. citations

11.3
avg, IF

4.51
L-index

#	Paper	IF	Citations
47	Evolutionary processes in the emergence and recent spread of the syphilis agent, <i>Treponema pallidum</i> . <i>Molecular Biology and Evolution</i> , 2021 ,	8.3	2
46	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of <i>Neisseria gonorrhoeae</i> at Pathogenwatch. <i>Genome Medicine</i> , 2021 , 13, 61	14.4	22
45	A global resource for genomic predictions of antimicrobial resistance and surveillance of <i>Salmonella</i> Typhi at pathogenwatch. <i>Nature Communications</i> , 2021 , 12, 2879	17.4	12
44	<i>Neisseria gonorrhoeae</i> Sequence Typing for Antimicrobial Resistance (NG-STAR) clonal complexes are consistent with genomic phylogeny and provide simple nomenclature, rapid visualization and antimicrobial resistance (AMR) lineage predictions. <i>Journal of Antimicrobial Chemotherapy</i> , 2021 , 76, 940-944	5.1	6
43	High susceptibility to zoliflodacin and conserved target (GyrB) for zoliflodacin among 1209 consecutive clinical <i>Neisseria gonorrhoeae</i> isolates from 25 European countries, 2018. <i>Journal of Antimicrobial Chemotherapy</i> , 2021 , 76, 1221-1228	5.1	9
42	Phylogenomics of reveals a new lineage and a complex evolutionary history. <i>Microbial Genomics</i> , 2021 , 7,	4.4	29
41	Lean, mean, learning machines. <i>Nature Reviews Microbiology</i> , 2020 , 18, 266	22.2	1
40	Genomic evolution of <i>Neisseria gonorrhoeae</i> since the preantibiotic era (1928-2013): antimicrobial use/misuse selects for resistance and drives evolution. <i>BMC Genomics</i> , 2020 , 21, 116	4.5	29
39	Genomic and Phenotypic Variability in <i>Neisseria gonorrhoeae</i> Antimicrobial Susceptibility, England. <i>Emerging Infectious Diseases</i> , 2020 , 26, 505-515	10.2	13
38	Phylogenomic analysis of <i>Neisseria gonorrhoeae</i> transmission to assess sexual mixing and HIV transmission risk in England: a cross-sectional, observational, whole-genome sequencing study. <i>Lancet Infectious Diseases</i> , 2020 , 20, 478-486	25.5	10
37	Increased power from conditional bacterial genome-wide association identifies macrolide resistance mutations in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020 , 11, 5374	17.4	18
36	Adaptation to the cervical environment is associated with increased antibiotic susceptibility in <i>Neisseria gonorrhoeae</i> . <i>Nature Communications</i> , 2020 , 11, 4126	17.4	26
35	Evaluation of parameters affecting performance and reliability of machine learning-based antibiotic susceptibility testing from whole genome sequencing data. <i>PLoS Computational Biology</i> , 2019 , 15, e1007349	5	34
34	Genomic determinants of speciation and spread of the complex. <i>Science Advances</i> , 2019 , 5, eaaw3307	14.3	37
33	Molecular epidemiology and whole genome sequencing analysis of clinical <i>Mycobacterium bovis</i> from Ghana. <i>PLoS ONE</i> , 2019 , 14, e0209395	3.7	10
32	The impact of antimicrobials on gonococcal evolution. <i>Nature Microbiology</i> , 2019 , 4, 1941-1950	26.6	53
31	Using genomics to understand antimicrobial resistance and transmission in <i>Neisseria gonorrhoeae</i> . <i>Microbial Genomics</i> , 2019 , 5,	4.4	7

30	Genome-wide epistasis and co-selection study using mutual information. <i>Nucleic Acids Research</i> , 2019 , 47, e112	20.1	19
29	Genetic variation regulates the activation and specificity of Restriction-Modification systems in <i>Neisseria gonorrhoeae</i> . <i>Scientific Reports</i> , 2019 , 9, 14685	4.9	10
28	Comparative genomics of <i>Mycobacterium africanum</i> Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. <i>Scientific Reports</i> , 2018 , 8, 11269	4.9	24
27	Antimicrobial resistance prediction and phylogenetic analysis of <i>Neisseria gonorrhoeae</i> isolates using the Oxford Nanopore MinION sequencer. <i>Scientific Reports</i> , 2018 , 8, 17596	4.9	41
26	Public health surveillance of multidrug-resistant clones of <i>Neisseria gonorrhoeae</i> in Europe: a genomic survey. <i>Lancet Infectious Diseases</i> , 2018 , 18, 758-768	25.5	112
25	Bringing <i>Treponema</i> into the spotlight. <i>Nature Reviews Microbiology</i> , 2017 , 15, 196	22.2	2
24	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. <i>Microbial Genomics</i> , 2017 , 3, e000131	4.4	283
23	Dynamics and impact of homologous recombination on the evolution of <i>Legionella pneumophila</i> . <i>PLoS Genetics</i> , 2017 , 13, e1006855	6	21
22	Genomic epidemiology of a national outbreak of post-surgical wound infections in Brazil. <i>Microbial Genomics</i> , 2017 , 3, e000111	4.4	15
21	Origin of modern syphilis and emergence of a pandemic <i>Treponema pallidum</i> cluster. <i>Nature Microbiology</i> , 2016 , 2, 16245	26.6	81
20	Linking an unchained malady. <i>Nature Reviews Microbiology</i> , 2016 , 14, 608	22.2	
19	The novel 2016 WHO <i>Neisseria gonorrhoeae</i> reference strains for global quality assurance of laboratory investigations: phenotypic, genetic and reference genome characterization. <i>Journal of Antimicrobial Chemotherapy</i> , 2016 , 71, 3096-3108	5.1	166
18	Genomic Analysis of Bacterial Outbreaks 2016 , 203-232		
17	Geographical and Temporal Structures of <i>Legionella pneumophila</i> Sequence Types in Comunitat Valenciana (Spain), 1998 to 2013. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 7106-13	4.8	9
16	Phylogenetic analysis of environmental <i>Legionella pneumophila</i> isolates from an endemic area (Alcoy, Spain). <i>Infection, Genetics and Evolution</i> , 2015 , 30, 45-54	4.5	6
15	Genomic Investigation of a Legionellosis Outbreak in a Persistently Colonized Hotel. <i>Frontiers in Microbiology</i> , 2015 , 6, 1556	5.7	24
14	Mixed infection by <i>Legionella pneumophila</i> in outbreak patients. <i>International Journal of Medical Microbiology</i> , 2014 , 304, 307-13	3.7	15
13	Recombination drives genome evolution in outbreak-related <i>Legionella pneumophila</i> isolates. <i>Nature Genetics</i> , 2014 , 46, 1205-11	36.3	60

12	Genetic Characterization of <i>Legionella pneumophila</i> Isolated from a Common Watershed in Comunidad Valenciana, Spain. <i>PLoS ONE</i> , 2013 , 8, e61564	3-7	5
11	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads		13
10	Increased antibiotic susceptibility in <i>Neisseria gonorrhoeae</i> through adaptation to the cervical environment		5
9	Increased power from bacterial genome-wide association conditional on known effects identifies <i>Neisseria gonorrhoeae</i> macrolide resistance mutations in the 50S ribosomal protein L4		4
8	Phylogenomics of <i>Mycobacterium africanum</i> reveals a new lineage and a complex evolutionary history		4
7	A global resource for genomic predictions of antimicrobial resistance and surveillance of <i>Salmonella Typhi</i> at Pathogenwatch		2
6	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of <i>Neisseria gonorrhoeae</i> at Pathogenwatch		1
5	Genomic determinants of speciation and spread of the <i>Mycobacterium tuberculosis</i> complex		1
4	Antimicrobial exposure in sexual networks drives divergent evolution in modern gonococci		4
3	Molecular epidemiology and whole genome sequencing analysis of clinical <i>Mycobacterium bovis</i> from Ghana		2
2	Genome-wide epistasis and co-selection study using mutual information		3
1	Evaluation of parameters affecting performance and reliability of machine learning-based antibiotic susceptibility testing from whole genome sequencing data		3