

Darina Cejkova

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/5740811/darina-cejkova-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

37
papers

983
citations

20
h-index

31
g-index

38
ext. papers

1,341
ext. citations

4
avg, IF

3.85
L-index

#	Paper	IF	Citations
37	Pyocin-mediated antagonistic interactions in <i>Pseudomonas</i> spp. isolated in James Ross Island, Antarctica. <i>Environmental Microbiology</i> , 2021 ,	5.2	0
36	Clinical Characteristics of Patients with Tick-Borne Encephalitis (TBE): A European Multicentre Study from 2010 to 2017. <i>Microorganisms</i> , 2021 , 9,	4.9	6
35	The distribution of antibiotic resistance genes in chicken gut microbiota commensals. <i>Scientific Reports</i> , 2021 , 11, 3290	4.9	3
34	Carbapenemase-Producing Gram-Negative Bacteria from American Crows in the United States. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 65,	5.9	1
33	Genomic analysis of <i>Escherichia coli</i> strains isolated from diseased chicken in the Czech Republic. <i>BMC Veterinary Research</i> , 2020 , 16, 189	2.7	16
32	Whole genome sequence of the <i>Treponema pallidum</i> subsp. endemicum strain Iraq B: A subpopulation of bejel treponemes contains full-length tprF and tprG genes similar to those present in <i>T. p.</i> subsp. pertenue strains. <i>PLoS ONE</i> , 2020 , 15, e0230926	3.7	3
31	Genome sequences of two Antarctic strains of <i>Pseudomonas prosekii</i> : insights into adaptation to extreme conditions. <i>Archives of Microbiology</i> , 2020 , 202, 447-454	3	2
30	Directly Sequenced Genomes of Contemporary Strains of Syphilis Reveal Recombination-Driven Diversity in Genes Encoding Predicted Surface-Exposed Antigens. <i>Frontiers in Microbiology</i> , 2019 , 10, 1691	5.7	15
29	Contact with adult hen affects development of caecal microbiota in newly hatched chicks. <i>PLoS ONE</i> , 2019 , 14, e0212446	3.7	49
28	Gut Anaerobes Capable of Chicken Caecum Colonisation. <i>Microorganisms</i> , 2019 , 7,	4.9	15
27	Use of 16S rRNA gene sequencing for prediction of new opportunistic pathogens in chicken ileal and cecal microbiota. <i>Poultry Science</i> , 2019 , 98, 2347-2353	3.9	20
26	Whole genome sequencing and function prediction of 133 gut anaerobes isolated from chicken caecum in pure cultures. <i>BMC Genomics</i> , 2018 , 19, 561	4.5	54
25	Effects of host genetics and environmental conditions on fecal microbiota composition of pigs. <i>PLoS ONE</i> , 2018 , 13, e0201901	3.7	28
24	Sequencing of <i>Treponema pallidum</i> subsp. <i>pallidum</i> from isolate UZ1974 using Anti-Treponemal Antibodies Enrichment: First complete whole genome sequence obtained directly from human clinical material. <i>PLoS ONE</i> , 2018 , 13, e0202619	3.7	9
23	Characterization of blaKPC-3-positive plasmids from an <i>Enterobacter aerogenes</i> isolated from a corvid in Canada. <i>Journal of Antimicrobial Chemotherapy</i> , 2018 , 73, 2573-2575	5.1	2
22	Complete genome sequences of two strains of <i>Treponema pallidum</i> subsp. <i>pertenue</i> from Indonesia: Modular structure of several treponemal genes. <i>PLoS Neglected Tropical Diseases</i> , 2018 , 12, e0006867	4.8	12
21	Complete genome sequences of two strains of <i>Treponema pallidum</i> subsp. <i>pertenue</i> from Ghana, Africa: Identical genome sequences in samples isolated more than 7 years apart. <i>PLoS Neglected Tropical Diseases</i> , 2017 , 11, e0005894	4.8	20

20	Two highly divergent lineages of exfoliative toxin B-encoding plasmids revealed in impetigo strains of <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2017 , 307, 291-296	3.7	8
19	Antibiotic Resistance, Core-Genome and Protein Expression in IncHI1 Plasmids in <i>Salmonella</i> Typhimurium. <i>Genome Biology and Evolution</i> , 2016 , 8, 1661-71	3.9	16
18	Microcin determinants are associated with B2 phylogroup of human fecal <i>Escherichia coli</i> isolates. <i>MicrobiologyOpen</i> , 2016 , 5, 490-8	3.4	21
17	Curcuma and <i>Scutellaria</i> plant extracts protect chickens against inflammation and <i>Salmonella</i> Enteritidis infection. <i>Poultry Science</i> , 2015 , 94, 2049-58	3.9	20
16	A Retrospective Study on Genetic Heterogeneity within <i>Treponema</i> Strains: Subpopulations Are Genetically Distinct in a Limited Number of Positions. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0004110	4.8	15
15	Characterization of Antibiotic Resistance Gene Abundance and Microbiota Composition in Feces of Organic and Conventional Pigs from Four EU Countries. <i>PLoS ONE</i> , 2015 , 10, e0132892	3.7	28
14	Succession and replacement of bacterial populations in the caecum of egg laying hens over their whole life. <i>PLoS ONE</i> , 2014 , 9, e115142	3.7	99
13	Whole genome sequence of the <i>Treponema pallidum</i> subsp. endemicum strain Bosnia A: the genome is related to yaws treponemes but contains few loci similar to syphilis treponemes. <i>PLoS Neglected Tropical Diseases</i> , 2014 , 8, e3261	4.8	39
12	Characterization of egg laying hen and broiler fecal microbiota in poultry farms in Croatia, Czech Republic, Hungary and Slovenia. <i>PLoS ONE</i> , 2014 , 9, e110076	3.7	50
11	Whole genome sequence of the <i>Treponema</i> Fribourg-Blanc: unspecified simian isolate is highly similar to the yaws subspecies. <i>PLoS Neglected Tropical Diseases</i> , 2013 , 7, e2172	4.8	45
10	Structure of <i>rrn</i> operons in pathogenic non-cultivable treponemes: sequence but not genomic position of intergenic spacers correlates with classification of <i>Treponema pallidum</i> and <i>Treponema paraluis-cuniculi</i> strains. <i>Journal of Medical Microbiology</i> , 2013 , 62, 196-207	3.2	25
9	Resequencing of <i>Treponema pallidum</i> ssp. <i>pallidum</i> strains Nichols and SS14: correction of sequencing errors resulted in increased separation of syphilis treponeme subclusters. <i>PLoS ONE</i> , 2013 , 8, e74319	3.7	53
8	Human <i>Escherichia coli</i> strains of different geographical and time source: bacteriocin types and their gene sequences are population-specific. <i>Environmental Microbiology Reports</i> , 2012 , 4, 459-66	3.7	10
7	Whole genome sequence of <i>Treponema pallidum</i> ssp. <i>pallidum</i> , strain Mexico A, suggests recombination between yaws and syphilis strains. <i>PLoS Neglected Tropical Diseases</i> , 2012 , 6, e1832	4.8	59
6	Whole genome sequences of three <i>Treponema pallidum</i> ssp. <i>pertenue</i> strains: yaws and syphilis treponemes differ in less than 0.2% of the genome sequence. <i>PLoS Neglected Tropical Diseases</i> , 2012 , 6, e1471	4.8	86
5	Complete genome sequence of <i>Treponema pallidum</i> strain DAL-1. <i>Standards in Genomic Sciences</i> , 2012 , 7, 12-21		32
4	Whole Genome Analyses of Treponemes: New Targets for Strain- and Subspecies-Specific Molecular Diagnostics 2011 ,		2
3	Complete genome sequence of <i>Treponema paraluis-cuniculi</i> , strain Cuniculi A: the loss of infectivity to humans is associated with genome decay. <i>PLoS ONE</i> , 2011 , 6, e20415	3.7	51

2	Genome analysis of <i>Treponema pallidum</i> subsp. <i>pallidum</i> and subsp. <i>pertenue</i> strains: most of the genetic differences are localized in six regions. <i>PLoS ONE</i> , 2010 , 5, e15713	3-7	48
1	Complete sequence of low-copy-number plasmid MccC7-H22 of probiotic <i>Escherichia coli</i> H22 and the prevalence of <i>mcc</i> genes among human <i>E. coli</i> . <i>Plasmid</i> , 2008 , 59, 1-10	3-3	21