Leonor Snchez-Bus

List of Publications by Citations

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	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. *Microbial Genomics*, **2017**, 3, e000131	4.4	283
46	The novel 2016 WHO Neisseria gonorrhoeae reference strains for global quality assurance of laboratory investigations: phenotypic, genetic and reference genome characterization. *Journal of Antimicrobial Chemotherapy*, **2016**, 71, 3096-3108	5.1	166
45	Public health surveillance of multidrug-resistant clones of Neisseria gonorrhoeae in Europe: a genomic survey. *Lancet Infectious Diseases, The*, **2018**, 18, 758-768	25.5	112
44	Origin of modern syphilis and emergence of a pandemic Treponema pallidum cluster. *Nature Microbiology*, **2016**, 2, 16245	26.6	81
43	Recombination drives genome evolution in outbreak-related Legionella pneumophila isolates. *Nature Genetics*, **2014**, 46, 1205-11	36.3	60
42	The impact of antimicrobials on gonococcal evolution. *Nature Microbiology*, **2019**, 4, 1941-1950	26.6	53
41	Antimicrobial resistance prediction and phylogenetic analysis of Neisseria gonorrhoeae isolates using the Oxford Nanopore MinION sequencer. *Scientific Reports*, **2018**, 8, 17596	4.9	41
40	Genomic determinants of speciation and spread of the complex. *Science Advances*, **2019**, 5, eaaw3307	14.3	37
39	Evaluation of parameters affecting performance and reliability of machine learning-based antibiotic susceptibility testing from whole genome sequencing data. *PLoS Computational Biology*, **2019**, 15, e1007349	5	34
38	Genomic evolution of Neisseria gonorrhoeae since the preantibiotic era (1928-2013): antimicrobial use/misuse selects for resistance and drives evolution. *BMC Genomics*, **2020**, 21, 116	4.5	29
37	Phylogenomics of reveals a new lineage and a complex evolutionary history. *Microbial Genomics*, **2021**, 7,	4.4	29
36	Adaptation to the cervical environment is associated with increased antibiotic susceptibility in Neisseria gonorrhoeae. *Nature Communications*, **2020**, 11, 4126	17.4	26
35	Comparative genomics of Mycobacterium africanum Lineage 5 and Lineage 6 from Ghana suggests distinct ecological niches. *Scientific Reports*, **2018**, 8, 11269	4.9	24
34	Genomic Investigation of a Legionellosis Outbreak in a Persistently Colonized Hotel. *Frontiers in Microbiology*, **2015**, 6, 1556	5.7	24
33	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of Neisseria gonorrhoeae at Pathogenwatch. *Genome Medicine*, **2021**, 13, 61	14.4	22
32	Dynamics and impact of homologous recombination on the evolution of Legionella pneumophila. *PLoS Genetics*, **2017**, 13, e1006855	6	21
31	Genome-wide epistasis and co-selection study using mutual information. *Nucleic Acids Research*, **2019**, 47, e112	20.1	19

30	Increased power from conditional bacterial genome-wide association identifies macrolide resistance mutations in Neisseria gonorrhoeae. *Nature Communications*, **2020**, 11, 5374	17.4	18
29	Mixed infection by Legionella pneumophila in outbreak patients. *International Journal of Medical Microbiology*, **2014**, 304, 307-13	3.7	15
28	Genomic epidemiology of a national outbreak of post-surgical wound infections in Brazil. *Microbial Genomics*, **2017**, 3, e000111	4.4	15
27	Genomic and Phenotypic Variability in Neisseria gonorrhoeae Antimicrobial Susceptibility, England. *Emerging Infectious Diseases*, **2020**, 26, 505-515	10.2	13
26	ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads		13
25	A global resource for genomic predictions of antimicrobial resistance and surveillance of Salmonella Typhi at pathogenwatch. *Nature Communications*, **2021**, 12, 2879	17.4	12
24	Molecular epidemiology and whole genome sequencing analysis of clinical Mycobacterium bovis from Ghana. *PLoS ONE*, **2019**, 14, e0209395	3.7	10
23	Phylogenomic analysis of Neisseria gonorrhoeae transmission to assess sexual mixing and HIV transmission risk in England: a cross-sectional, observational, whole-genome sequencing study. *Lancet Infectious Diseases, The*, **2020**, 20, 478-486	25.5	10
22	Genetic variation regulates the activation and specificity of Restriction-Modification systems in Neisseria gonorrhoeae. *Scientific Reports*, **2019**, 9, 14685	4.9	10
21	Geographical and Temporal Structures of Legionella pneumophila Sequence Types in Comunitat Valenciana (Spain), 1998 to 2013. *Applied and Environmental Microbiology*, **2015**, 81, 7106-13	4.8	9
20	High susceptibility to zoliflodacin and conserved target (GyrB) for zoliflodacin among 1209 consecutive clinical Neisseria gonorrhoeae isolates from 25 European countries, 2018. *Journal of Antimicrobial Chemotherapy*, **2021**, 76, 1221-1228	5.1	9
19	Using genomics to understand antimicrobial resistance and transmission in Neisseria gonorrhoeae. *Microbial Genomics*, **2019**, 5,	4.4	7
18	Phylogenetic analysis of environmental Legionella pneumophila isolates from an endemic area (Alcoy, Spain). *Infection, Genetics and Evolution*, **2015**, 30, 45-54	4.5	6
17	Neisseria gonorrhoeae 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. *Journal of Antimicrobial Chemotherapy*, **2021**, 76, 940-944	5.1	6
16	Genetic Characterization of Legionella pneumophila Isolated from a Common Watershed in Comunidad Valenciana, Spain. *PLoS ONE*, **2013**, 8, e61564	3.7	5
15	Increased antibiotic susceptibility in Neisseria gonorrhoeae through adaptation to the cervical environment		5
14	Increased power from bacterial genome-wide association conditional on known effects identifies Neisseria gonorrhoeae macrolide resistance mutations in the 50S ribosomal protein L4		4
13	Phylogenomics of Mycobacterium africanum reveals a new lineage and a complex evolutionary history		4

12	Antimicrobial exposure in sexual networks drives divergent evolution in modern gonococci		4
11	Genome-wide epistasis and co-selection study using mutual information		3
10	Evaluation of parameters affecting performance and reliability of machine learning-based antibiotic susceptibility testing from whole genome sequencing data		3
9	Bringing Treponema into the spotlight. *Nature Reviews Microbiology*, **2017**, 15, 196	22.2	2
8	Evolutionary processes in the emergence and recent spread of the syphilis agent, Treponema pallidum. *Molecular Biology and Evolution*, **2021**,	8.3	2
7	A global resource for genomic predictions of antimicrobial resistance and surveillance of Salmonella Typhi at Pathogenwatch		2
6	Molecular epidemiology and whole genome sequencing analysis of clinical Mycobacterium bovis from Ghana		2
5	Lean, mean, learning machines. *Nature Reviews Microbiology*, **2020**, 18, 266	22.2	1
4	A community-driven resource for genomic epidemiology and antimicrobial resistance prediction of Neisseria gonorrhoeae at Pathogenwatch		1
3	Genomic determinants of speciation and spread of the Mycobacterium tuberculosis complex		1
2	Linking an unchained malady. *Nature Reviews Microbiology*, **2016**, 14, 608	22.2	
1	Genomic Analysis of Bacterial Outbreaks **2016**, 203-232		