

Corinna Glasner

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

4,538
citations

185998

28
h-index

114278

63
g-index

104
all docs

104
docs citations

104
times ranked

7026
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping twenty years of antimicrobial resistance research trends. <i>Artificial Intelligence in Medicine</i> , 2022, 123, 102216.	3.8	14
2	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. <i>Eurosurveillance</i> , 2022, 27, .	3.9	5
3	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.	2.8	8
4	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.	1.3	8
5	Compliance to Screening Protocols for Multidrug-Resistant Microorganisms at the Emergency Departments of Two Academic Hospitals in the Dutch-German Cross-Border Region. <i>Tropical Medicine and Infectious Disease</i> , 2021, 6, 15.	0.9	3
6	<i>Bdellovibrio bacteriovorus</i> : a potential "living antibiotic" to control bacterial pathogens. <i>Critical Reviews in Microbiology</i> , 2021, 47, 630-646.	2.7	25
7	Staphylococcal cassette chromosome mec containing a novel mec gene complex, B4. <i>Journal of Antimicrobial Chemotherapy</i> , 2021, 76, 1986-1990.	1.3	3
8	The tripartite insurance model (TIM): a financial incentive to prevent outbreaks of infections due to multidrug-resistant microorganisms in hospitals. <i>Clinical Microbiology and Infection</i> , 2021, 27, 665-667.	2.8	1
9	Misidentification of methicillin-resistant <i>Staphylococcus aureus</i> by the Cepheid Xpert MRSA NxG assay, the Netherlands, February to March 2021. <i>Eurosurveillance</i> , 2021, 26, .	3.9	3
10	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.	1.5	7
11	<i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> virulence factors as biomarkers of infection. <i>Biological Chemistry</i> , 2021, 402, 1565-1573.	1.2	9
12	Long-read sequencing-based in silico phage typing of vancomycin-resistant <i>Enterococcus faecium</i> . <i>BMC Genomics</i> , 2021, 22, 758.	1.2	5
13	The Visual Dictionary of Antimicrobial Stewardship, Infection Control, and Institutional Surveillance Data. <i>Frontiers in Microbiology</i> , 2021, 12, 743939.	1.5	1
14	Insight Into the Anti-staphylococcal Activity of JBC 1847 at Sub-Inhibitory Concentration. <i>Frontiers in Microbiology</i> , 2021, 12, 786173.	1.5	1
15	<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.	1.5	87
16	Improved diagnostic policy for respiratory tract infections essential for patient management in the emergency department. <i>Future Microbiology</i> , 2020, 15, 623-632.	1.0	6
17	Prevention and Control of Multidrug-Resistant Bacteria in The Netherlands and Germany-The Impact of Healthcare Structures. <i>International Journal of Environmental Research and Public Health</i> , 2020, 17, 2337.	1.2	7
18	Detection of extended-spectrum beta-lactamase (ESBL) genes and plasmid replicons in <i>Enterobacteriaceae</i> using PlasmidSPAdes assembly of short-read sequence data. <i>Microbial Genomics</i> , 2020, 6, .	1.0	3

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19	Epidemic of carbapenem-resistant <i>Klebsiella pneumoniae</i> in Europe is driven by nosocomial spread. <i>Nature Microbiology</i> , 2019, 4, 1919-1929.	5.9	476
20	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.	1.8	18
21	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.	1.8	16
22	Applied shotgun metagenomics approach for the genetic characterization of dengue viruses. <i>Journal of Biotechnology</i> , 2019, 306, 100009.	1.9	6
23	Reduced Fitness Costs of <i>mcr-1.2</i> Compared to Mutated <i>pmrB</i> in Isogenic Colistin-Resistant KPC-3-Producing <i>Klebsiella pneumoniae</i> . <i>MSphere</i> , 2019, 4, .	1.3	5
24	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.	1.1	11
25	Development of a reference data set for assigning <i>Streptococcus</i> and <i>Enterococcus</i> species based on next generation sequencing of the 16S-23S rRNA region. <i>Antimicrobial Resistance and Infection Control</i> , 2019, 8, 178.	1.5	12
26	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.	1.3	19
27	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.	2.1	13
28	Changing epidemiology of methicillin-resistant <i>Staphylococcus aureus</i> in 42 hospitals in the Dutch-German border region, 2012 to 2016: results of the search-and-follow-policy. <i>Eurosurveillance</i> , 2019, 24, .	3.9	10
29	Title is missing!. , 2019, 14, e0226828.		0
30	Title is missing!. , 2019, 14, e0226828.		0
31	Title is missing!. , 2019, 14, e0226828.		0
32	Title is missing!. , 2019, 14, e0226828.		0
33	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.	1.1	35
34	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.	1.5	51
35	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.	1.6	17
36	Extended-spectrum beta-lactamase producing Enterobacteriaceae (ESBL-E) isolated from bean sprouts in the Netherlands. <i>PLoS ONE</i> , 2018, 13, e0203338.	1.1	12

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37	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.	1.8	10
38	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, .	1.8	12
39	Evaluation of an Accelerated Workflow for Surveillance of ESBL (CTX-M)-Producing <i>Escherichia coli</i> Using Amplicon-Based Next-Generation Sequencing and Automated Analysis. <i>Microorganisms</i> , 2018, 6, 6.	1.6	5
40	Defining Multidrug Resistance of Gram-Negative Bacteria in the Dutchâ€“German Border Regionâ€“Impact of National Guidelines. <i>Microorganisms</i> , 2018, 6, 11.	1.6	11
41	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.	1.3	6
42	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.	1.8	75
43	Complete-genome sequencing elucidates outbreak dynamics of CA-MRSA USA300 (ST8-spa t008) in an academic hospital of Paramaribo, Republic of Suriname. <i>Scientific Reports</i> , 2017, 7, 41050.	1.6	33
44	Reprint of â€œApplication of next generation sequencing in clinical microbiology and infection preventionâ€œ. <i>Journal of Biotechnology</i> , 2017, 250, 2-10.	1.9	34
45	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.	1.6	110
46	<i>Staphylococcus aureus</i> from the German general population is highly diverse. <i>International Journal of Medical Microbiology</i> , 2017, 307, 21-27.	1.5	67
47	Application of next generation sequencing in clinical microbiology and infection prevention. <i>Journal of Biotechnology</i> , 2017, 243, 16-24.	1.9	414
48	Genetic loci of <i>Staphylococcus aureus</i> associated with anti-neutrophil cytoplasmic autoantibody (ANCA)-associated vasculitides. <i>Scientific Reports</i> , 2017, 7, 12211.	1.6	24
49	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.	4.6	522
50	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.	1.5	11
51	Epidemiology of Extended-Spectrum Î²-Lactamase-Producing <i>E. coli</i> and Vancomycin-Resistant Enterococci in the Northern Dutchâ€“German Cross-Border Region. <i>Frontiers in Microbiology</i> , 2017, 8, 1914.	1.5	30
52	Diagnostic Evasion of Highly-Resistant Microorganisms: A Critical Factor in Nosocomial Outbreaks. <i>Frontiers in Microbiology</i> , 2017, 8, 2128.	1.5	3
53	PVL overexpression due to genomic rearrangements and mutations in the <i>S. aureus</i> reference strain ATCC25923. <i>BMC Research Notes</i> , 2017, 10, 576.	0.6	0
54	Combating the complex global challenge of antimicrobial resistance: what can Antimicrobial Stewardship contribute?. <i>Gastroenterology Insights</i> , 2017, 9, 7158.	0.7	7

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55	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.	1.8	19
56	Epidemiology of <i>Staphylococcus aureus</i> in a burn unit of a tertiary care center in Ghana. <i>PLoS ONE</i> , 2017, 12, e0181072.	1.1	25
57	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. <i>Microbial Genomics</i> , 2016, 2, e000093.	1.0	470
58	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.	1.8	15
59	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.	1.5	31
60	Virulence, Antimicrobial Resistance Properties and Phylogenetic Background of Non-H7 Enteropathogenic <i>Escherichia coli</i> O157. <i>Frontiers in Microbiology</i> , 2016, 7, 1540.	1.5	11
61	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.	1.6	117
62	Measuring the impact of antimicrobial stewardship programs. <i>Expert Review of Anti-Infective Therapy</i> , 2016, 14, 569-575.	2.0	41
63	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, .	1.8	192
64	Multicenter evaluation of molecular and culture-dependent diagnostics for <i>Shigella</i> species and Enteroinvasive <i>Escherichia coli</i> in the Netherlands. <i>Journal of Microbiological Methods</i> , 2016, 131, 10-15.	0.7	6
65	Extracellular Proteome and Citrullinome of the Oral Pathogen <i>Porphyromonas gingivalis</i> . <i>Journal of Proteome Research</i> , 2016, 15, 4532-4543.	1.8	62
66	Preclinical studies and prospective clinical applications for bacteria-targeted imaging: the future is bright. <i>Clinical and Translational Imaging</i> , 2016, 4, 253-264.	1.1	30
67	Whole-Genome Multilocus Sequence Typing of Extended-Spectrum-Beta-Lactamase-Producing Enterobacteriaceae. <i>Journal of Clinical Microbiology</i> , 2016, 54, 2919-2927.	1.8	97
68	Positive impact of infection prevention on the management of nosocomial outbreaks at an academic hospital. <i>Future Microbiology</i> , 2016, 11, 1249-1259.	1.0	4
69	An integrated stewardship model: antimicrobial, infection prevention and diagnostic (AID). <i>Future Microbiology</i> , 2016, 11, 93-102.	1.0	71
70	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.	1.1	36
71	A peptide factor secreted by <i>Staphylococcus pseudintermedius</i> exhibits properties of both bacteriocins and virulence factors. <i>Scientific Reports</i> , 2015, 5, 14569.	1.6	45
72	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.	1.8	28

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73	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.	1.5	52
74	Comprehensive Characterization of <i>Escherichia coli</i> O104:H4 Isolated from Patients in the Netherlands. <i>Frontiers in Microbiology</i> , 2015, 6, 1348.	1.5	16
75	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.	1.1	27
76	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.	1.5	66
77	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.	1.6	20
78	Genetic Diversity of <i>Staphylococcus aureus</i> in Buruli Ulcer. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003421.	1.3	21
79	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.	1.3	27
80	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.	1.3	7
81	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.	1.8	68
82	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.	1.1	13
83	Carbapenemase-Producing <i>Klebsiella pneumoniae</i> in Romania: A Six-Month Survey. <i>PLoS ONE</i> , 2015, 10, e0143214.	1.1	39
84	Carbapenemase-producing Enterobacteriaceae in Europe: assessment by national experts from 38 countries, May 2015. <i>Eurosurveillance</i> , 2015, 20, .	3.9	332
85	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.	1.5	42
86	Infection prevention in a connected world: The case for a regional approach. <i>International Journal of Medical Microbiology</i> , 2013, 303, 380-387.	1.5	66
87	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.	1.5	6
88	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.	1.5	12
89	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.	0.3	40
90	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.	1.8	26

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91	Specific Targeting of the Metallophosphoesterase YkuE to the Bacillus Cell Wall Requires the Twin-arginine Translocation System. <i>Journal of Biological Chemistry</i> , 2012, 287, 29789-29800.	1.6	23
92	Two cases of severe sepsis caused by <i>Bacillus pumilus</i> in neonatal infants. <i>Journal of Medical Microbiology</i> , 2012, 61, 596-599.	0.7	43