

CURRICULUM VITAE: ANNA JOHNNING

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Affiliations	Fraunhofer-Chalmers Centre Department of Systems and Data Analysis Chalmers University of Technology/University of Gothenburg Department of Mathematical Sciences Division of Applied Mathematics and Statistics CARe – Centre for Antibiotic Resistance Research in Gothenburg	

ACADEMIC DEGREES

2010–2014	PhD in Medicine from the University of Gothenburg.
Project title	<i>Fluoroquinolone resistance in the environment and the human gut</i> – <i>Analyses of bacterial DNA sequences to explore the underlying mechanisms</i> Supervised by Professor D. G. Joakim Larsson (Biomedicine, University of Gothenburg), Professor Erik Kristiansson (Mathematical Sciences, Chalmers University of Technology) & Professor Edward R. B. Moore (Biomedicine, University of Gothenburg)
2007–2009	MSc in Bioinformatics and Systems Biology from Chalmers University of Technology
Thesis title	<i>Analysis of variance for cancer diagnostics using qPCR markers</i> Supervised by Professor Marita Olsson (Mathematical Sciences, Chalmers University of Technology) & Daniel Lindh (MultiD Analyses AB)
2004–2007	BSc in Bioengineering from Chalmers University of Technology
Thesis title	<i>Statistical analysis of errors in EST databases</i> Supervised by Professor Erik Kristiansson & Dr Alexandra Jauhiainen (Mathematical Sciences, Chalmers University of Technology)

EMPLOYMENT

2018–current	Applied researcher at the Department of Systems and Data Analysis, Fraunhofer-Chalmers Centre
2016–current	Researcher at the Department of Mathematical Sciences, Chalmers University of Technology/University of Gothenburg, in Professor Erik Kristiansson’s group
2014–2016	Postdoctoral researcher at the Department of Mathematical Sciences, Chalmers University of Technology/University of Gothenburg, in Professor Erik Kristiansson’s group
2014–2015	Bioinformatics specialist at 1928 diagnostics (30% position)
2010–2014	PhD student at the Institute of Biomedicine, the Sahlgrenska Academy, University of Gothenburg, in Joakim Larsson’s group
2009	R&D engineer at MultiD Analyses AB

PUBLICATIONS

Peer-reviewed

- Lund, D., Coertze, R. D., Parras-Moltó, M., Berglund, F., Flach, C. F., Johnning, A., Larsson, D. G. J., & Kristiansson, E. (2023). **Extensive screening reveals previously undiscovered aminoglycoside resistance genes in human pathogens.** *Communications Biology*, 6(1), 812.
- Hallbäck, E. T., Johnning, A., Myhrman, S., Studahl, M., Hentz, E., Elfvin, A., & Adlerberth, I. (2023). **Outbreak of OXA-48-producing Enterobacteriaceae in a neonatal intensive care unit in Western Sweden.** *European Journal of Clinical Microbiology & Infectious Diseases*, 1-9.
- Inda-Díaz, J. S., Lund, D., Parras-Moltó, M., Johnning, A., Bengtsson-Palme, J., & Kristiansson, E. (2023). **Latent antibiotic-resistance genes are abundant, diverse, and mobile in human, animal, and environmental microbiomes.** *Microbiome*, 11(1), 44.
- Nyblom, M.* , Johnning, A.* , Frykholm, K., Wrande, M., Müller, V., Goyal, G., Robertsson, M., Dvirnas, A., Sewunet, T., Kk., S., Ambjörnsson, T., Giske, C. G., Sandegren, L., Kristiansson, E., & Westerlund, F. (2023). **Strain-level bacterial typing directly from patient samples using optical DNA mapping.** *Communications Medicine*, 3(1), 31. (*Authors contributed equally)
- Lund, D., Kieffer, N., Parras-Moltó, M., Ebmeyer, S., Berglund, F., Johnning, A., Larsson, D. G. J., & Kristiansson, E. (2022). **Large-scale characterization of the macrolide resistome reveals high diversity and several new pathogen-associated genes.** *Microbial Genomics*, 8(1).
- Torstensson, E., Goyal, G., Johnning, A., Westerlund, F., & Ambjörnsson, T. (2021). **Combining dense and sparse labeling in optical DNA mapping.** *Plos one*, 16(11), e0260489.
- Leander, J., Almquist, J., Johnning, A., Larsson, J., & Jirstrand, M. (2021). **Nonlinear mixed effects modeling of deterministic and stochastic dynamical systems in Wolfram Mathematica.** *IFAC-PapersOnLine*, 54(7), 409-414.
- Berglund, F., Johnning, A., Larsson, D. G. J., & Kristiansson, E. (2020). **An updated phylogeny of the metallo- β -lactamases.** *Journal of Antimicrobial Chemotherapy*, 76(1), 117-123.
- Berglund, F., Böhm, M. E., Martinsson, A., Ebmeyer, S., Österlund, T., Johnning, A., Larsson, D. G. J., & Kristiansson, E. (2020). **Comprehensive screening of genomic and metagenomic data reveals a large diversity of tetracycline resistance genes.** *Microbial Genomics*, mgen000455.
- Müller, V.* , Nyblom, M.* , Johnning, A.* , Wrande, M., Dvirnas, A., Kk, S., Giske, C. G., Ambjörnsson, T., Sandegren, L., Kristiansson, E. & Westerlund, F. (2020). **Cultivation-free typing of bacteria using optical DNA mapping.** *ACS Infectious Diseases*, 6(5), 1076-1084. (*Authors contributed equally)

Karlsson, R., Thorsell, A., Gomila, M., Salvà-Serra, F., Jakobsson, H. E., Gonzales-Siles, L., Jaén-Luchoro, D., Skovbjerg, S., Fuchs, J., Karlsson, A., Boulund, F., Johnning, A., Kristiansson, E., & Moore, E. (2020). **Discovery of species-unique peptide biomarkers of bacterial pathogens by tandem mass spectrometry-based proteotyping.** *Molecular & Cellular Proteomics*, 19(3), 518-528.

Johnning, A., Karami, N., Tång-Hallbäck, E., Müller, V., Nyberg, L., Pereira, M. B., Stewart, C., Ambjörnsson, T., Westerlund, F., Adlerberth, I., & Kristiansson, E. (2018). **The resistomes of six carbapenem-resistant pathogens – a critical genotype-phenotype analysis.** *Microbial genomics*, 4(11): e000233.

Boulund, F., Karlsson, R., Gonzales-Siles, L., Johnning, A., Karami, N., Omar, A. B., Åhrén, C., Moore, E. R. B., & Kristiansson, E. (2017). **Typing and characterization of bacteria using bottom-up tandem mass spectrometry proteomics.** *Molecular & Cellular Proteomics*, 16(6): 1052-1063.

Bengtsson-Palme, J., Boulund, F., Edström, R., Feizi, A., Johnning, A., Jonsson, V. A., Karlsson, F. H., Pal, C., Pereira, M. B., Rehammar, A., Sanchez, J., Sanli, K., & Thorell, K. (2016). **Strategies to improve usability and preserve accuracy in biological sequence databases.** *Proteomics*, 16(18), 2454-2460.

Johnning, A., Kristiansson, E., Fick, J., Weijdegård, B., & Larson, D. G. J. (2015). **Resistance mutations in *gyrA* and *parC* are common in *Escherichia* communities of both fluoroquinolone-polluted and uncontaminated aquatic environments.** *Frontiers in microbiology*, 6, 1355.

Johnning, A., Kristiansson, E., Angelin, M., Marathe, N., Shouche, Y. S., Johansson, A., & Larsson, D. G. J. (2015). **Quinolone resistance mutations in the microbiota of Swedish travellers to India.** *BMC Microbiology*, 15(1): 1-8.

Flach, C. F., Johnning, A., Nilsson, I., Smalla, K., Kristiansson, E., & Larsson, D. G. J. (2015). **Isolation of novel *IncA/C* and *IncN* fluoroquinolone resistance plasmids from an antibiotic-polluted lake.** *Journal of Antimicrobial Chemotherapy*, 70(10): 2709-2717.

Johnning, A., Moore, E. R. B., Svensson-Stadler, L., Shouche, Y. S., Larsson, D. G. J., & Kristiansson, E. (2013). **Acquired genetic mechanisms of a multiresistant bacterium isolated from a treatment plant receiving wastewater from antibiotic production.** *Applied and Environmental Microbiology*, 79(23), 7256-7263.

Boulund, F., Johnning, A., Pereira, M. B., Larsson, D. G. J., & Kristiansson, E. (2012). **A novel method to discover fluoroquinolone antibiotic resistance (*qnr*) genes in fragmented nucleotide sequences.** *BMC genomics*, 13(1), 695.

TEACHING

2024	Co-supervision of master student Erik Aerts 30 hp, Chalmers University of Technology <i>TBD</i>
2024	Supervision of master student Jesper Olsson 30+15 hp, Chalmers University of Technology <i>TBD</i>
2024	Co-supervision of master student Michaela Holmström 60 hp, Chalmers University of Technology <i>TBD</i>
2023–2024	Introduction to bioinformatics 7.5 hp, advanced level, Chalmers University of Technology <i>Teaching assistant responsible for computer exercise sessions and report correction</i>
2023	Co-supervision of master student Alice Schiller 30 hp, Chalmers University of Technology <i>Large-scale screening of genomic data identifies novel mobile colistin resistance genes and reveals high over-representation in Pseudomonadota</i>
2022	Supervision of master student Oskar Gustafsson 30 hp, Chalmers University of Technology <i>Improving antibiotic resistance prediction through the integration of natural language processing models – Pre-training transformers to utilize both genotype and phenotype data</i>
2022–current	Mathematical statistics/Introduction to mathematical statistics 7.5 hp, undergraduate level. Chalmers University of Technology <i>Lecturer, examiner, and course administrator responsible for 180 students</i>
2021	Innovation och teknik – läkare Advanced level. Region Västra Götaland <i>Guest lecturer</i>
2021	Co-supervision of master student Sofia Johansson 30 hp, Chalmers University of Technology <i>High-resolution identification of vancomycin-resistant enterococci using optical DNA mapping</i>
2020–current	Co-supervision of PhD student David Lund Chalmers University of Technology
2020–2023	Co-supervision of PhD student Juan Inda Diaz University of Gothenburg <i>New AI-based methods for studying antibiotic-resistant bacteria</i>

- 2020** **Co-supervision of master student** Karin Ytterberg
60 hp, Chalmers University of Technology
Characterisation of the accessory genomes of predatory bacterial species
- 2020** **Co-supervision of master student** Beatrice Skyman
30 hp, Chalmers University of Technology
Prediction of antibiotic-resistant bacteria using deep neural networks
- 2019–2020** **Co-supervision of master student** David Lund
60 hp, Chalmers University of Technology
Identification of macrolide resistance genes in genomic and metagenomic data
- 2019** **Co-supervision of master student** Hampus Lane
30 hp, Chalmers University of Technology
Predicting antibiotic resistance phenotypes using neural networks
- 2018–2019** **DNA som en tidsspegel: från Neandertalare till framtida klimatförändringar**
3 hp, undergraduate level. University of Gothenburg.
Guest lecturer
- 2018–2019** **Co-supervision of PhD student** Fanny Berglund
Chalmers University of Technology
Identification of novel antibiotic resistance genes through large-scale data analysis
- 2017–2018** **Introduction to Bioinformatics**
7.5 hp, advanced level. Chalmers University of Technology
Lecturer and course administrator responsible for 60 students
- 2016–2017** **Supervision of master student** Martin Boström
30 hp, Chalmers University of Technology
Automated identification of antibiotic resistance mutations in bacterial genomes – Creation of the ARM-find pipeline
- 2016** **Statistics and probability**
3 hp, undergraduate level. Chalmers University of Technology
Lecturer, examiner, and course administrator responsible for 100 students
- 2015–2016** **Supervision of master student** Stefan Ebmeyer
60 hp, Chalmers University of Technology
Explorative analysis of the resistome of 362 globally collected ETEC isolates
- 2015** **Mathematical statistics**
7.5 hp, undergraduate level, Chalmers University of Technology
Teaching assistant responsible for exercise sessions
- 2014–2016** **Mathematical statistics and discrete mathematics**
7.5 hp, undergraduate level, Chalmers University of Technology
Teaching assistant responsible for exercise sessions, grading of reports and exams

2011	Large Scale Genomic Techniques, Analysis, and Modelling 7.5 hp, advanced level, Chalmers University of Technology <i>Guest lecturer</i>
2010	Co-supervision of master student Fredrik Boulund 30 hp, Chalmers University of Technology <i>Exploring antibiotic resistance genes in the human intestinal microbiome – Development of a framework for large-scale annotation of next-generation sequencing data</i>
2010	Co-supervision of summer student Fredrik Boulund 15 hp, Gothenburg University
Project title	<i>A computational pipeline for identification of novel qnr fluoroquinolone resistance genes in large metagenomic databases</i>
2010	Large Scale Genomic Techniques, Analysis, and Modelling 7.5 hp, Chalmers University of Technology <i>Lectured on qPCR and supervised a computer lab in microarray data analysis</i>
Examples of course evaluations	"Hon var den här kursens stora behållning och kan vara den enskilt största anledningen till att iaf jag klarade tentan.", "Anna är den bästa övningsledaren jag haft under in tid på Chalmers.", "Anna Johnning är en mycket duktig lärare.", "En så pass pedagogisk person är sällsynt på högskola – åtminstone inom matematik."

PRESENTATIONS

2023 Seminar title	The Infectious Diseases Clinic, Östra Hospital, Gothenburg. 30-minute seminar <i>Prediktion av antibiotika-resistens med hjälp av AI</i>
2023 Talk title	7th Annual CARE Conference, Gothenburg. 15-minute talk <i>Robust statistical tool for defining wild-type distributions of antimicrobial inhibition-zone diameters and calculating ECOFFs</i>
2021 Talk title	5th Annual CARE Conference, Gothenburg. 15-minute talk <i>AI for bacterial diagnostics</i>
2021 Seminar title	The Gothenburg Bioinformatics Network – GOTBIN, Gothenburg. 40-minute seminar <i>Bacterial Identification by Optical DNA Mapping</i>
2019 Talk title	4th Annual CARE Conference, Gothenburg. 15-minute talk <i>Optical DNA mapping for bacterial diagnostics</i>
2017 Seminar title	The Division of Physical Resource Theory, Chalmers, Gothenburg. 30-minute seminar <i>Attack of the Killer Bugs! An introduction to Antibiotic Resistance</i>
2017 Talk title	2nd Annual CARE Conference, Gothenburg. 15-minute talk <i>A detailed analysis of the resistomes of six carbapenem-resistant pathogens</i>
2016 Talk title	Microbiology Spring Meeting, Helsingborg. 15-minute talk <i>The genomes of carbapenem-resistant pathogens of five different species isolated at a Swedish hospital</i>
2016 Poster title	26th ECCMID 2015, Amsterdam. Poster presentation <i>Prediction of antibiotic resistance phenotypes using the genomes of carbapenem-resistant pathogens of five different species isolated at a Swedish hospital</i>
2015 Talk title	14th Swedish Bioinformatics Workshop 2015, Stockholm. 30-minute talk <i>Predicting antibiotic resistance phenotypes of five carbapenem-resistant isolates using whole-genome sequencing</i> Awarded Best Presentation at the workshop
2015 Poster title	6th Congress of European Microbiologists by FEMS, Maastricht. Poster pr. <i>The genomes of carbapenem-resistant pathogens of five different species isolated at a Swedish hospital</i>
2015 Poster title	25th ECCMID 2015, Copenhagen. Poster presentation <i>The genomes of carbapenem-resistant pathogens of five different species isolated at a Swedish hospital</i>
2014 Poster title	13th Swedish Bioinformatics Workshop 2014, Gothenburg. Poster pr. <i>Predicting antibiotic resistance profile in five carbapenem-resistant isolates using whole-genome sequencing</i>

2013	Sustainability 2013, Gothenburg. 6-minute talk followed by a panel debate
Talk title	<i>Antibiotic pollution</i>
2012	4th Annual Next Generation Sequencing Congress, London. Poster pr.
Poster title	<i>The Genome of an Extensively Drug-Resistant Bacterium</i>
2011	11th Swedish Bioinformatics Workshop, Lund. 20-minute talk
Talk title	<i>The genome of an extensively drug-resistance bacterium</i>
2011	Veterinary Congress, Uppsala. 30-minute talk
Talk title	<i>Antibiotikaproduktionens miljöförroreningar – en onödig källa till resistens?</i>
2011	4th Congress of European Microbiologists by FEMS, Geneva. Poster highlight
Poster title	<i>The genome of an extensively drug-resistant bacterium isolated from a wastewater treatment plant receiving effluent from antibiotic manufacturing</i>
2011	Adlerbert Research Foundation seminar, Gothenburg. 30-minute talk
Talk title	<i>Antibiotika i miljön – En orsak till resistens?</i>
2011	SETAC Europe 21st Annual Meeting, Milan. Poster presentation
Poster title	<i>The genome of an extensively drug-resistant bacterium isolated from a wastewater treatment plant receiving effluent from antibiotic manufacturing</i>
2011	11th SocBiN Conference, Helsinki. 15-minute talk & poster presentation
Talk title	<i>The genome of an extensively drug-resistant bacterium isolated from a wastewater treatment plant receiving effluent from antibiotic manufacturing</i>
2011	Microbiology Spring Meeting, Uppsala. 15-minute talk
Talk title	<i>The genome of an extensively drug-resistant bacterium isolated from a wastewater treatment plant receiving effluent from antibiotic manufacturing</i>
2010	Deep Sequencing Techniques: Bioscience Applications, Statistical and Computational Practices and Challenges, Gothenburg. 20-minute talk
Talk title	<i>The genome of an extensively drug-resistant bacterium</i>
2010	35th FEBS Congress: Molecules of Life, Gothenburg. Poster presentation
Poster title	<i>Whole-genome sequencing of a multi-resistant bacterium isolated from a wastewater treatment plant receiving effluent from antibiotic drug manufacturing</i>
2010	10th Swedish bioinformatics workshop, Gothenburg. Poster presentation
Poster title	<i>Whole-genome sequencing of a multi-resistant bacterium isolated from a wastewater treatment plant receiving effluent from antibiotic drug manufacturing</i>

GRANTS AND AWARDS

2024	Vetenskapsrådet & JPIAMR, principal investigator, 3.5 Mkr (1 036 kEUR to consortium)
2022	Erling-Persson Foundation, co-applicant, 9 Mkr
2021	Vinnova, co-applicant, 3.7 Mkr
2021	Chalmers Artificial Intelligence Research Centre (CHAIR), co-applicant, 1.2 Mkr
2020	Centre for Antibiotic Resistance Research (CARE), principal investigator, 596 276 kr
2010–2013, 2015, 2018	Adlerbert Research Foundation, a total of 232 500 kr
2015	Awarded Best Presentation at the Swedish Bioinformatics Workshop
2012	Knut och Alice Wallenbergs stiftelse, 9 000 kr
2012	Wilhelm och Martina Lundgrens vetenskapsfond, 8 000 kr
2011	Resebidrag ur donationsmedel för ograduerade forskare vid Sahlgrenska akademin, 8 000 kr
2010	Hvitfeldtska resestipendium, 18 000 kr