

SANDRA REUTER

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Website:

<https://www.uniklinik-freiburg.de/institute-for-infection-prevention-and-control/microbial-genome-analysis.html>

EDUCATION AND RESEARCH EXPERIENCE

11/2020 – PRESENT JUNIOR RESEARCH GROUP LEADER, MEDICAL CENTER – UNIVERSITY OF FREIBURG, GERMANY

TAPIR – Tracking Acquisition of Pathogens In Real-time

05/2016 – 10/2020 POSTDOCTORAL RESEARCHER, MEDICAL CENTER – UNIVERSITY OF FREIBURG, GERMANY

Translation of bacterial whole genome sequencing into medical microbiological practice, including ISO 17025 accreditation

Carbapenem-nonsusceptible *Klebsiella pneumoniae*

01/2015 – 04/2016 RESEARCH ASSOCIATE, UNIVERSITY OF CAMBRIDGE, UK

Hospital-acquired infections and translation of bacterial whole genome sequencing into clinical practice

Methicillin-resistant *Staphylococcus aureus* (MRSA), antimicrobial resistance and plasmid carriage in carbapenem-resistant *Enterobacteriales*

12/2011 – 12/2014 POSTDOCTORAL RESEARCH FELLOW, WELLCOME SANGER INSTITUTE, UK

Population framework for MRSA in the UK, antibiotic resistance prediction from the genotype

Emerging alert organisms (*Legionella pneumophila*, *Enterococcus faecium*)

10/2008 – 09/2011 PhD THESIS, NOTTINGHAM TRENT UNIVERSITY, UK

Evolutionary dynamics of the *Yersinia enterocolitica* Complex

Joint project supervision with Wellcome Sanger Institute

03/2006 – 03/2008 MSc. BIOLOGY, TECHNICAL UNIVERSITY MUNICH, GERMANY

11/2005 – 02/2006 WORK EXPERIENCE TROPICAL MEDICINE AND HYGIENE, HEIDELBERG UNIVERSITY HOSPITAL, GERMANY

07/2004 – 06/2005 BSc. MOLECULAR BIOLOGY AND BIOMEDICAL SCIENCE, MURDOCH UNIVERSITY, AUSTRALIA

10/2002 – 09/2005 BSc. BIOLOGY WITH BIOMEDICAL SCIENCES, UNIVERSITY OF APPLIED SCIENCES BONN-RHEIN-SIEG, GERMANY

COMPETENCIES AND SKILLS

Professional Interests Hospital-acquired pathogens and infections
Population genomics
Genomic epidemiology
Genomic basis of antimicrobial resistance

Teaching Skills Medizindidaktik I Qualification, Kompetenzzentrum Medizindidaktik Baden-Württemberg

Teaching Undergraduate Seminar Aktuelle Impffragen (Current Vaccination Questions)
Lecture in Hospital Epidemiology
Laboratory assistance in Microbiology Laboratory Module

Postgraduate Principal course organiser EUCIC Advance Module “Dynamics of Disease Transmission: From Genomes to Infection Control, from Beds to Bases and Bytes”; Freiburg 2019
Bioinformatics workshop Stellenbosch University Tygerberg Campus, Cape Town 2019

	Principal course organiser ESCMID “Capacity-Building Workshop: Whole-Genome Sequencing for Clinical Microbiology and Hospital Epidemiology”; Freiburg 2017 Course instructor Wellcome Trust Advanced Courses: “Working with Pathogen Genomes”, Hinxton 2012, 2014; “Molecular Basis of Bacterial Infection: Contemporary Research Approaches”, Hinxton 2013
Supervision	current PhD students: Stefany Ayala Montaña, Ifeoluwa Janet Akintayo, Mabel Budia Silva Co-supervision of PhD students: Kedišaletše Moloto, Yolandi Snyman (Stellenbosch University, Cape Town, South Africa), Rocío Gabriela Stucchi (Universidad Buenos Aires, Argentina) MSc students (IMBS Freiburg): Valentina Valenzuela Dallos, Ivan Dario Acevedo Monterrosa
Society Activities	ESGEM – ESCMID Study Group on Epidemiological Markers: Executive Committee 2023-2025, Education Officer; Programme committee for IMMEX-XIII, Conference and Workshop Coordinator Microbiology Society: Editor for Microbial Genomics

SARS-COV-2 PANDEMIC – IMPACT ON WORK

Lab closure, lab technician on loan to virology 15.03.-30.04.2020
Support of local infection prevention and control through Sars-CoV-2 sequence analysis
Delay in compute server set-up (instead of 05/2020 was 09/2021), delay in ordering further computer servers (instead of 11/2020 ordered 01/2022, delivered 11/2022) and installing second server (ongoing)

GRANTS

2018-2020 German-Israeli Foundation (GIF) – co-PI
A multicentre study of the evolution and spread of NDM-producing bacteria across bacterial clones and species; €237.940

2020-2023 JPI-AMR Resistenzen 01KI1910 – co-PI
k-STaR (A K-mer based approach for institutional AMR Surveillance, Transmission monitoring, and Rapid diagnostics); €359.896,63

2020-2025 Nachwuchsförderung in den Infektionswissenschaften 01KI2018 - PI
TAPIR – Tracking of Acquisition of Pathogens In Real-time; €1.960.196,25

2021-2024 NUM (Network of University Medicine) Infrastructure Project 01KX2121 – co-PI
GenSurv – Genomic Pathogen Surveillance and Translational Research; €570.415,31

2022-2023 NUM Research Project 01KX2121 – co-PI
MolTraX – Molecular Surveillance and Infection Chain Tracing for Local Public Health Authorities; €67.153,21

2024-2025 NUM Research Project – co-PI
GenSurv+ – Genomic Pathogen Surveillance and Translational Research plus; €39.663,20

PUBLICATIONS

MAJOR PUBLICATIONS LAST 5 YEARS

Budia-Silva, M., Kostyanov, T., Ayala-Montaña, S., Bravo-Ferrer Acosta, J., Garcia-Castillo, M., Cantón, R., Goossens, H., Rodríguez-Baño, J., Grundmann, H., and **Reuter, S.** (2024). International and regional spread of carbapenem-resistant *Klebsiella pneumoniae* in Europe. *Nat Comm* **15**(1): 5092

Donker, T., Papathannasopoulou, A., Ghosh, H., Kociurzynski, R., Felder, M., Grundmann, H., and **Reuter, S.** (2024). Direct estimation of fitness advantage from genomic surveillance data without prior lineage classification. *PNAS* 121(25):e2314262121.

Aracil-Gisbert, S., Fernández-De-Bobadilla, M.D., Guerra-Pinto, N., Serrano-Calleja, S., Pérez-Cobas, A.E., Soriano, C., de Pablo, R., Lanza, V.F., Pérez-Viso, B., **Reuter, S.**, Hasman, H., Cantón, R., Baquero, F., and Coque, T.M. (2024). The ICU environment contributes to the endemicity of the "Serratia marcescens complex" in the hospital setting. *mBio* 15(5).

Reuter, S., Müller, C., Wille, J., Xanthopoulou, K., Stefanik, D., Hackel, M., Grundmann, H., Higgins, P.G., and Seifert, H. (2023). A global view on carbapenem-resistant *Acinetobacter baumannii*. *mBio* 14(6):e02260-23.

Afolayan, A.O., Rigatou, A., Grundmann, H., Pantazatou, A., Daikos, G., and **Reuter, S.** (2023). The art of taking turns to rule: Carbapenemase-producing ST258, ST147, and ST11 *Klebsiella pneumoniae* lineages variably dominated within a Greek hospital over a 15-year period. *MGen* 9(8):001082.

Werner, G., Couto, N., Feil, E.J., Novais, Â., Hegstad, K., Howden, B.P., Friedrich, A.W., and **Reuter, S.** (2023). Taking hospital pathogen surveillance to the next level. *MGen* 9(4):001008, on behalf of ESGEM study group.

David, S., Cohen, V., **Reuter, S.**, Sheppard, A.E., Giani, T., Parkhill, J., Rossolini, G.M., Feil, E.J., Grundmann, H., Aanensen, D.M. and the ESCMID Study Group for Epidemiological Markers (ESGEM) (2020). Integrated chromosomal and plasmid sequence analyses reveal diverse modes of carbapenemase gene spread among *Klebsiella pneumoniae*. *PNAS* 117(40): 25043-25054.

David, S., **Reuter, S.**, Harris, S.R., Glasner, C., Feltwell, T., Argimon, S., Abudahab, K., Goater, R., Giani, T., Aspbury, M., Sjunnebo, S., Feil, E.J., Rossolini, G.M., Aanensen, D.M., Grundmann, H., the European Survey of Carbapenemase-Producing Enterobacteriaceae (EuSCAPE) Working Group, and the ESCMID Study Group for Epidemiological Markers (ESGEM) (2019). Epidemic of carbapenem-resistant *Klebsiella pneumoniae* in Europe is driven by nosocomial spread: Inference from a continent-wide population analysis. *Nat Microbiol* 4(11): 1919-1929.

MAJOR PUBLICATIONS PRIOR TO 2018

Reuter, S., Ludden, C., Judge, K., Gouliouris, T., Blane, B., Coll, F., Naydenova, P., Hunt, M., Hopkins, K., Brown, N.M., Woodford, N., Parkhill, J., and Peacock, S.J. (2017). Sharing of carbapenemase-encoding plasmids between Enterobacteriaceae in UK sewage uncovered by MinION sequencing. *MGen* 3 (7): e000114.

Reuter, S., Török, M.E., Holden, M.T.G., Reynolds, R., Raven, K.E., Blane, B., Donker, T., Bentley, S.D., Aanensen, D.M., Grundmann, H., Feil, E.J., Spratt, B.G., Parkhill, J., and Peacock, S.J. (2016). Building a genomic framework for prospective MRSA surveillance in the United Kingdom and the Republic of Ireland. *Genome Res*, 26 (2): 263 – 270.

Raven, K.E., **Reuter, S.**, Gouliouris, T., Reynolds, R., Russell, J.E., Brown, N.M., Török, M.E., Parkhill, J., and Peacock, S.J. (2016). Whole-genome sequencing defines the population structure and evolution of vancomycin resistance in *Enterococcus faecalis*. *Nat Microbiol*, 1 (3): 15033.

Page, A.J., Cummins, C.A., Hunt, M., Wong, V.K., **Reuter, S.**, Holden, M.T.G., Fookes, M., Falush, D., Keane, J.A., and Parkhill, J. (2015). Roary: Rapid large-scale prokaryote pan genome analysis. *Bioinformatics*, 31 (22): 3691 – 3693.

Reuter, S., Connor, T.R., [...], Wren, B.W., Parkhill, J., Carniel, E., Achtman, M., McNally, A., and Thomson, N.R. (2014). Parallel independent evolution of pathogenicity within the genus *Yersinia*. *Proc Nat Acad Sci USA*, 111(8): 6768 – 73.

Reuter, S., Ellington, M.J., Cartwright, E.J.P., Köser, C.U., Török, M.E., Gouliouris, T., Harris, S.R., Brown, N.M., Holden, M.T.G., Quail, M., Parkhill, J., Smith, G.P., Bentley, S.D., and Peacock, S.J. (2013). Rapid whole genome sequencing to improve diagnostic and public health microbiology. *JAMA Int Med*, 173 (15): 1397 – 1404.

FULL PUBLICATION LIST: <https://scholar.google.co.uk/citations?user=PjLm1ysAAAAJ&hl=en>

REFEREES

Prof. Hajo Grundmann
Emeritus Director Institute for Infection
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Medical Center – University of Freiburg

Prof. Sharon Peacock
Professor of Public Health and Microbiology
University of Cambridge

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OTHER INTERESTS

I enjoy music and play classical guitar as well as double base. I am also acting as a senior in the local Lutheran church congregation. I support our local parkrun community (run director).