Matthias Wielscher

Mobile: 0043-650-8641043 Email: matthias.wielscher@meduniwien.ac.at

Home address:	Martinstraße 91, 1180 Wien, Austria
Work address:	Medical University of Vienna, Währinger Gürtel 18-20, 1090 Vienna
ORCID:	https://orcid.org/0000-0003-4138-1383
Webpages:	https://www.meduniwien.ac.at/researcher/matthias_wielscher https://www.imperial.ac.uk/people/m.wielscher

Employments

since 09/2022	**Senior Research Associate** Medical University of Vienna, Dept. of Laboratory Medicine
since 01/2020	**Senior Research Associate** Medical University of Vienna, Dept. of Dermatology
06/2018 -12/2019	**Bioinformatician / Senior Analyst** Genomics England (100k Genomes Project)
since 06/2018	**Consultant for Genetic Epidemiology** Imperial College, Dept. of Epidemiology and Biostatistics
07/2015- 05/2018	**Research Associate** Imperial College, Dept. of Epidemiology and Biostatistics
01/2011-04/2015	**PhD Student** AIT, Department of Health and Environment
2009-2011	**Research Assistant** AIT, Department of Health and Environment
2008-2009	**MSc Student** AIT, Department of Health and Environment

Education

2011-2015	**PhD thesis** University of Natural Resources and Life Science, *Title: Differential DNA methylation signatures in interstitial lung disease and lung cancer reveal novel biomarkers*
2012-2013	Training in Statistics at Technical University of Vienna
2008-2009	**MSc Thesis** University of Vienna, *Title: DNA methylation analysis for minimal-invasive Breast cancer diagnostic testing*
2002-2007	**Degree program Genetics/Microbiology** University of Vienna, Austria

Leaves

02/2014 – 10/2014	Paternal Leave 1
10/2009 – 06/2010	Paternal Leave 2

Main research area

At the Department of Dermatology, I set up a pipeline to investigate skin resident bacteria and phage genomes. For this we combined several large scale publicly available data sets and novel data sets.

I have a strong interest in genetic epidemiology and have actively collaborated with the Department of Epidemiology on multiple projects, contributing my expertise in genetic epidemiology to their endeavors. Recently, we have compiled a comprehensive Austrian whole exome dataset (n=150) aimed at identifying rare and common genetic variants that elevate the risk of skin cancer susceptibility following organ transplantation at the General Hospital of Vienna.

At the Department of Laboratory Medicine, I am managing the NGS pipelines used for WES based clinical diagnosis, while testing new reporting standards and variant calling and annotation approaches.

Major scientific contributions/additional research achievements

Research Data generation: While working in Genomics England Research environment I aggregated and quality controlled 640 million variants across 60.000 patients from individual whole genome datasets to one joint dataset. The dataset occupied 120 TB of storage and to our best knowledge was the largest call set outside of the US at the time.

Software: Most of my applications and code is publicly available on GitHub https://github.com/Mwielscher . This includes: scripts and instructions for GWAS, Mendelian Randomization, Triangulation analysis, GATK based germline variant calling, GATK somatic variant calling, setting up a secure cloud environment, RNA sequencing, single cell RNA sequencing and Identification of phages in meta-genomic datasets.

Project Coordination: I have coordinated a large-scale epigenome wide association study with contributors from more than 100 different Institutions worldwide. I am also member of several genetic consortia such as GIANT, GLGC and Spirometer.

Research Grant preparation: I have been involved in successful Grant applications: PREcisE - A precision nutri-epigenetic approach to tackle the mother-to-child transmission of impaired glucose and GENEROSITY - A sustainable and multi-actor approach to prevent another generation of childhood obesity in Europe. In Austria, I consistently develop and submit grant proposals to a range of major funding agencies, including the FWF, WWTF, and as academic partner in FFG programs. My commitment to securing research funding is ongoing, with current proposals under review and some advancing to later stages in the evaluation process."

Scholarly activities: I am a topic Editor for Frontiers in Genetics and I am reviewing regularly for International Journal of Epidemiology and American Journal of Epidemiology as well as occasionally several other journals.

Patent: I hold a patent for serum DNA methylation markers. ***Diagnosis of Lung Cancer***. European Patent Application EP14194732.5, filed 25-11-2014 and U.S. application PCT /EP2015/077478

Publications

total number of publications: **51**
total number of citations: **4131**
h index: **31**
https://scholar.google.com/citations?user=tWrztwwAAAAJ&hl=de

Wielscher M, Pfisterer K, Samardzic D, Balsini P, Bangert C, Jaeger K, Buchberger M, Selitsch B, Pjevac P, Willinger B, Weninger W, **The Phageome in Normal and Inflamed Human Skin.** Available at SSRN: http://dx.doi.org/10.2139/ssrn.4294793 In Press at Science Advances|AAAS

Sunder-Plassmann R, Geusau A, Endler G, Weninger W and **Wielscher M**. **Identification of Genetic Risk Factors for Keratinocyte Cancer in Immunosuppressed Solid Organ Transplant Recipients: A Case-Control Study.**
Cancers (Basel). 2023 Jun 26;15(13):3354. doi: 10.3390/cancers15133354.

Wielscher M, Mandaviya P, Kuehnel B, Joehanes R, Mustafa R [..], Jarvelin MR. ***DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases.*** Nat Commun. 2022 May 3;13(1):2408. doi: 10.1038/s41467-022-29792-6.

Wielscher M, Amaral AFS, van der Plaat D, Sebert S, Wain L, Sebert S, Mosen-Ansorena D, Auvinen J, Herzig A, Dehghan A, Jarvis D, Jarvelin MR. ***Genetic correlation and causal relationships between cardio-metabolic traits and Lung function Impairment.*** Genome Med. 2021 Jun 21;13(1):104. doi: 10.1186/s13073-021-00914-x.

Wielscher M, Vierlinger K, Kegler U, Ziesche R, Gsur A, Weinhausel A. ***Diagnostic Performance of Plasma DNA Methylation Profiles in Lung Cancer, Pulmonary Fibrosis and COPD.*** EBioMedicine 2015, 2(8):929-936.

Wielscher M, Liou W, Pulverer W, Singer CF, Rappaport-Fuerhauser C, Kandioler D, Egger G, Weinhausel A. ***Cytosine 5-Hydroxymethylation of the LZTS1 Gene Is Reduced in Breast Cancer.*** Translational oncology 2013, 6(6):715-721.

Wielscher M, Pulverer W, Peham J, Hofner M, Rappaport CF, Singer C, Jungbauer C, Nohammer C, Weinhausel A. ***Methyl-binding domain protein-based DNA isolation from human blood serum combines DNA analyses and serum-autoantibody testing***. BMC clinical pathology 2011, 11:11.

Imboden M*, **Wielscher M***, Rezwan FI*, et al. ***Epigenome-wide association study of lung function level and its change.*** Eur Respir J. 2019 Jul 4;54(1):1900457. doi: 10.1183/13993003.00457-2019. Print 2019 Jul. * contributed equally

100,000 Genomes Project Pilot Investigators, amongst authors **Wielscher M,** Caulfield M. ***100,000 Genomes Pilot on Rare-Disease Diagnosis in Health Care - Preliminary Report.*** N Engl J Med. 2021 Nov 11;385(20):1868-1880. doi: 10.1056/NEJMoa2035790.