Angelika Fruth

List of Publications by Year
in descending order

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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	Epidemic Profile of Shiga-Toxinâ€“ProducingEscherichia coliO104:H4 Outbreak in Germany. New England Journal of Medicine, 2011, 365, 1771-1780.	27.0	1,008
2	Characterisation of the Escherichia coli strain associated with an outbreak of haemolytic uraemic syndrome in Germany, 2011: a microbiological study. Lancet Infectious Diseases, The, 2011, 11, 671-676.	9.1	673
3	Host cell interactions of outer membrane vesicle-associated virulence factors of enterohemorrhagic Escherichia coli O157: Intracellular delivery, trafficking and mechanisms of cell injury. PLoS Pathogens, 2017, 13, e1006159.	4.7	176
4	Virulence from vesicles: Novel mechanisms of host cell injury by Escherichia coli O104:H4 outbreak strain. Scientific Reports, 2015, 5, 13252.	3.3	122
5	Characterization of Escherichia coli Isolates from Hospital Inpatients or Outpatients with Urinary Tract Infection. Journal of Clinical Microbiology, 2014, 52, 407-418.	3.9	120
6	Clonal spread and interspecies transmission of clinically relevant ESBL-producingEscherichia coliof ST410â€”another successful pandemic clone?. FEMS Microbiology Ecology, 2016, 92, fiv155.	2.7	120
7	Molecular characterisation of extended-spectrum Î²-lactamase (ESBL)-producing Escherichia coli isolates from hospital and ambulatory patients in Germany. Veterinary Microbiology, 2017, 200, 130-137.	1.9	71
8	Molecular epidemiological view on Shiga toxin-producing Escherichia coli causing human disease in Germany: Diversity, prevalence, and outbreaks. International Journal of Medical Microbiology, 2015, 305, 697-704.	3.6	46
9	A molecular scheme for Yersinia enterocolitica patho-serotyping derived from genome-wide analysis. International Journal of Medical Microbiology, 2014, 304, 275-283.	3.6	42
10	Two Novel EHEC/EAEC Hybrid Strains Isolated from Human Infections. PLoS ONE, 2014, 9, e95379.	2.5	39
11	Shiga toxin-producing Escherichia coli O103:H2 outbreak in Germany after school trip to Austria due to raw cow milk, 2017 â€“ The important role of international collaboration for outbreak investigations. International Journal of Medical Microbiology, 2018, 308, 539-544.	3.6	35
12	Bacteriophage Sf6 Tailspike Protein for Detection of Shigella flexneri Pathogens. Viruses, 2018, 10, 431.	3.3	25
13	Whole-Genome-Based Public Health Surveillance of Less Common Shiga Toxin-Producing Escherichia coli Serovars and Untypeable Strains Identifies Four Novel O Genotypes. Journal of Clinical Microbiology, 2019, 57, .	3.9	25
14	Novel type of pilus associated with a Shiga-toxigenic E. coli hybrid pathovar conveys aggregative adherence and bacterial virulence. Emerging Microbes and Infections, 2018, 7, 1-16.	6.5	21
15	Population structure-guided profiling of antibiotic resistance patterns in clinical Listeria monocytogenes isolates from Germany identifies pbpB3 alleles associated with low levels of cephalosporin resistance. Emerging Microbes and Infections, 2020, 9, 1804-1813.	6.5	18
16	Genome-wide insights into population structure and host specificity of Campylobacter jejuni. Scientific Reports, 2021, 11, 10358.	3.3	18
17	Molecular epidemiology of Salmonella enterica serovar Kottbus isolated in Germany from humans, food and animals. Veterinary Microbiology, 2014, 170, 97-108.	1.9	12
18	Extended-spectrum beta-lactamase-producing Shiga toxin gene (stx1)-positive Escherichia coli O91:H14 carrying blaCTX-M-15 on an IncI1-ST31 plasmid isolated from a human patient in Germany. International Journal of Medical Microbiology, 2015, 305, 404-407.	3.6	12

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19	The Superior Adherence Phenotype of E. coli O104:H4 is Directly Mediated by the Aggregative Adherence Fimbriae Type I. Virulence, 2021, 12, 346-359.	4.4	9
20	Attack of the clones: whole genome-based characterization of two closely related enterohemorrhagic Escherichia coli O26 epidemic lineages. BMC Genomics, 2018, 19, 647.	2.8	7
21	Genetic diversity and pathogenic potential of Shiga toxin-producing Escherichia coli (STEC) derived from German flour. International Journal of Food Microbiology, 2021, 347, 109197.	4.7	7
22	Correlation between the genomic o454-nlpD region polymorphisms, virulence gene equipment and phylogenetic group of extraintestinal Escherichia coli (ExPEC) enables pathotyping irrespective of host, disease and source of isolation. Gut Pathogens, 2014, 6, 37.	3.4	6
23	The use of a salmonella bacteriophage in bearded dragons: application, passage time and reisolation. Tierarztliche Praxis Ausgabe K: Kleintiere - Heimtiere, 2019, 47, 247-256.	0.5	3
24	Influence of Salmonella specific bacteriophages (O1; S16) on the shedding of naturally occurring Salmonella and an orally applied Salmonella Eastbourne strain in bearded dragons (Pogona vitticeps). Veterinary Medicine and Science, 2021, 7, 534-547.	1.6	3
25	Zoonotic bacteria in clinically healthy goats in petting zoo settings of zoological gardens in Germany. Zoonoses and Public Health, 2022, , .	2.2	3
26	Simple differentiation of Salmonella Typhi, Paratyphi and Choleraesuis from Salmonella species using the eazyplex TyphiTyper LAMP assay. Journal of Medical Microbiology, 2020, 69, 817-823.	1.8	2