

Angelika Fruth

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

2,623
citations

623734

14
h-index

552781

26
g-index

26
all docs

26
docs citations

26
times ranked

3170
citing authors

#	ARTICLE	IF	CITATIONS
1	Zoonotic bacteria in clinically healthy goats in petting zoo settings of zoological gardens in Germany. <i>Zoonoses and Public Health</i> , 2022, , .	2.2	3
2	Influence of <i>Salmonella</i> specific bacteriophages (O1; S16) on the shedding of naturally occurring <i>Salmonella</i> and an orally applied <i>Salmonella</i> Eastbourne strain in bearded dragons (<i>Pogona vitticeps</i>). <i>Veterinary Medicine and Science</i> , 2021, 7, 534-547.	1.6	3
3	The Superior Adherence Phenotype of <i>E. coli</i> O104:H4 is Directly Mediated by the Aggregative Adherence Fimbriae Type I. <i>Virulence</i> , 2021, 12, 346-359.	4.4	9
4	Genome-wide insights into population structure and host specificity of <i>Campylobacter jejuni</i> . <i>Scientific Reports</i> , 2021, 11, 10358.	3.3	18
5	Genetic diversity and pathogenic potential of Shiga toxin-producing <i>Escherichia coli</i> (STEC) derived from German flour. <i>International Journal of Food Microbiology</i> , 2021, 347, 109197.	4.7	7
6	Population structure-guided profiling of antibiotic resistance patterns in clinical <i>Listeria monocytogenes</i> isolates from Germany identifies <i>pbpB3</i> alleles associated with low levels of cephalosporin resistance. <i>Emerging Microbes and Infections</i> , 2020, 9, 1804-1813.	6.5	18
7	Simple differentiation of <i>Salmonella</i> Typhi, Paratyphi and Choleraesuis from <i>Salmonella</i> species using the eazyplex TyphiTyper LAMP assay. <i>Journal of Medical Microbiology</i> , 2020, 69, 817-823.	1.8	2
8	Whole-Genome-Based Public Health Surveillance of Less Common Shiga Toxin-Producing <i>Escherichia coli</i> Serovars and Untypeable Strains Identifies Four Novel O Genotypes. <i>Journal of Clinical Microbiology</i> , 2019, 57, .	3.9	25
9	The use of a salmonella bacteriophage in bearded dragons: application, passage time and reisolation. <i>Tierärztliche Praxis Ausgabe K: Kleintiere - Heimtiere</i> , 2019, 47, 247-256.	0.5	3
10	Novel type of pilus associated with a Shiga-toxigenic <i>E. coli</i> hybrid pathovar conveys aggregative adherence and bacterial virulence. <i>Emerging Microbes and Infections</i> , 2018, 7, 1-16.	6.5	21
11	Attack of the clones: whole genome-based characterization of two closely related enterohemorrhagic <i>Escherichia coli</i> O26 epidemic lineages. <i>BMC Genomics</i> , 2018, 19, 647.	2.8	7
12	Shiga toxin-producing <i>Escherichia coli</i> O103:H2 outbreak in Germany after school trip to Austria due to raw cow milk, 2017 – The important role of international collaboration for outbreak investigations. <i>International Journal of Medical Microbiology</i> , 2018, 308, 539-544.	3.6	35
13	Bacteriophage Sf6 Tailspike Protein for Detection of <i>Shigella flexneri</i> Pathogens. <i>Viruses</i> , 2018, 10, 431.	3.3	25
14	Molecular characterisation of extended-spectrum β -lactamase (ESBL)-producing <i>Escherichia coli</i> isolates from hospital and ambulatory patients in Germany. <i>Veterinary Microbiology</i> , 2017, 200, 130-137.	1.9	71
15	Host cell interactions of outer membrane vesicle-associated virulence factors of enterohemorrhagic <i>Escherichia coli</i> O157: Intracellular delivery, trafficking and mechanisms of cell injury. <i>PLoS Pathogens</i> , 2017, 13, e1006159.	4.7	176
16	Clonal spread and interspecies transmission of clinically relevant ESBL-producing <i>Escherichia coli</i> of ST410 – another successful pandemic clone?. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiv155.	2.7	120
17	Virulence from vesicles: Novel mechanisms of host cell injury by <i>Escherichia coli</i> O104:H4 outbreak strain. <i>Scientific Reports</i> , 2015, 5, 13252.	3.3	122
18	Extended-spectrum beta-lactamase-producing Shiga toxin gene (stx1)-positive <i>Escherichia coli</i> O91:H14 carrying blaCTX-M-15 on an Inc11-ST31 plasmid isolated from a human patient in Germany. <i>International Journal of Medical Microbiology</i> , 2015, 305, 404-407.	3.6	12

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19	Molecular epidemiological view on Shiga toxin-producing <i>Escherichia coli</i> causing human disease in Germany: Diversity, prevalence, and outbreaks. <i>International Journal of Medical Microbiology</i> , 2015, 305, 697-704.	3.6	46
20	Correlation between the genomic <i>o454-nlpD</i> region polymorphisms, virulence gene equipment and phylogenetic group of extraintestinal <i>Escherichia coli</i> (ExPEC) enables pathotyping irrespective of host, disease and source of isolation. <i>Gut Pathogens</i> , 2014, 6, 37.	3.4	6
21	Molecular epidemiology of <i>Salmonella enterica</i> serovar Kottbus isolated in Germany from humans, food and animals. <i>Veterinary Microbiology</i> , 2014, 170, 97-108.	1.9	12
22	A molecular scheme for <i>Yersinia enterocolitica</i> patho-serotyping derived from genome-wide analysis. <i>International Journal of Medical Microbiology</i> , 2014, 304, 275-283.	3.6	42
23	Characterization of <i>Escherichia coli</i> Isolates from Hospital Inpatients or Outpatients with Urinary Tract Infection. <i>Journal of Clinical Microbiology</i> , 2014, 52, 407-418.	3.9	120
24	Two Novel EHEC/EAEC Hybrid Strains Isolated from Human Infections. <i>PLoS ONE</i> , 2014, 9, e95379.	2.5	39
25	Epidemic Profile of Shiga-Toxin-Producing <i>Escherichia coli</i> O104:H4 Outbreak in Germany. <i>New England Journal of Medicine</i> , 2011, 365, 1771-1780.	27.0	1,008
26	Characterisation of the <i>Escherichia coli</i> strain associated with an outbreak of haemolytic uraemic syndrome in Germany, 2011: a microbiological study. <i>Lancet Infectious Diseases</i> , The, 2011, 11, 671-676.	9.1	673