

Curriculum Vitæ – Dr. rer. nat. Felix M. Key

CONTACT INFORMATION	Max Planck Institute for Infection Biology Charitéplatz 1 Campus Charité Mitte 10117 Berlin Germany Phone: +49 (0) 30 28460474 Email: key@mpiib-berlin.mpg.de Web: website
EDUCATION	Ph.D., Population Genetics (<i>summa cum laude</i>) Dec 2010 - Apr 2016 Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany. Dissertation: <i>Human adaptation in the light of ancient and modern genomes</i> . Advisor: Aida M. Andrés. Reviewer: Svante Pääbo and Lluis Quintana-Murci.
	Diploma, Human Biology Oct 2004 - Apr 2010 University of Greifswald, Greifswald, Germany Major: Immunology, Minor: Microbiology, Ecotoxicology Thesis: <i>Influence of polymicrobial sepsis on a subsequent immune response</i> Advisor: Barbara Broeker
PROFESSIONAL EXPERIENCE	Independent Max Planck Research Group Leader (W2) since Sep 2020 Max Planck Institute for Infection Biology, Berlin, Germany Field: <i>Evolutionary Pathogenomics</i>
	Postdoctoral fellow Aug 2018 - Aug 2020 Massachusetts Institute of Technology, Cambridge, USA Topic: <i>Within-host microbial evolution, Population Genetics</i> Advisor: Tami D. Lieberman
	Postdoctoral associate Jul 2016 - Aug 2018 Max Planck Institute for the Science of Human History, Jena, Germany Topic: <i>Ancient Microbial Genomics, Metagenomics, Archaeogenetics</i> Advisor: Johannes Krause
	Ph.D. Student Dec 2010 - Jun 2016 Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany Topic: <i>Human adaptation in the light of ancient and modern genomes</i> Advisor: Aida M. Andrés (now at UCL)
	Diploma Student May 2009 - Apr 2010 University of Greifswald, Greifswald, Germany Topic: <i>Influence of polymicrobial sepsis on a subsequent immune response</i> Advisor: Barbara Broeker
	Internship Sep 2007 - Mar 2008 University of British Columbia, Vancouver, Canada

SELECTED
RESEARCH
ARTICLES

Biomedical Research Centre
Topic: *p53-dependent transcription and tumor suppression are not affected in Set7/9-deficient mice*
Advisor: [Fabio Rossi](#)

[Google Scholar](#) for a complete list of publications

8. **Felix M. Key**, Veda D Khadka, Carolina Romo-González, Kimbria J Blake, Liwen Deng, Tucker C Lynn, Jean C Lee, Isaac M Chiu, Maria Teresa García-Romero, Tami D Lieberman
On-person adaptive evolution of *Staphylococcus aureus* during atopic dermatitis increases disease severity. *Cell Host & Microbe* (2023)
[weblink](#)

7. Arthur Kocher, Luka Papac, Rodrigo Barquera, **Felix M Key**, [164 co-authors], Wolfgang Haak, Johannes Krause, Denise Kühnert
Ten millennia of hepatitis B virus evolution. *Science* (2021)
[weblink](#)

6. **Felix M. Key**, Cosimo Posth, Luis R. Esquivel Gomez, [40 co-authors], Denise Kuehnert, Alexander Herbig, Johannes Krause
Emergence of human-adapted *Salmonella enterica* is linked to the Neolithization process. *Nature Ecol & Evol* (2020)
[weblink](#)

5. Ron Hübner*, **Felix M. Key***, Christina Warinner, Kirsten Bos, Johannes Krause, Alexander Herbig
HOPS: Automated detection and authentication of pathogen DNA in archaeological remains. *Genome Biology* (2019)
[weblink](#)

4. **Felix M. Key**, Muslihudeen Abdul-Aziz, Roger Mundry, Benjamin Peter, Mauro D'Amato, Megan Dennis, Joshua Schmidt, Aida Andrés.
Local adaptation of a human cold receptor along a latitudinal cline. *PLoS Genetics* e1007298 (2018)
[weblink](#)

3. Ben Krause-Kyora*, Julian Susat*, **Felix M. Key**, Denise Kühnert, Esther Bosse, Alexander Immel, Christoph Rinne, Sabin-Christin Kornell, Diego Yepes, Sören Franzenburg, Henrike O Heyne, Thomas Meier, Sandra Lösch, Harald Meller, Susanne Friederich, Nicole Nicklisch, Kurt W Alt, Stefan Schreiber, Andreas Tholey, Alexander Herbig, Almut Nebel, Johannes Krause
Neolithic and medieval virus genomes reveal complex evolution of Hepatitis B *eLife*. (2018)
[weblink](#)

2. **Felix M. Key**, Qiaomei Fu, Frédéric Romagné, Michael Lachmann, Aida M. Andrés.

Human adaptation and population differentiation in the light of ancient genomes.
Nature Communications, 7:10775. (2016). [weblink](#)

1. **Felix M. Key**, Benjamin Peter, Megan Y Dennis, Emilia Huerta-Sánchez, Wei Tang, Ludmila Prokunina-Olsson, Rasmus Nielsen, Aida M Andrés.
 Selection on a Variant Associated with Improved Viral Clearance Drives Local, Adaptive Pseudogenization of Interferon Lambda 4 (*IFNL4*). **PLoS Genetics**, 10:e1004681. (2014)
[weblink](#)
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GRANTS AND FUNDING

Grant	Jan 2025 - Dec 2028
Volkswagen Foundation - Pioneering Research program	500,000Euro
Grant	Oct 2021 - Aug 2023
Klaus Tschira Boost Fund	80,000Euro
Core Funding	Sep 2020 - Feb 2026
Independent Max Planck Research Group	1,895,000Euro
Grant	Mar 2020 - Jun 2023
EASI Genomics Transnational Access Projects	50,000Euro
Postdoctoral Stipend	Aug 2018 - Aug 2020
German Research Foundation <i>Forschungsstipendium</i>	130,000Euro
PhD Stipend	Dec 2010 - Dec 2014
International Max Planck Research School 'The Leipzig School of Human Origins'	
Travel Grant	Sep 2007
Deutsche Akademische Austauschdienst (for Internship at BRC in Vancouver, Canada)	

AWARDS

PLoS Genetics Research Prize	2019
Award for highly recognised research article published in 2018: Key et al. Plos Genetics	

PRESENTATIONS & PUBLIC OUTREACHG (SELECTED)

Talk	Wuerzburg (Germany), Jun 2024
7th Joint Microbiology & Infection Conference. <i>Microbiome translocation and within-patient evolution promotes opportunistic, nosocomial infections.</i>	
Talk	Zurich (Switzerland), Apr 2024
Invited talk at University Zurich. <i>Pathogen emergence during prehistory.</i>	
Talk	Paris (France), Apr 2022
Invited talk at Pasteur Institute. <i>Microbial on-person evolution during chronic disease.</i>	

Talk

Boston (USA), Nov 2019

Science of the human past meeting. *Microbial genomics in the era of ancient DNA.*

Talk

New York (USA), Jul 2019

CSHL Microbiome. *Spread and adaptation of *Staphylococcus aureus* on the lesions on children with atopic dermatitis.*

Talk

Heidelberg (Germany), Mar 2018

EMBO Conference on Reconstructing the Human Past. *6,500 year old *Salmonella enterica* genomes link human-host adaptation to animal domestication.*

Talk

Austin (USA), Jul 2017

Annual meeting of the Society for Molecular Biology and Evolution. *High-throughput pathogen detection in ancient metagenomic data.*

Talk

Vienna (Austria), July 2015

Annual meeting of the Society for Molecular Biology and Evolution. *Ancient Genomes improve our understanding of human population differentiation.*

Talk

Zurich (Switzerland), April 2015.

Swiss Society for Medical Genetics. *Using Ancient and Present-Day Human Genomes to Understand Local Adaptation and Medically-Relevant Phenotypes.*

Talk

Berkeley (USA), April 2013

Department of Integrative Biology (UC Berkeley). *Adaptive Pseudogenization of IFNL4 - A gene that underlies variation of Hepatitis C clearance.*

TEACHING &
TRAINEES

1. **Current advisees** at *Evolutionary Pathogenomics* lab (MPI IB):
PhD students (Ian Light [*2021], Martin Fenk [*2021], Veronica Rozek [*2023], Lilly Bartsch [*2024]) and postdoctoral associate (Thomas Silvers [*2024])
 2. **Past advisees** at *Evolutionary Pathogenomics* lab (MPI IB) and before:
Postdoctoral associate (Anne K. Runge), MS thesis (Remmora Gomaid), BS thesis (Laura Osterheldt) and internships (Lisa Skroblin, Fatumata Sow, Elina Coquery, Levin Alleweldt, Muslihudeen Abdul-Aziz, Katalina Bobowik)
 3. **Teaching** Master course Immunobiology May 2024
Taught in Lecture Series at Freie University (Berlin)
 4. **Teaching** Graduate School for Infectious Disease and Immunology May 2021
Taught in Lecture Series Infection Biology
 5. **Teaching** Graduate School: IMPRS of Human Origin Jun 2016
Taught module about ongoing research projects at MPI EVA.
 6. **Teaching** Programming for Evolutionary Biology Course Feb 2016
Population Genomics together with Stefan Laurent (Jensen Lab, U Lausanne).
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