

# Claire Bertelli

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7444502/publications.pdf>

Version: 2024-02-01

61  
papers

4,252  
citations

201575

27  
h-index

123376

61  
g-index

65  
all docs

65  
docs citations

65  
times ranked

5816  
citing authors

#	ARTICLE	IF	CITATIONS
1	IslandViewer 4: expanded prediction of genomic islands for larger-scale datasets. <i>Nucleic Acids Research</i> , 2017, 45, W30-W35.	6.5	1,251
2	EDGAR 2.0: an enhanced software platform for comparative gene content analyses. <i>Nucleic Acids Research</i> , 2016, 44, W22-W28.	6.5	398
3	Genome of <i>Acanthamoeba castellanii</i> highlights extensive lateral gene transfer and early evolution of tyrosine kinase signaling. <i>Genome Biology</i> , 2013, 14, R11.	13.9	296
4	Rapid bacterial genome sequencing: methods and applications in clinical microbiology. <i>Clinical Microbiology and Infection</i> , 2013, 19, 803-813.	2.8	186
5	Lausannevirus, a giant amoebal virus encoding histone doublets. <i>Environmental Microbiology</i> , 2011, 13, 1454-1466.	1.8	164
6	Genotypes Associated with <i>Listeria monocytogenes</i> Isolates Displaying Impaired or Enhanced Tolerances to Cold, Salt, Acid, or Desiccation Stress. <i>Frontiers in Microbiology</i> , 2017, 8, 369.	1.5	147
7	Improved genomic island predictions with IslandPath-DIMOB. <i>Bioinformatics</i> , 2018, 34, 2161-2167.	1.8	127
8	<i>Bifidobacterium longum</i> Bacteremia in Preterm Infants Receiving Probiotics. <i>Clinical Infectious Diseases</i> , 2015, 60, 924-927.	2.9	117
9	The <i>Waddlia</i> Genome: A Window into Chlamydial Biology. <i>PLoS ONE</i> , 2010, 5, e10890.	1.1	104
10	Microbial genomic island discovery, visualization and analysis. <i>Briefings in Bioinformatics</i> , 2019, 20, 1685-1698.	3.2	86
11	Reduced Chlorine in Drinking Water Distribution Systems Impacts Bacterial Biodiversity in Biofilms. <i>Frontiers in Microbiology</i> , 2018, 9, 2520.	1.5	73
12	High Throughput Sequencing and Proteomics to Identify Immunogenic Proteins of a New Pathogen: The Dirty Genome Approach. <i>PLoS ONE</i> , 2009, 4, e8423.	1.1	70
13	Lateral gene exchanges shape the genomes of amoeba-resisting microorganisms. <i>Frontiers in Cellular and Infection Microbiology</i> , 2012, 2, 110.	1.8	70
14	Genomic characterisation of an international <i>Pseudomonas aeruginosa</i> reference panel indicates that the two major groups draw upon distinct mobile gene pools. <i>FEMS Microbiology Letters</i> , 2018, 365, .	0.7	67
15	The SIB Swiss Institute of Bioinformatics's™ resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016, 44, D27-D37.	6.5	64
16	Taxogenomics of the order Chlamydiales. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2015, 65, 1381-1393.	0.8	61
17	Comparative genome analysis of <i>Pseudomonas knackmussii</i> 13, the first bacterium known to degrade chloroaromatic compounds. <i>Environmental Microbiology</i> , 2015, 17, 91-104.	1.8	52
18	Insight into cross-talk between intra-amoebal pathogens. <i>BMC Genomics</i> , 2011, 12, 542.	1.2	47

#	ARTICLE	IF	CITATIONS
19	Letter to the editor: SARS-CoV-2 detection by real-time RT-PCR. <i>Eurosurveillance</i> , 2020, 25, .	3.9	41
20	Distinct Genomic Features Characterize Two Clades of <i>Corynebacterium diphtheriae</i> : Proposal of <i>Corynebacterium diphtheriae</i> Subsp. <i>diphtheriae</i> Subsp. nov. and <i>Corynebacterium diphtheriae</i> Subsp. <i>lausannense</i> Subsp. nov.. <i>Frontiers in Microbiology</i> , 2018, 9, 1743.	1.5	38
21	RNA pentaloop structures as effective targets of regulators belonging to the RsmA/CsrA protein family. <i>RNA Biology</i> , 2013, 10, 1030-1041.	1.5	37
22	Phylogenomics reveal that <i>Mycobacterium kansasii</i> subtypes are species-level lineages. Description of <i>Mycobacterium pseudokansasii</i> sp. nov., <i>Mycobacterium innocens</i> sp. nov. and <i>Mycobacterium attenuatum</i> sp. nov.. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2019, 69, 1696-1704.	0.8	37
23	<i>Cedratvirus lausannensis</i> “digging into <i>Pithoviridae</i> diversity. <i>Environmental Microbiology</i> , 2017, 19, 4022-4034.	1.8	36
24	Genome of the carbapenemase-producing clinical isolate <i>Elizabethkingia miricola</i> EM_CHUV and comparative genomics with <i>Elizabethkingia meningoseptica</i> and <i>Elizabethkingia anophelis</i> : evidence for intrinsic multidrug resistance trait of emerging pathogens. <i>International Journal of Antimicrobial Agents</i> , 2017, 49, 93-97.	1.1	34
25	Environmental Metagenomic Assemblies Reveal Seven New Highly Divergent Chlamydial Lineages and Hallmarks of a Conserved Intracellular Lifestyle. <i>Frontiers in Microbiology</i> , 2018, 9, 79.	1.5	34
26	Comparative genomics of koala, cattle and sheep strains of <i>Chlamydia pecorum</i> . <i>BMC Genomics</i> , 2014, 15, 667.	1.2	33
27	Assessment of SARS-CoV-2 Genome Sequencing: Quality Criteria and Low-Frequency Variants. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0094421.	1.8	33
28	Sequencing and characterizing the genome of <i>Estrella lausannensis</i> as an undergraduate project: training students and biological insights. <i>Frontiers in Microbiology</i> , 2015, 6, 101.	1.5	32
29	SARS-CoV-2 N501Y Introductions and Transmissions in Switzerland from Beginning of October 2020 to February 2021”Implementation of Swiss-Wide Diagnostic Screening and Whole Genome Sequencing. <i>Microorganisms</i> , 2021, 9, 677.	1.6	32
30	Recommendations for accurate genotyping of SARS-CoV-2 using amplicon-based sequencing of clinical samples. <i>Clinical Microbiology and Infection</i> , 2021, 27, 1036.e1-1036.e8.	2.8	32
31	Lausannevirus Seroprevalence among Asymptomatic Young Adults. <i>Intervirology</i> , 2013, 56, 430-433.	1.2	29
32	Genome sequencing and functional characterization of the non-pathogenic <i>Klebsiella pneumoniae</i> KpGe bacteria. <i>Microbes and Infection</i> , 2018, 20, 293-301.	1.0	28
33	Decreased Fetal Movements: A Sign of Placental SARS-CoV-2 Infection with Perinatal Brain Injury. <i>Viruses</i> , 2021, 13, 2517.	1.5	28
34	Low prevalence of <i>Chlamydia trachomatis</i> infection in asymptomatic young Swiss men. <i>BMC Infectious Diseases</i> , 2008, 8, 45.	1.3	27
35	Trimethylamine-N-Oxide Postprandial Response in Plasma and Urine Is Lower After Fermented Compared to Non-Fermented Dairy Consumption in Healthy Adults. <i>Nutrients</i> , 2020, 12, 234.	1.7	27
36	Molecular diagnosis and enrichment culture identified a septic pseudoarthrosis due to an infection with <i>Erysipelatoclostridium ramosum</i> . <i>International Journal of Infectious Diseases</i> , 2019, 81, 167-169.	1.5	26

#	ARTICLE	IF	CITATIONS
37	The Genome of the Toluene-Degrading <i>Pseudomonas veronii</i> Strain 1YdBTEX2 and Its Differential Gene Expression in Contaminated Sand. <i>PLoS ONE</i> , 2016, 11, e0165850.	1.1	24
38	CRISPR System Acquisition and Evolution of an Obligate Intracellular <i>Chlamydia</i> -Related Bacterium. <i>Genome Biology and Evolution</i> , 2016, 8, 2376-2386.	1.1	23
39	Whole-genome sequencing for rapid, reliable and routine investigation of <i>Mycobacterium tuberculosis</i> transmission in local communities. <i>New Microbes and New Infections</i> , 2019, 31, 100582.	0.8	21
40	Sequencing the Obligate Intracellular <i>Rhadinobdychlamydia helvetica</i> within Its Tick Host <i>Ixodes ricinus</i> to Investigate Their Symbiotic Relationship. <i>Genome Biology and Evolution</i> , 2019, 11, 1334-1344.	1.1	21
41	Comparative genomics of <i>Neisseria meningitidis</i> strains: new targets for molecular diagnostics. <i>Clinical Microbiology and Infection</i> , 2016, 22, 568.e1-568.e7.	2.8	18
42	Crescent and star shapes of members of the Chlamydiales order: impact of fixative methods. <i>Antonie Van Leeuwenhoek</i> , 2013, 104, 521-532.	0.7	17
43	<i>Criblamydia sequanensis</i> Harbors a Megaplasmid Encoding Arsenite Resistance. <i>Genome Announcements</i> , 2014, 2, .	0.8	16
44	External Quality Assessment of SARS-CoV-2 Sequencing: an ESGMD-SSM Pilot Trial across 15 European Laboratories. <i>Journal of Clinical Microbiology</i> , 2022, 60, JCM0169821.	1.8	13
45	ChlamDB: a comparative genomics database of the phylum Chlamydiae and other members of the Planctomycetes-Verrucomicrobiae-Chlamydiae superphylum. <i>Nucleic Acids Research</i> , 2020, 48, D526-D534.	6.5	11
46	Enabling genomic island prediction and comparison in multiple genomes to investigate bacterial evolution and outbreaks. <i>Microbial Genomics</i> , 2022, 8, .	1.0	10
47	NGS-Based <i>S. aureus</i> Typing and Outbreak Analysis in Clinical Microbiology Laboratories: Lessons Learned From a Swiss-Wide Proficiency Test. <i>Frontiers in Microbiology</i> , 2020, 11, 591093.	1.5	9
48	One Year Genome Evolution of Lausannevirus in Allopatric versus Sympatric Conditions. <i>Genome Biology and Evolution</i> , 2017, 9, 1432-1449.	1.1	8
49	Resistome Analysis of a Carbapenemase (OXA-48)-Producing and Colistin-Resistant <i>Klebsiella pneumoniae</i> Strain. <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	1.4	8
50	AB569, a nontoxic chemical tandem that kills major human pathogenic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4921-4930.	3.3	6
51	<i>Chlamydia pneumoniae</i> and <i>Mycoplasma pneumoniae</i> in children with cystic fibrosis: impact on bacterial respiratory microbiota diversity. <i>Pathogens and Disease</i> , 2021, 79, .	0.8	6
52	Building up a clinical microbiota profiling: a quality framework proposal. <i>Critical Reviews in Microbiology</i> , 2022, 48, 356-375.	2.7	6
53	Insights into Mobile Genetic Elements of the Biocide-Degrading Bacterium <i>Pseudomonas nitroreducens</i> HBP-1. <i>Genes</i> , 2020, 11, 930.	1.0	5
54	Genome sequencing of <i>Mycobacterium tuberculosis</i> clinical isolates revealed isoniazid resistance mechanisms undetected by conventional molecular methods. <i>International Journal of Antimicrobial Agents</i> , 2020, 56, 106068.	1.1	5

#	ARTICLE	IF	CITATIONS
55	Pathogenic Determinants of the <i>Mycobacterium kansasii</i> Complex: An Unsuspected Role for Distributive Conjugal Transfer. <i>Microorganisms</i> , 2021, 9, 348.	1.6	5
56	Performance evaluation of the Becton Dickinson Kiestraâ„¢ IdentifA/SusceptA. <i>Clinical Microbiology and Infection</i> , 2020, 27, 1167.e9-1167.e17.	2.8	4
57	Microbiota and Metabolite Modifications after Dietary Exclusion of Dairy Products and Reduced Consumption of Fermented Food in Young and Older Men. <i>Nutrients</i> , 2021, 13, 1905.	1.7	4
58	Piperacillin/tazobactam selects an ampC derepressed <i>E.Âcloacae</i> complex mutant in a diabetic osteoarticular infection. <i>Clinical Microbiology and Infection</i> , 2021, 27, 475-477.	2.8	3
59	Unexpected associations between respiratory viruses and bacteria with Pulmonary Function Testing in children suffering from Cystic Fibrosis (MUCOVIB study). <i>Journal of Cystic Fibrosis</i> , 2022, 21, e158-e164.	0.3	2
60	Prevalence of multidrug-resistant bacteria colonisation among asylum seekers in western Switzerland. <i>Journal of Infection Prevention</i> , 2021, 22, 173-176.	0.5	1
61	Phyla Related to Planctomycetes: Members of Phylum Chlamydiae and Their Implications for Planctomycetes <i>Cell Biology</i> . , 2013, , 229-241.		1