

Curriculum Vitæ – Felix M. Key

CONTACT INFORMATION
Max Planck Institute for Infection Biology
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Campus Charité Mitte
10117 Berlin
Germany
Email: fkey@mit.edu
Web: [website](#)

PROFESSIONAL EXPERIENCE

Max Planck Research Group Leader since Sep 2020
Max Planck Institute for Infection Biology, Berlin, Germany
Field: *Evolutionary pathogenomics*

Postdoctoral fellow Aug 2018 - Jul 2020
Massachusetts Institute of Technology, Cambridge, USA
Topic: *Microbial intrahost evolution, Metagenomics, Population Genetics*
Advisor: Tami D. Lieberman

Postdoctoral associate Jul 2016 - Aug 2018
Max Planck Institute for the Science of Human History, Jena, Germany
Topic: *Population Genetics, ancient DNA, Metagenomics*
Advisor: Johannes Krause & Alexander Herbig

Postdoctoral associate May 2016 - Jun 2016
Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany
Topic: *Human adaptation along a latitudinal cline*
Advisor: Aida M. Andrés

Ph.D. Student Dec 2010 - Apr 2016
Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany
Topic: *Human adaptation in the light of ancient and modern genomes*
Advisor: Aida M. Andrés

Diploma Student May 2009 - Apr 2010
University of Greifswald, Greifswald, Germany
Topic: *Influence of polymicrobial sepsis on a subsequent immune response*
Advisor: Barbara Broecker

Internship Sep 2007 - Mar 2008
University of British Columbia, Vancouver, Canada
Biomedical Research Centre
Topic: *p53-dependent transcription and tumor suppression are not affected in Set7/9-deficient mice*
Advisor: Bernhard Lehnertz & Fabio Rossi

Student Assistant Apr 2007 - Aug 2007
Department of Microbiology, University of Greifswald, Greifswald, Germany
Advisor: Michael Hecker

EDUCATION

Ph.D., Population Genetics (*summa cum laude*) Dec 2010 - Apr 2016
Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany.
Dissertation: *Human adaptation in the light of ancient and modern genomes*.
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: *Influence of polymicrobial sepsis on a subsequent immune response*
Advisor: Barbara Broecker

RESEARCH
ARTICLES

13. **Felix M. Key**, Cosimo Posth, Luis R. Esquivel Gomez, Ron Huebler, Maria Spyrou, Gunnar Neumann, Anja Furtwaengler, Susanna Sabin, Marta Burri, Antje Wisgott, Aditya Kumar Lankapalli, Ashild J. Vagene, Matthias Meyer, Sarah Nagel, Rezeda Tukhbatova, Alexandr Khohlov, Andrey Chizhevsky, Svend Hansen, Andrey B. Belinsky, Alexey Kalmykov, Anatoly R. Kantorovich, Vladimir E. Maslov, Philipp W Stockhammer, Stefania Vai, Monica Zavattaro, Alessandro Riga, David Caramelli, Robin Skeates, Jessica Beckett, Maria Giuseppina Gradoli, Noah Steuri, Albert Hafner, Marianne Ramstein, Inga Siebke, Sandra Loesch, Yilmaz Selim Erdal, Nabil-Fareed Alikhan, Zhemin Zhou, Mark Achtman, Kirsten Bos, Sabine Reinhold, Wolfgang Haak, Denise Kuehnert, Alexander Herbig, Johannes Krause
Emergence of human-adapted *Salmonella enterica* is linked to the Neolithization process. *Nature Ecol & Evol* (2020)
12. 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)
11. Maria A Spyrou, Marcel Keller, Rezeda I Tukhbatova, Christiana L Scheib, Elizabeth A Nelson, Aida Andrades Valtueña, Gunnar U Neumann, Don Walker, Amelie Alterauge, Niamh Carty, Craig Cessford, Hermann Fetz, Michaël Gourvenec, Robert Hartle, Michael Henderson, Kristin von Heyking, Sarah A Inskip, Sacha Kacki, **Felix M Key**, Elizabeth L Knox, Christian Later, Prishita Maheshwari-Aplin, Joris Peters, John E Robb, Jürgen Schreiber, Toomas Kivisild, Dominique Castex, Sandra Lösch, Michaela Harbeck, Alexander Herbig, Kirsten I Bos, Johannes Krause
Phylogeography of the second plague pandemic revealed through analysis of historical *Yersinia pestis* genomes *Nature Communications* (2019).
10. David Reher, **Felix M. Key**, Aida Andres, Janet Kelso
Immune gene diversity in archaic and present-day humans. *Genome Biology and Evolution* (2019).
9. **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)
8. 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)
 7. Aida Andrades Valtuena, Alissa Mittnik, **Felix M. Key**, Wolfgang Haak, Raili Allmae, Andrej Belinskij, Mantas Daubaras, Michal Feldman, Rimantas Jankauskas, Ivor Jankovic, Ken Massy, Mario Novak, Saskia Pfrengle, Sabine Reinhold, Mario Slaus, Maria A Spyrou, Anna Szecsenyi-Nagy, Mari Torv, Svend Hansen, Kirsten I Bos, Philipp W Stockhammer, Alexander Herbig, Johannes Krause.
The Stone Age Plague: 1000 years of Persistence in Eurasia. *Current Biology*, 27, 3683–3691. (2017)
 6. Kay Prüfer, Cesare de Filippo, Steffi Grote, Fabrizio Mafessoni, Petra Korlevic, Mateja Hajdinjak, Benjamin Vernot, Laurits Skov, Pingsun Hsieh, Stephane Peyregne, David Reher, Charlotte Hopfe, Sarah Nagel, Tomislav Maricic, Qiaomei Fu, Christoph Theunert, Rebekah Rogers, Pontus Skoglund, Manjusha Chintalapati, Michael Dannemann, Bradley J. Nelson, **Felix M. Key**, Pavao Rudan, Zeljko Kucan, Ivan Gusic, Liubov V. Golovanova, Vladimir B. Doronichev, Nick Patterson, David Reich, Evan E. Eichler, Montgomery Slatkin, Mikkel H. Schierup, Aida Andrés, Janet Kelso, Matthias Meyer, Svante Pääbo
A high-coverage Neandertal genome from Vindija Cave in Croatia. *Science* 10.1126/science.aao1887 (2017)
 5. **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).
 4. Cesare de Filippo, **Felix M. Key**, Silvia Ghirrotto, Andrea Benazzo, Juan R. Meneu, Antje Weihmann, NISC Comparative Sequence Program, Genís Parra, Eric D. Green, and Aida M. Andrés.
Recent selection changes in human genes under long-term balancing selection. *Molecular Biology and Evolution*, 33(6):1435–1447. (2016)
 3. **Felix M. Key**, Benjamin Peter, Megan Y Dennis, Emilia Huerta-Sanchez, 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)
 2. Bernhard Lehnertz, Jason C Rogalski, **Felix M. Schulze**, Lin Yi, Shujun Lin, Jürgen Kast, Fabio MV Rossi.

p53-dependent transcription and tumor suppression are not affected in Set7/9-deficient mice. *Molecular Cell*, 43.4.673-680. (2011)

1. Anna-Barbara Stittrich, Claudia Haftmann, Evridiki Sgouroudis, Anja Andrea Köhl, Ahmed Nabil Hegazy, Isabel Panse, Rene Riedel, Michael Flossdorf, Jun Dong, Franziska Fuhrmann, Gitta Anne Heinz, Zhuo Fang, Na Li, Ute Bissels, Farahnaz Hatam, Angelina Jahn, Ben Hammoud, Mareen Matz, **Felix M. Schulze**, Ria Baumgrass, Andreas Bosio, Hans-Joachim Mollenkopf, Joachim Grün, Andreas Thiel, Wei Chen, Thomas Höfer, Christoph Loddenkemper, Max Löhning, Hyun-Dong Chang, Nikolaus Rajewsky, Andreas Radbruch, Mir-Farzin Mashreghi.
The microRNA miR-182 is induced by IL-2 and promotes clonal expansion of activated helper T lymphocytes. *Nature Immunology*, 11.1057-1062. (2011)

REVIEWS

2. **Felix M. Key**, Cosimo Posth, Johannes Krause, Alexander Herbig, Kirsten Bos. Mining Metagenomic Data Sets for Ancient DNA: Recommended Protocols for Authentication. *Trends in Genetics*, Vol. 33, No. 8 (2017)
1. **Felix M. Key***, Joao C. Teixeira*, Cesare de Filippo, Aida M. Andres. Advantageous diversity maintained by balancing selection in humans. *Current opinion in Genetics & Development*, 29.45-51. (2014)

PRESENTATIONS &
PUBLIC
OUTREACH

Talk Boston (USA), Mar 2020
MIT IMES. *Spread and adaptation of Staphylococcus aureus on the lesions on children with atopic dermatitis.*

Talk Boston (USA), Nov 2019
Science of the human past meeting. *Microbial evolutionary 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 Boston (USA), Nov 2018
Harvard Medical School. *Microbial evolutionary genomics in the era of ancient DNA.*

Talk Austin (USA), Jul 2017
Annual meeting of the Society for Molecular Biology and Evolution. *High-throughput pathogen detection in ancient metagenomic data.*

Talk Ploen (Germany), Feb 2017
The One Past Health Workshop. *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 Lucca (Italy), February 2015
Gordon Research Seminar. *Using Ancient Genomes to Dissect Modern Human Population Differentiation.*

Seminar Leipzig (Germany), January 2015
Evangelisches Schulzentrum (High School). *What makes us human?*

Poster Leicester (UK), April 2014
EMBO Conference on Human Evolution in the Genomic Era. *Selection on a variant associated with improved viral clearance drives local, adaptive pseudogenization of interferon lambda 4 (IFNL4).*

Poster New York (USA), May 2013
CSHL The Biology of Genomes. *Selection on a variant associated with improved viral clearance drives local, adaptive pseudogenization of interferon lambda 4 (IFNL4).*

Talk Seattle (USA), April 2013
Institute for Systems Biology. *Adaptive Pseudogenization of IFNL4 - A gene that underlies variation of Hepatitis C clearance.*

Talk Berkeley (USA), April 2013
Department of Integrative Biology (UC Berkeley). *Adaptive Pseudogenization of IFNL4 - A gene that underlies variation of Hepatitis C clearance.*

Poster Dublin (Ireland), May 2012
Annual meeting of the Society for Molecular Biology and Evolution. *Natural Selection in the MHC-I peptide loading pathway.*

Postdoctoral Stipend Aug 2018 - Jul 2020
German Research Foundation 'Forschungsstipendium'

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)

TEACHING &
TRAINEES

1. Graduate School: IMPRS of Human Origin Jun 2016
Taught module about research projects at MPI EVA.
 2. Programming for Evolutionary Biology Feb 2016
Taught module *Population Genomics* together with Stefan Laurent (Jensen Lab, U Lausanne).
 3. Muslihudeen Abdul-Aziz - Intern Feb 2015 - Oct 2015
Topic: Local Adaptation in Europeans
Current Position: PhD Candidate (Lab of Alan Cooper), ACAD, U Adelaide, Australia
 4. Katalina Bobowik - Intern Sep 2014 - May 2015
Topic: Natural Selection of Protein Extending Variant
Current Position: PhD Candidate (Lab of Irene Gallego Romero), U Melbourne, Australia
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SKILLS

Bash
R
Python
awk
sed
L^AT_EX

MEMBERSHIPS

Society for Molecular Biology and Evolution
