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## Employment

01/2024 - now  
Associate Professor, UMC Utrecht  
05/2018 - 12/2023  
Assistant Professor, UMC Utrecht  
08/2015 - 04/2018  
Senior Bioinformatician, UMC Utrecht  
01/2012 - 07/2015  
Postdoctoral researcher, Erasmus MC  
09/2011 - 12/2011  
Postdoctoral researcher, RIVM  
03/2011 - 04/2011  
Visiting Scientist, Stellenbosch University, SA  
09/2007 - 08/2011  
PhD student, RIVM and Radboud UMC  
01/2004 - 08/2007  
Sequencing Manager, Microsynth AG

## Research outputs

### Dissemination of IncQ1 Plasmids Harboring NTE<sub>KPC</sub>-IId in a Brazilian Hospital

Boralli, C. M. D. S., Paganini, J. A., Meneses, R. S., Mata, C. P. S. M. D., Leite, E. M. M., Schürch, A. C., Paganelli, F. L., Willems, R. J. L. & Camargo, I. L. B. C., Jan 2025, In: *Microorganisms*. 13, 1, 16 p., 180.

### Pan-pathogen deep sequencing of nosocomial bacterial pathogens in Italy in spring 2020: a prospective cohort study

Thorpe, H. A., Pesonen, M., Corbella, M., Pesonen, H., Gaiarsa, S., Boinett, C. J., Tonkin-Hill, G., Mäklin, T., Pöntinen, A. K., MacAlasdair, N., Gladstone, R. A., Arredondo-Alonso, S., Kallonen, T., Jamrozy, D., Lo, S. W., Chaguza, C., Blackwell, G. A., Honkela, A., Schürch, A. C. & Willems, R. J. L. & 8 others, Merla, C., Petazzoni, G., Feil, E. J., Cambieri, P., Thomson, N. R., Bentley, S. D., Sasser, D. & Corander, J., Oct 2024, In: *The Lancet. Microbe*. 5, 10, p. 100890 100890.

### PlasmidEC and gplas2: an optimized short-read approach to predict and reconstruct antibiotic resistance plasmids in *Escherichia coli*.

Paganini, J. A., Kerkvliet, J. J., Vader, L., Plantinga, N. L., Meneses, R., Corander, J., Willems, R. J. L., Arredondo-Alonso, S. & Schürch, A. C., Feb 2024, In: *Microbial genomics*. 10, 2, 001193.

### Metagenomic assembly is the main bottleneck in the identification of mobile genetic elements

Kerkvliet, J. J., Bossers, A., Kers, J. G., Meneses, R., Willems, R. & Schürch, A. C., 2024, In: *PeerJ*. 12, p. e16695 e16695.

### Mge-cluster: a reference-free approach for typing bacterial plasmids

Arredondo-Alonso, S., Gladstone, R. A., Pöntinen, A. K., Gama, J. A., Schürch, A. C., Lanza, V. F., Johnsen, P. J., Samuelsen, Ø., Tonkin-Hill, G. & Corander, J., 1 Sept 2023, In: *NAR genomics and bioinformatics*. 5, 3, 15 p., lqad066.

### Characterization of bla<sub>KPC-2</sub> and bla<sub>NDM-1</sub> Plasmids of a *K. pneumoniae* ST11 Outbreak Clone

Boralli, C. M. D. S., Paganini, J. A., Meneses, R. S., Mata, C. P. S. M. D., Leite, E. M. M., Schürch, A. C., Paganelli, F. L., Willems, R. J. L. & Camargo, I. L. B. C., May 2023, In: *Antibiotics*. 12, 5, 926.

### A high-throughput multiplexing and selection strategy to complete bacterial genomes

Pöntinen, A. K., Cléon, F., Gladstone, R. A., Schürch, A. C., Johnsen, P. J., Samuelsen, Ø. & Corander, J., 9 Dec 2021, In: *GigaScience*. 10, 12, giab079.

### **Recovering escherichia coli plasmids in the absence of long-read sequencing data**

Paganini, J. A., Plantinga, N. L., Arredondo-alonso, S., Willems, R. J. L. & Schürch, A. C., 28 Jul 2021, In: Microorganisms. 9, 8, p. 1-20 1613.

### **Comparative genomics of ESBL-producing Escherichia coli (ESBL-Ec) reveals a similar distribution of the 10 most prevalent ESBL-Ec clones and ESBL genes among human community faecal and extra-intestinal infection isolates in the Netherlands (2014-17)**

Verschuuren, T. D., van Hout, D., Arredondo-Alonso, S., Fluit, A. C., Reuland, E. A., Top, J., Schürch, A. C., Bosch, T., Bonten, M. J. M., Kluytmans, J. A. J. W. & Willems, R. J. L., 12 Mar 2021, In: The Journal of antimicrobial chemotherapy. 76, 4, p. 901-908 8 p.

### **Apparent nosocomial adaptation of Enterococcus faecalis predates the modern hospital era**

Pöntinen, A. K., Top, J., Arredondo-Alonso, S., Tonkin-Hill, G., Freitas, A. R., Novais, C., Gladstone, R. A., Pesonen, M., Meneses, R., Pesonen, H., Lees, J. A., Jamrozny, D., Bentley, S. D., Lanza, V. F., Torres, C., Peixe, L., Coque, T. M., Parkhill, J., Schürch, A. C. & Willems, R. J. L. & 1 others, Corander, J., 9 Mar 2021, In: Nature Communications. 12, 1, 13 p., 1523.

### **Mode and dynamics of vanA-type vancomycin resistance dissemination in Dutch hospitals**

Arredondo-Alonso, S., Top, J., Corander, J., Willems, R. J. L. & Schürch, A. C., 20 Jan 2021, In: Genome Medicine. 13, 1, p. 1-18 18 p., 9.

### **gplas: a comprehensive tool for plasmid analysis using short-read graphs**

Arredondo-Alonso, S., Bootsma, M., Hein, Y., Rogers, M. R. C., Corander, J., Willems, R. J. L. & Schürch, A. C., 15 Jun 2020, In: Bioinformatics (Oxford, England). 36, 12, p. 3874-3876 3 p.

### **Plasmids shaped the recent emergence of the major nosocomial pathogen Enterococcus faecium**

Arredondo-Alonso, S., Top, J., McNally, A., Puranen, S., Pesonen, M., Pensar, J., Marttinen, P., Braat, J. C., Rogers, M. R. C., van Schaik, W., Kaski, S., Willems, R. J. L., Corander, J. & Schürch, A. C., 11 Feb 2020, In: mBio. 11, 1, 17 p., e03284-19.

### **Extended-spectrum beta-lactamase (ESBL)-producing and non-ESBL-producing Escherichia coli isolates causing bacteremia in the Netherlands (2014 - 2016) differ in clonal distribution, antimicrobial resistance gene and virulence gene content**

van Hout, D., Verschuuren, T. D., Buijning-Verhagen, P. C. J., Bosch, T., Schürch, A. C., Willems, R. J. L., Bonten, M. J. M. & Kluytmans, J. A. J. W., 1 Jan 2020, In: PLoS ONE. 15, 1, p. 1-14 14 p., e0227604.

### **Genomic rearrangements uncovered by genome-wide co-evolution analysis of a major nosocomial pathogen, enterococcus faecium**

Top, J., Arredondo-Alonso, S., Schürch, A. C., Puranen, S., Pesonen, M., Pensar, J., Willems, R. J. L. & Corander, J., 2020, In: Microbial genomics. 6, 12, p. 1-8 8 p., 000488.

### **Sequence-Based Epidemiology of an OXA-48 Plasmid during Hospital Outbreak**

Hidalgo, L., de Been, M., Rogers, M. R. C., Schürch, A. C., Scharringa, J., van der Zee, A., Bonten, M. J. M. & Fluit, A. C., Dec 2019, In: Antimicrobial Agents and Chemotherapy. 63, 12, e01204-19.

### **Prevalence, risk factors and genetic characterisation of extended-spectrum beta-lactamase and carbapenemase-producing Enterobacteriaceae (ESBL-E and CPE): a community-based cross-sectional study, the Netherlands, 2014 to 2016**

van den Bunt, G., van Pelt, W., Hidalgo, L., Scharringa, J., de Greeff, S. C., Schurch, A. C., Mughini-Gras, L., Bonten, M. J. M. & Fluit, A. C., 1 Oct 2019, In: Eurosurveillance. 24, 41, p. 29-39 11 p.

### **Draft Genome Sequence of Haemophilus haemolyticus Strain 16/010 O, Isolated from a Sputum Sample from a Cystic Fibrosis Patient**

Fluit, A. C., Bayjanov, J. R., Tunney, M., Elborn, J. S., Rogers, M. R. C., Schürch, A. C. & Ekkelenkamp, M. B., 6 Jun 2019, In: Microbiology resource announcements. 8, 23, e0024319.

**datacarpentry/shell-genomics: Data Carpentry: Introduction to the shell for genomics data**

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**Design of the EPIGENEC Study: Assessing the EPIdemiology and GENetics of Escherichia coli in the Netherlands**

van Hout, D., Verschuuren, T., Bruijning-Verhagen, P., Bosch, T., Reuland, A., Fluit, A., Schürch, A., Willems, R., de Greeff, S. C., van 't Veen, A., Kluijtmans, J. & Bonten, M., 7 Feb 2019, (Preprints).

**Corrigendum: Mlplasmids: A user-friendly tool to predict plasmid-and chromosome-derived sequences for single species, (Microbial Genomics), (2018), 4, 10.1099/mgen.0.000224**

Arredondo-Alonso, S., Rogers, M. R. C., Braat, J. C., Verschuuren, T. D., Top, J., Corander, J., Willems, R. J. L. & Schürch, A. C., 1 Jan 2019, In: Microbial genomics. 5, 1, 000249.

**mlplasmids: a user-friendly tool to predict plasmid- and chromosome-derived sequences for single species**

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**Whole genome sequencing options for bacterial strain typing and epidemiologic analysis based on single nucleotide polymorphism versus gene-by-gene-based approaches**

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**Identification of HCV Resistant Variants against Direct Acting Antivirals in Plasma and Liver of Treatment Naïve Patients**

Raj, V. S., Hundie, G. B., Schürch, A. C., Smits, S. L., Pas, S. D., Le Pogam, S., Janssen, H. L. A., De Knecht, R. J., Osterhaus, A. D. M. E., Najera, I., Boucher, C. A. & Haagmans, B. L., 1 Dec 2017, In: Scientific Reports. 7, 1, 4688.

**On the (im)possibility of reconstructing plasmids from whole-genome short-read sequencing data**

Arredondo-Alonso, S., Willems, R. J., van Schaik, W. & Schürch, A. C., 1 Oct 2017, In: Microbial genomics. 3, 10, 000128.

**Challenges and opportunities for whole-genome sequencing-based surveillance of antibiotic resistance**

Schürch, A. C. & van Schaik, W., 1 Jan 2017, In: Annals of the New York Academy of Sciences. 1388, 1, p. 108-120 13 p.

**CRISPR/Cas9-Mediated Genome Editing of Herpesviruses Limits Productive and Latent Infections**

van Diemen, F. R., Kruse, E. M., Hooykaas, M. J. G., Bruggeling, C. E., Schürch, A. C., van Ham, P. M., Imhof, S. M., Nijhuis, M., Wiertz, E. J. H. J. & Lebbink, R. J., 1 Jun 2016, In: PLoS Pathogens. 12, 6, e1005701.

**Recovering full-length viral genomes from metagenomes**

Smits, S. L., Bodewes, R., Ruiz-González, A., Baumgärtner, W., Koopmans, M. P., Osterhaus, A. D. M. E. & Schürch, A. C., 1 Jan 2015, In: Frontiers in Microbiology. 6, OCT, 1069.

**Metagenomic survey for viruses in Western Arctic caribou, Alaska, through iterative assembly of taxonomic units**

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**New viruses in idiopathic human diarrhea cases, the Netherlands**

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**Genetic relatedness of dolphin rhabdovirus with fish rhabdoviruses**

Siegers, J. Y., van de Bildt, M. W. G., van Elk, C. E., Schürch, A., Tordo, N., Kuiken, T., Bodewes, R. & Osterhaus, A. D. M. E., Jun 2014, In: Emerging infectious diseases. 20, 6, p. 1081-1082 2 p.

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De Beer, J. L., Akkerman, O. W., Schürch, A., Mulder, A., Van Der Werf, T. S., Van Der Zanden, A. G. M., Van Ingen, J. & Van Soolingen, D., May 2014, In: *Journal of Clinical Microbiology*. 52, 5, p. 1338-1342 5 p.

Assembly of viral genomes from metagenomes

Smits, S. L., Bodewes, R., Ruiz-Gonzalez, A., Baumgärtner, W., Koopmans, M. P., Osterhaus, A. D. M. E. & Schürch, A., 2014, In: *Frontiers in Microbiology*. 5, DEC, 714.

Inferring patient to patient transmission of *Mycobacterium tuberculosis* from whole genome sequencing data

Bryant, J. M., Schürch, A., van Deutekom, H., Harris, S. R., de Beer, J. L., de Jager, V., Kremer, K., van Hijum, S. A. F. T., Siezen, R. J., Borgdorff, M., Bentley, S. D., Parkhill, J. & van Soolingen, D., 27 Feb 2013, In: *BMC Infectious Diseases*. 13, 1, 110.

Novel cyclovirus in human cerebrospinal fluid, Malawi, 2010-2011

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Combined species identification, genotyping, and drug resistance detection of *mycobacterium tuberculosis* cultures by mlpA on a bead-based array

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DNA fingerprinting of *Mycobacterium tuberculosis*: From phage typing to whole-genome sequencing

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European 2 - A clonal complex of *Mycobacterium bovis* dominant in the Iberian Peninsula

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Comparative analysis of *mycobacterium tuberculosis* *pe* and *ppe* genes reveals high sequence variation and an apparent absence of selective constraints

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Proteogenomic analysis of polymorphisms and gene annotation divergences in prokaryotes using a clustered mass spectrometry-friendly database

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The tempo and mode of molecular evolution of *Mycobacterium tuberculosis* at patient-to-patient scale

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Physical mapping and identification of a candidate for the leaf rust resistance gene Lr1 of wheat

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