

Corinna Glasner

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

4,538
citations

186265
28
h-index

114465
63
g-index

104
all docs

104
docs citations

104
times ranked

7026
citing authors

#	ARTICLE	IF	CITATIONS
1	Occurrence of carbapenemase-producing <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> in the European survey of carbapenemase-producing Enterobacteriaceae (EuSCAPE): a prospective, multinational study. <i>Lancet Infectious Diseases</i> , The, 2017, 17, 153-163.	9.1	522
2	Epidemic of carbapenem-resistant <i>Klebsiella pneumoniae</i> in Europe is driven by nosocomial spread. <i>Nature Microbiology</i> , 2019, 4, 1919-1929.	13.3	476
3	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. <i>Microbial Genomics</i> , 2016, 2, e000093.	2.0	470
4	Application of next generation sequencing in clinical microbiology and infection prevention. <i>Journal of Biotechnology</i> , 2017, 243, 16-24.	3.8	414
5	Carbapenemase-producing Enterobacteriaceae in Europe: assessment by national experts from 38 countries, May 2015. <i>Eurosurveillance</i> , 2015, 20, .	7.0	332
6	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive <i>Staphylococcus aureus</i> in Europe. <i>MBio</i> , 2016, 7, .	4.1	192
7	Use of whole-genome sequencing to trace, control and characterize the regional expansion of extended-spectrum β -lactamase producing ST15 <i>Klebsiella pneumoniae</i> . <i>Scientific Reports</i> , 2016, 6, 20840.	3.3	117
8	Targeted next-generation sequencing of the 16S-23S rRNA region for culture-independent bacterial identification - increased discrimination of closely related species. <i>Scientific Reports</i> , 2017, 7, 3434.	3.3	110
9	Whole-Genome Multilocus Sequence Typing of Extended-Spectrum-Beta-Lactamase-Producing Enterobacteriaceae. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2919-2927.	3.9	97
10	<i>Enterococcus faecium</i> : from microbiological insights to practical recommendations for infection control and diagnostics. <i>Antimicrobial Resistance and Infection Control</i> , 2020, 9, 130.	4.1	87
11	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. <i>Journal of Clinical Microbiology</i> , 2017, 55, 908-913.	3.9	75
12	An integrated stewardship model: antimicrobial, infection prevention and diagnostic (AID). <i>Future Microbiology</i> , 2016, 11, 93-102.	2.0	71
13	Is Shiga Toxin-Negative <i>Escherichia coli</i> O157:H7 Enteropathogenic or Enterohemorrhagic <i>Escherichia coli</i> ? Comprehensive Molecular Analysis Using Whole-Genome Sequencing. <i>Journal of Clinical Microbiology</i> , 2015, 53, 3530-3538.	3.9	68
14	<i>Staphylococcus aureus</i> from the German general population is highly diverse. <i>International Journal of Medical Microbiology</i> , 2017, 307, 21-27.	3.6	67
15	Infection prevention in a connected world: The case for a regional approach. <i>International Journal of Medical Microbiology</i> , 2013, 303, 380-387.	3.6	66
16	Are cases of Methicillin-resistant <i>Staphylococcus aureus</i> clonal complex (CC) 398 among humans still livestock-associated?. <i>International Journal of Medical Microbiology</i> , 2015, 305, 110-113.	3.6	66
17	Extracellular Proteome and Citrullinome of the Oral Pathogen <i>Porphyromonas gingivalis</i> . <i>Journal of Proteome Research</i> , 2016, 15, 4532-4543.	3.7	62
18	Characterization of a CTX-M-15 Producing <i>Klebsiella Pneumoniae</i> Outbreak Strain Assigned to a Novel Sequence Type (1427). <i>Frontiers in Microbiology</i> , 2015, 6, 1250.	3.5	52

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19	Daptomycin Resistant <i>Staphylococcus aureus</i> Clinical Strain With Novel Non-synonymous Mutations in the <i>mprF</i> and <i>vraS</i> Genes: A New Insight Into Daptomycin Resistance. <i>Frontiers in Microbiology</i> , 2018, 9, 2705.	3.5	51
20	A peptide factor secreted by <i>Staphylococcus pseudintermedius</i> exhibits properties of both bacteriocins and virulence factors. <i>Scientific Reports</i> , 2015, 5, 14569.	3.3	45
21	Two cases of severe sepsis caused by <i>Bacillus pumilus</i> in neonatal infants. <i>Journal of Medical Microbiology</i> , 2012, 61, 596-599.	1.8	43
22	Carriage of <i>Staphylococcus aureus</i> in Thika Level 5 Hospital, Kenya: a cross-sectional study. <i>Antimicrobial Resistance and Infection Control</i> , 2014, 3, 22.	4.1	42
23	Measuring the impact of antimicrobial stewardship programs. <i>Expert Review of Anti-Infective Therapy</i> , 2016, 14, 569-575.	4.4	41
24	High Anti- <i>Staphylococcal</i> Antibody Titers in Patients with Epidermolysis Bullosa Relate to Long-Term Colonization with Alternating Types of <i>Staphylococcus aureus</i> . <i>Journal of Investigative Dermatology</i> , 2013, 133, 847-850.	0.7	40
25	Carbapenemase-Producing <i>Klebsiella pneumoniae</i> in Romania: A Six-Month Survey. <i>PLoS ONE</i> , 2015, 10, e0143214.	2.5	39
26	Clonal Structure and Characterization of <i>Staphylococcus aureus</i> Strains from Invasive Infections in Paediatric Patients from South Poland: Association between Age, <i>spa</i> Types, Clonal Complexes, and Genetic Markers. <i>PLoS ONE</i> , 2016, 11, e0151937.	2.5	36
27	Expansion of KPC-producing <i>Klebsiella pneumoniae</i> with various <i>mgrB</i> mutations giving rise to colistin resistance: the role of IS L3 on plasmids. <i>International Journal of Antimicrobial Agents</i> , 2018, 51, 260-265.	2.5	35
28	Reprint of “Application of next generation sequencing in clinical microbiology and infection prevention” <i>Journal of Biotechnology</i> , 2017, 250, 2-10.	3.8	34
29	Complete-genome sequencing elucidates outbreak dynamics of CA-MRSA USA300 (ST8- <i>spa</i> t008) in an academic hospital of Paramaribo, Republic of Suriname. <i>Scientific Reports</i> , 2017, 7, 41050.	3.3	33
30	MRSA Prevalence and Associated Risk Factors among Health-Care Workers in Non-outbreak Situations in the Dutch-German EUREGIO. <i>Frontiers in Microbiology</i> , 2016, 7, 1273.	3.5	31
31	Preclinical studies and prospective clinical applications for bacteria-targeted imaging: the future is bright. <i>Clinical and Translational Imaging</i> , 2016, 4, 253-264.	2.1	30
32	Epidemiology of Extended-Spectrum β -Lactamase-Producing <i>E. coli</i> and Vancomycin-Resistant Enterococci in the Northern Dutch-German Cross-Border Region. <i>Frontiers in Microbiology</i> , 2017, 8, 1914.	3.5	30
33	Genetic characterization of Shiga toxin-producing <i>Escherichia coli</i> O26:H11 strains isolated from animal, food, and clinical samples. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 74.	3.9	28
34	Molecular Typing of Enterobacteriaceae from Pig Holdings in North-Western Germany Reveals Extended- Spectrum and AmpC β -Lactamases Producing but no Carbapenem Resistant Ones. <i>PLoS ONE</i> , 2015, 10, e0134533.	2.5	27
35	Whole-genome analysis of an oxacillin-susceptible CC80 <i>mecA</i> -positive <i>Staphylococcus aureus</i> clinical isolate: insights into the mechanisms of cryptic methicillin resistance. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 2956-2964.	3.0	27
36	Novel Twin-Arginine Translocation Pathway-Dependent Phenotypes of <i>Bacillus subtilis</i> Unveiled by Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 796-807.	3.7	26

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37	<i>Bdellovibrio bacteriovorus</i> : a potential “living antibiotic”™ to control bacterial pathogens. <i>Critical Reviews in Microbiology</i> , 2021, 47, 630-646.	6.1	25
38	Epidemiology of <i>Staphylococcus aureus</i> in a burn unit of a tertiary care center in Ghana. <i>PLoS ONE</i> , 2017, 12, e0181072.	2.5	25
39	Genetic loci of <i>Staphylococcus aureus</i> associated with anti-neutrophil cytoplasmic autoantibody (ANCA)-associated vasculitides. <i>Scientific Reports</i> , 2017, 7, 12211.	3.3	24
40	Specific Targeting of the Metallophosphoesterase YkuE to the <i>Bacillus</i> Cell Wall Requires the Twin-arginine Translocation System. <i>Journal of Biological Chemistry</i> , 2012, 287, 29789-29800.	3.4	23
41	Genetic Diversity of <i>Staphylococcus aureus</i> in Buruli Ulcer. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003421.	3.0	21
42	Low anti-staphylococcal IgG responses in granulomatosis with polyangiitis patients despite long-term <i>Staphylococcus aureus</i> exposure. <i>Scientific Reports</i> , 2015, 5, 8188.	3.3	20
43	Incidence, clinical implications and impact on public health of infections with <i>Shigella</i> spp. and entero-invasive <i>Escherichia coli</i> (EIEC): results of a multicenter cross-sectional study in the Netherlands during 2016–2017. <i>BMC Infectious Diseases</i> , 2019, 19, 1037.	2.9	19
44	Signatures of cytoplasmic proteins in the exoproteome distinguish community- and hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> USA300 lineages. <i>Virulence</i> , 2017, 8, 891-907.	4.4	19
45	Development and Validation of a Reference Data Set for Assigning <i>Staphylococcus</i> Species Based on Next-Generation Sequencing of the 16S-23S rRNA Region. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 278.	3.9	18
46	Antimicrobial Resistance in Class 1 Integron-Positive Shiga Toxin-Producing <i>Escherichia coli</i> Isolated from Cattle, Pigs, Food and Farm Environment. <i>Microorganisms</i> , 2018, 6, 99.	3.6	17
47	Comprehensive Characterization of <i>Escherichia coli</i> O104:H4 Isolated from Patients in the Netherlands. <i>Frontiers in Microbiology</i> , 2015, 6, 1348.	3.5	16
48	Exoproteome Heterogeneity among Closely Related <i>Staphylococcus aureus</i> t437 Isolates and Possible Implications for Virulence. <i>Journal of Proteome Research</i> , 2019, 18, 2859-2874.	3.7	16
49	Identification of Secreted Exoproteome Fingerprints of Highly-Virulent and Non-Virulent <i>Staphylococcus aureus</i> Strains. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 51.	3.9	15
50	Mapping twenty years of antimicrobial resistance research trends. <i>Artificial Intelligence in Medicine</i> , 2022, 123, 102216.	6.5	14
51	MRSA Carriage in Community Outpatients: A Cross-Sectional Prevalence Study in a High-Density Livestock Farming Area along the Dutch-German Border. <i>PLoS ONE</i> , 2015, 10, e0139589.	2.5	13
52	Rapid Analysis of Diagnostic and Antimicrobial Patterns in R (RadaR): Interactive Open-Source Software App for Infection Management and Antimicrobial Stewardship. <i>Journal of Medical Internet Research</i> , 2019, 21, e12843.	4.3	13
53	Rapid and high-resolution distinction of community-acquired and nosocomial <i>Staphylococcus aureus</i> isolates with identical pulsed-field gel electrophoresis patterns and spa types. <i>International Journal of Medical Microbiology</i> , 2013, 303, 70-75.	3.6	12
54	Extended-spectrum beta-lactamase producing Enterobacteriaceae (ESBL-E) isolated from bean sprouts in the Netherlands. <i>PLoS ONE</i> , 2018, 13, e0203338.	2.5	12

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55	Evaluation of a Culture-Dependent Algorithm and a Molecular Algorithm for Identification of <i>Shigella</i> spp., <i>Escherichia coli</i> , and Enteroinvasive <i>E. coli</i> . <i>Journal of Clinical Microbiology</i> , 2018, 56, .	3.9	12
56	Development of a reference data set for assigning <i>Streptococcus</i> and <i>Enterococcus</i> species based on next generation sequencing of the 16Sâ€“23S rRNA region. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 178.	4.1	12
57	Virulence, Antimicrobial Resistance Properties and Phylogenetic Background of Non-H7 Enteropathogenic <i>Escherichia coli</i> O157. <i>Frontiers in Microbiology</i> , 2016, 7, 1540.	3.5	11
58	Methicillin Resistant <i>Staphylococcus aureus</i> Transmission in a Ghanaian Burn Unit: The Importance of Active Surveillance in Resource-Limited Settings. <i>Frontiers in Microbiology</i> , 2017, 8, 1906.	3.5	11
59	Defining Multidrug Resistance of Gram-Negative Bacteria in the Dutchâ€“German Border Regionâ€“Impact of National Guidelines. <i>Microorganisms</i> , 2018, 6, 11.	3.6	11
60	Decreasing prevalence of contamination with extended-spectrum beta-lactamase-producing Enterobacteriaceae (ESBL-E) in retail chicken meat in the Netherlands. <i>PLoS ONE</i> , 2019, 14, e0226828.	2.5	11
61	Joint Genomic and Proteomic Analysis Identifies Meta-Trait Characteristics of Virulent and Non-virulent <i>Staphylococcus aureus</i> Strains. <i>Frontiers in Cellular and Infection Microbiology</i> , 2018, 8, 313.	3.9	10
62	Changing epidemiology of methicillin-resistant <i>Staphylococcus aureus</i> in 42 hospitals in the Dutchâ€“German border region, 2012 to 2016: results of the search-and-follow-policy. <i>Eurosurveillance</i> , 2019, 24, .	7.0	10
63	<i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> virulence factors as biomarkers of infection. <i>Biological Chemistry</i> , 2021, 402, 1565-1573.	2.5	9
64	Predominance of CTX-M-15-producing ST131 strains among ESBL-producing <i>Escherichia coli</i> isolated from asylum seekers in the Netherlands. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 70-76.	3.0	8
65	The unintended contribution of clinical microbiology laboratories to climate change and mitigation strategies: a combination of descriptive study, short survey, literature review and opinion. <i>Clinical Microbiology and Infection</i> , 2022, 28, 1245-1250.	6.0	8
66	Genome-wide analysis reveals two novel mosaic regions containing an ACME with an identical DNA sequence in the MRSA ST398-t011 and MSSA ST8-t008 isolates. <i>Journal of Antimicrobial Chemotherapy</i> , 2015, 70, 1298-1302.	3.0	7
67	Combating the complex global challenge of antimicrobial resistance: what can Antimicrobial Stewardship contribute?. <i>Gastroenterology Insights</i> , 2017, 9, 7158.	1.2	7
68	Prevention and Control of Multidrug-Resistant Bacteria in The Netherlands and Germanyâ€“The Impact of Healthcare Structures. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 2337.	2.6	7
69	Molecular Characterisation of Vancomycin-Resistant <i>Enterococcus faecium</i> Isolates Belonging to the Lineage ST117/CT24 Causing Hospital Outbreaks. <i>Frontiers in Microbiology</i> , 2021, 12, 728356.	3.5	7
70	High-resolution typing by MLVF unveils extensive heterogeneity of European livestock-associated methicillin-resistant <i>Staphylococcus aureus</i> isolates with the sequence type 398. <i>International Journal of Medical Microbiology</i> , 2013, 303, 124-127.	3.6	6
71	Multicenter evaluation of molecular and culture-dependent diagnostics for <i>Shigella</i> species and Entero-invasive <i>Escherichia coli</i> in the Netherlands. <i>Journal of Microbiological Methods</i> , 2016, 131, 10-15.	1.6	6
72	European external quality assessments for identification, molecular typing and characterization of <i>Staphylococcus aureus</i> . <i>Journal of Antimicrobial Chemotherapy</i> , 2018, 73, 2662-2666.	3.0	6

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73	Applied shotgun metagenomics approach for the genetic characterization of dengue viruses. Journal of Biotechnology, 2019, 306, 100009.	3.8	6
74	Improved diagnostic policy for respiratory tract infections essential for patient management in the emergency department. Future Microbiology, 2020, 15, 623-632.	2.0	6
75	Evaluation of an Accelerated Workflow for Surveillance of ESBL (CTX-M)-Producing Escherichia coli Using Amplicon-Based Next-Generation Sequencing and Automated Analysis. Microorganisms, 2018, 6, 6.	3.6	5
76	Reduced Fitness Costs of mcr-1.2 Compared to Mutated pmrB in Isogenic Colistin-Resistant KPC-3-Producing Klebsiella pneumoniae. MSphere, 2019, 4, .	2.9	5
77	Long-read sequencing-based in silico phage typing of vancomycin-resistant Enterococcus faecium. BMC Genomics, 2021, 22, 758.	2.8	5
78	A prospective multicentre screening study on multidrug-resistant organisms in intensive care units in the Dutch-German cross-border region, 2017 to 2018: the importance of healthcare structures. Eurosurveillance, 2022, 27, .	7.0	5
79	Positive impact of infection prevention on the management of nosocomial outbreaks at an academic hospital. Future Microbiology, 2016, 11, 1249-1259.	2.0	4
80	Diagnostic Evasion of Highly-Resistant Microorganisms: A Critical Factor in Nosocomial Outbreaks. Frontiers in Microbiology, 2017, 8, 2128.	3.5	3
81	Compliance to Screening Protocols for Multidrug-Resistant Microorganisms at the Emergency Departments of Two Academic Hospitals in the Dutch-German Cross-Border Region. Tropical Medicine and Infectious Disease, 2021, 6, 15.	2.3	3
82	Staphylococcal cassette chromosome mec containing a novel mec gene complex, B4. Journal of Antimicrobial Chemotherapy, 2021, 76, 1986-1990.	3.0	3
83	Misidentification of methicillin-resistant Staphylococcus aureus by the Cepheid Xpert MRSA NxG assay, the Netherlands, February to March 2021. Eurosurveillance, 2021, 26, .	7.0	3
84	Detection of extended-spectrum beta-lactamase (ESBL) genes and plasmid replicons in Enterobacteriaceae using PlasmidSPAdes assembly of short-read sequence data. Microbial Genomics, 2020, 6, .	2.0	3
85	The tripartite insurance model (TIM): a financial incentive to prevent outbreaks of infections due to multidrug-resistant microorganisms in hospitals. Clinical Microbiology and Infection, 2021, 27, 665-667.	6.0	1
86	The Visual Dictionary of Antimicrobial Stewardship, Infection Control, and Institutional Surveillance Data. Frontiers in Microbiology, 2021, 12, 743939.	3.5	1
87	Insight Into the Anti-staphylococcal Activity of JBC 1847 at Sub-Inhibitory Concentration. Frontiers in Microbiology, 2021, 12, 786173.	3.5	1
88	PVL overexpression due to genomic rearrangements and mutations in the S. aureus reference strain ATCC25923. BMC Research Notes, 2017, 10, 576.	1.4	0
89	Title is missing!. , 2019, 14, e0226828.		0
90	Title is missing!. , 2019, 14, e0226828.		0

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91	Title is missing!., 2019, 14, e0226828.		0
92	Title is missing!., 2019, 14, e0226828.		0