Corinna Glasner

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Mapping twenty years of antimicrobial resistance research trends. Artificial Intelligence in Medicine, 2022, 123, 102216.	6.5	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. Eurosurveillance, 2022, 27, .	7.0	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. Clinical Microbiology and Infection, 2022, 28, 1245-1250.	6.0	8
4	Predominance of CTX-M-15-producing ST131 strains among ESBL-producing <i>Escherichia coli</i> isolated from asylum seekers in theÂNetherlands. Journal of Antimicrobial Chemotherapy, 2021, 76, 70-76.	3.0	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. Tropical Medicine and Infectious Disease, 2021, 6, 15.	2.3	3
6	<i>Bdellovibrio bacteriovorus</i> : a potential â€~living antibiotic' to control bacterial pathogens. Critical Reviews in Microbiology, 2021, 47, 630-646.	6.1	25
7	Staphylococcal cassette chromosome mec containing a novel mec gene complex, B4. Journal of Antimicrobial Chemotherapy, 2021, 76, 1986-1990.	3.0	3
8	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
9	Misidentification of meticillin-resistant Staphylococcus aureus by the Cepheid Xpert MRSA NxG assay, the Netherlands, February to March 2021. Eurosurveillance, 2021, 26, .	7.0	3
10	Molecular Characterisation of Vancomycin-Resistant Enterococcus faecium Isolates Belonging to the Lineage ST117/CT24 Causing Hospital Outbreaks. Frontiers in Microbiology, 2021, 12, 728356.	3.5	7
11	<i>Pseudomonas aeruginosa</i> and <i>Staphylococcus aureus</i> virulence factors as biomarkers of infection. Biological Chemistry, 2021, 402, 1565-1573.	2.5	9
12	Long-read sequencing-based in silico phage typing of vancomycin-resistant Enterococcus faecium. BMC Genomics, 2021, 22, 758.	2.8	5
13	The Visual Dictionary of Antimicrobial Stewardship, Infection Control, and Institutional Surveillance Data. Frontiers in Microbiology, 2021, 12, 743939.	3.5	1
14	Insight Into the Anti-staphylococcal Activity of JBC 1847 at Sub-Inhibitory Concentration. Frontiers in Microbiology, 2021, 12, 786173.	3.5	1
15	Enterococcus faecium: from microbiological insights to practical recommendations for infection control and diagnostics. Antimicrobial Resistance and Infection Control, 2020, 9, 130.	4.1	87
16	Improved diagnostic policy for respiratory tract infections essential for patient management inÂthe emergency department. Future Microbiology, 2020, 15, 623-632.	2.0	6
17	Prevention and Control of Multidrug-Resistant Bacteria in The Netherlands and Germany—The Impact of Healthcare Structures. International Journal of Environmental Research and Public Health, 2020, 17, 2337.	2.6	7
18	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

CORINNA GLASNER

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19	Epidemic of carbapenem-resistant Klebsiella pneumoniae in Europe is driven by nosocomial spread. Nature Microbiology, 2019, 4, 1919-1929.	13.3	476
20	Development and Validation of a Reference Data Set for Assigning Staphylococcus Species Based on Next-Generation Sequencing of the 16S-23S rRNA Region. Frontiers in Cellular and Infection Microbiology, 2019, 9, 278.	3.9	18
21	Exoproteome Heterogeneity among Closely Related <i>Staphylococcus aureus</i> t437 Isolates and Possible Implications for Virulence. Journal of Proteome Research, 2019, 18, 2859-2874.	3.7	16
22	Applied shotgun metagenomics approach for the genetic characterization of dengue viruses. Journal of Biotechnology, 2019, 306, 100009.	3.8	6
23	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
24	Decreasing prevalence of contamination with extended-spectrum beta-lactamase-producing Enterobacteriaceae (ESBL-E) in retail chicken meat in the Netherlands. PLoS ONE, 2019, 14, e0226828.	2.5	11
25	Development of a reference data set for assigning Streptococcus and Enterococcus species based on next generation sequencing of the 16S–23S rRNA region. Antimicrobial Resistance and Infection Control, 2019, 8, 178.	4.1	12
26	Incidence, clinical implications and impact on public health of infections with Shigella spp. and entero-invasive Escherichia coli (EIEC): results of a multicenter cross-sectional study in the Netherlands during 2016–2017. BMC Infectious Diseases, 2019, 19, 1037.	2.9	19
27	Rapid Analysis of Diagnostic and Antimicrobial Patterns in R (RadaR): Interactive Open-Source Software App for Infection Management and Antimicrobial Stewardship. Journal of Medical Internet Research, 2019, 21, e12843.	4.3	13
28	Changing epidemiology of meticillin-resistant Staphylococcus aureus in 42 hospitals in the Dutch–German border region, 2012 to 2016: results of the search-and-follow-policy. Eurosurveillance, 2019, 24, .	7.0	10
29	Title is missing!. , 2019, 14, e0226828.		0
30	Title is missing!. , 2019, 14, e0226828.		0
31	Title is missing!. , 2019, 14, e0226828.		Ο
32	Title is missing!. , 2019, 14, e0226828.		0
33	Expansion of KPC-producing Klebsiella pneumoniae with various mgrB mutations giving rise to colistin resistance: the role of IS L3 on plasmids. International Journal of Antimicrobial Agents, 2018, 51, 260-265.	2.5	35
34	Daptomycin Resistant Staphylococcus aureus Clinical Strain With Novel Non-synonymous Mutations in the mprF and vraS Genes: A New Insight Into Daptomycin Resistance. Frontiers in Microbiology, 2018, 9, 2705.	3.5	51
35	Antimicrobial Resistance in Class 1 Integron-Positive Shiga Toxin-Producing Escherichia coli Isolated from Cattle, Pigs, Food and Farm Environment. Microorganisms, 2018, 6, 99.	3.6	17
36	Extended-spectrum beta-lactamase producing Enterobacteriaceae (ESBL-E) isolated from bean sprouts in the Netherlands. PLoS ONE, 2018, 13, e0203338.	2.5	12

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37	Joint Genomic and Proteomic Analysis Identifies Meta-Trait Characteristics of Virulent and Non-virulent Staphylococcus aureus Strains. Frontiers in Cellular and Infection Microbiology, 2018, 8, 313.	3.9	10
38	Evaluation of a Culture-Dependent Algorithm and a Molecular Algorithm for Identification of Shigella spp., Escherichia coli, and Enteroinvasive E. coli. Journal of Clinical Microbiology, 2018, 56, .	3.9	12
39	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
40	Defining Multidrug Resistance of Gram-Negative Bacteria in the Dutch–German Border Region—Impact of National Guidelines. Microorganisms, 2018, 6, 11.	3.6	11
41	European external quality assessments for identification, molecular typing and characterization of Staphylococcus aureus. Journal of Antimicrobial Chemotherapy, 2018, 73, 2662-2666.	3.0	6
42	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. Journal of Clinical Microbiology, 2017, 55, 908-913.	3.9	75
43	Complete-genome sequencing elucidates outbreak dynamics of CA-MRSA USA300 (ST8-spa t008) in an academic hospital of Paramaribo, Republic of Suriname. Scientific Reports, 2017, 7, 41050.	3.3	33
44	Reprint of "Application of next generation sequencing in clinical microbiology and infection prevention― Journal of Biotechnology, 2017, 250, 2-10.	3.8	34
45	Targeted next-generation sequencing of the 16S-23S rRNA region for culture-independent bacterial identification - increased discrimination of closely related species. Scientific Reports, 2017, 7, 3434.	3.3	110
46	Staphylococcus aureus from the German general population is highly diverse. International Journal of Medical Microbiology, 2017, 307, 21-27.	3.6	67
47	Application of next generation sequencing in clinical microbiology and infection prevention. Journal of Biotechnology, 2017, 243, 16-24.	3.8	414
48	Genetic loci of Staphylococcus aureus associated with anti-neutrophil cytoplasmic autoantibody (ANCA)-associated vasculitides. Scientific Reports, 2017, 7, 12211.	3.3	24
49	Occurrence of carbapenemase-producing Klebsiella pneumoniae and Escherichia coli in the European survey of carbapenemase-producing Enterobacteriaceae (EuSCAPE): a prospective, multinational study. Lancet Infectious Diseases, The, 2017, 17, 153-163.	9.1	522
50	Methicillin Resistant Staphylococcus aureus Transmission in a Ghanaian Burn Unit: The Importance of Active Surveillance in Resource-Limited Settings. Frontiers in Microbiology, 2017, 8, 1906.	3.5	11
51	Epidemiology of Extended-Spectrum β-Lactamase-Producing E. coli and Vancomycin-Resistant Enterococci in the Northern Dutch–German Cross-Border Region. Frontiers in Microbiology, 2017, 8, 1914.	3.5	30
52	Diagnostic Evasion of Highly-Resistant Microorganisms: A Critical Factor in Nosocomial Outbreaks. Frontiers in Microbiology, 2017, 8, 2128.	3.5	3
53	PVL overexpression due to genomic rearrangements and mutations in the S. aureus reference strain ATCC25923. BMC Research Notes, 2017, 10, 576.	1.4	0
54	Combating the complex global challenge of antimicrobial resistance: what can Antimicrobial Stewardship contribute?. Gastroenterology Insights, 2017, 9, 7158.	1.2	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. Virulence, 2017, 8, 891-907.	4.4	19
56	Epidemiology of Staphylococcus aureus in a burn unit of a tertiary care center in Ghana. PLoS ONE, 2017, 12, e0181072.	2.5	25
57	Microreact: visualizing and sharing data for genomic epidemiology and phylogeography. Microbial Genomics, 2016, 2, e000093.	2.0	470
58	Identification of Secreted Exoproteome Fingerprints of Highly-Virulent and Non-Virulent Staphylococcus aureus Strains. Frontiers in Cellular and Infection Microbiology, 2016, 6, 51.	3.9	15
59	MRSA Prevalence and Associated Risk Factors among Health-Care Workers in Non-outbreak Situations in the Dutch-German EUREGIO. Frontiers in Microbiology, 2016, 7, 1273.	3.5	31
60	Virulence, Antimicrobial Resistance Properties and Phylogenetic Background of Non-H7 Enteropathogenic Escherichia coli O157. Frontiers in Microbiology, 2016, 7, 1540.	3.5	11
61	Use of whole-genome sequencing to trace, control and characterize the regional expansion of extended-spectrum β-lactamase producing ST15 Klebsiella pneumoniae. Scientific Reports, 2016, 6, 20840.	3.3	117
62	Measuring the impact of antimicrobial stewardship programs. Expert Review of Anti-Infective Therapy, 2016, 14, 569-575.	4.4	41
63	Whole-Genome Sequencing for Routine Pathogen Surveillance in Public Health: a Population Snapshot of Invasive Staphylococcus aureus in Europe. MBio, 2016, 7, .	4.1	192
64	Multicenter evaluation of molecular and culture-dependent diagnostics for Shigella species and Entero-invasive Escherichia coli in the Netherlands. Journal of Microbiological Methods, 2016, 131, 10-15.	1.6	6
65	Extracellular Proteome and Citrullinome of the Oral Pathogen <i>Porphyromonas gingivalis</i> . Journal of Proteome Research, 2016, 15, 4532-4543.	3.7	62
66	Preclinical studies and prospective clinical applications for bacteria-targeted imaging: the future is bright. Clinical and Translational Imaging, 2016, 4, 253-264.	2.1	30
67	Whole-Genome Multilocus Sequence Typing of Extended-Spectrum-Beta-Lactamase-Producing Enterobacteriaceae. Journal of Clinical Microbiology, 2016, 54, 2919-2927.	3.9	97
68	Positive impact of infection prevention on the management of nosocomial outbreaks at an academic hospital. Future Microbiology, 2016, 11, 1249-1259.	2.0	4
69	An integrated stewardship model: antimicrobial, infection prevention and diagnostic (AID). Future Microbiology, 2016, 11, 93-102.	2.0	71
70	Clonal Structure and Characterization of Staphylococcus aureus Strains from Invasive Infections in Paediatric Patients from South Poland: Association between Age, spa Types, Clonal Complexes, and Genetic Markers. PLoS ONE, 2016, 11, e0151937.	2.5	36
71	A peptide factor secreted by Staphylococcus pseudintermedius exhibits properties of both bacteriocins and virulence factors. Scientific Reports, 2015, 5, 14569.	3.3	45
72	Genetic characterization of Shiga toxin-producing Escherichia coli O26:H11 strains isolated from animal, food, and clinical samples. Frontiers in Cellular and Infection Microbiology, 2015, 5, 74.	3.9	28

CORINNA GLASNER

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73	Characterization of a CTX-M-15 Producing Klebsiella Pneumoniae Outbreak Strain Assigned to a Novel Sequence Type (1427). Frontiers in Microbiology, 2015, 6, 1250.	3.5	52
74	Comprehensive Characterization of Escherichia coli O104:H4 Isolated from Patients in the Netherlands. Frontiers in Microbiology, 2015, 6, 1348.	3.5	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. PLoS ONE, 2015, 10, e0134533.	2.5	27
76	Are cases of Methicillin-resistant Staphylococcus aureus clonal complex (CC) 398 among humans still livestock-associated?. International Journal of Medical Microbiology, 2015, 305, 110-113.	3.6	66
77	Low anti-staphylococcal IgG responses in granulomatosis with polyangiitis patients despite long-term Staphylococcus aureus exposure. Scientific Reports, 2015, 5, 8188.	3.3	20
78	Genetic Diversity of Staphylococcus aureus in Buruli Ulcer. PLoS Neglected Tropical Diseases, 2015, 9, e0003421.	3.0	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. Journal of Antimicrobial Chemotherapy, 2015, 70, 2956-2964.	3.0	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. Journal of Antimicrobial Chemotherapy, 2015, 70, 1298-1302.	3.0	7
81	Is Shiga Toxin-Negative Escherichia coli O157:H7 Enteropathogenic or Enterohemorrhagic Escherichia coli? Comprehensive Molecular Analysis Using Whole-Genome Sequencing. Journal of Clinical Microbiology, 2015, 53, 3530-3538.	3.9	68
82	MRSA Carriage in Community Outpatients: A Cross-Sectional Prevalence Study in a High-Density Livestock Farming Area along the Dutch-German Border. PLoS ONE, 2015, 10, e0139589.	2.5	13
83	Carbapenemase-Producing Klebsiella pneumoniae in Romania: A Six-Month Survey. PLoS ONE, 2015, 10, e0143214.	2.5	39
84	Carbapenemase-producing Enterobacteriaceae in Europe: assessment by national experts from 38 countries, May 2015. Eurosurveillance, 2015, 20, .	7.0	332
85	Carriage of Staphylococcus aureus in Thika Level 5 Hospital, Kenya: a cross-sectional study. Antimicrobial Resistance and Infection Control, 2014, 3, 22.	4.1	42
86	Infection prevention in a connected world: The case for a regional approach. International Journal of Medical Microbiology, 2013, 303, 380-387.	3.6	66
87	High-resolution typing by MLVF unveils extensive heterogeneity of European livestock-associated methicillin-resistant Staphylococcus aureus isolates with the sequence type 398. International Journal of Medical Microbiology, 2013, 303, 124-127.	3.6	6
88	Rapid and high-resolution distinction of community-acquired and nosocomial Staphylococcus aureus isolates with identical pulsed-field gel electrophoresis patterns and spa types. International Journal of Medical Microbiology, 2013, 303, 70-75.	3.6	12
89	High Anti-Staphylococcal Antibody Titers in Patients with Epidermolysis Bullosa Relate to Long-Term Colonization with Alternating Types of Staphylococcus aureus. Journal of Investigative Dermatology, 2013, 133, 847-850.	0.7	40
90	Novel Twin-Arginine Translocation Pathway-Dependent Phenotypes of <i>Bacillus subtilis</i> Unveiled by Quantitative Proteomics. Journal of Proteome Research, 2013, 12, 796-807.	3.7	26

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91	Specific Targeting of the Metallophosphoesterase YkuE to the Bacillus Cell Wall Requires the Twin-arginine Translocation System. Journal of Biological Chemistry, 2012, 287, 29789-29800.	3.4	23
92	Two cases of severe sepsis caused by Bacillus pumilus in neonatal infants. Journal of Medical Microbiology, 2012, 61, 596-599.	1.8	43