

Jun-Prof. Dr. Lars Barquist

Junior Group Leader

Helmholtz Institute for RNA-based Infection Research (HIRI)

Josef-Schneider-Str. 2 / Building D15

97080 Würzburg | Germany

+49 931 31 82513

lars.barquist@helmholtz-hiri.de | www.helmholtz-hiri.de



Education

2014 PhD, Biological Sciences, Cambridge University, UK
2007 BA, Biomathematics, Rutgers University, NJ, USA

Positions

2018 - present Junior Professor (W1), Institute for Molecular Infection Biology (IMIB), Würzburg, Germany
2018 - present Junior Group Leader, Helmholtz Institute for RNA-based Infection Research (HIRI), Würzburg, Germany
2013 - 2017 Postdoc, RNA Biology, Institute for Molecular Infection Biology (IMIB), Würzburg, Germany
2012 - 2013 Visitor, European Bioinformatics Institute (EMBL-EBI), Hinxton, UK
2009 - 2013 Graduate Student, Wellcome Trust Sanger Institute, Hinxton, UK
2007 - 2009 Specialist, Department of Bioengineering, UC Berkeley, CA, USA

Awards & Honors

Alexander von Humboldt Research Fellow (2014 - 2016)

Selected Publications

- Popella L, Jung J, Popova K, Đurica-Mitic S, **Barquist L**#, Vogel J# (2021)
Global RNA profiles show target selectivity and physiological effects of peptide-delivered antisense antibiotics
Nucleic Acids Research 49(8):4705-4724
- Mika-Gospodorz B*, Giengkam S*, Westermann AJ, Wongsantichon J, Kion-Crosby W, Chuenklin S, Wang LC, Sunyakumthorn P, Sobota RM, Subbian S, **Barquist L**#, Salje J# (2020)
*Dual RNA-seq of *Orientia tsutsugamushi* informs on host-pathogen interactions for this neglected intracellular human pathogen*
Nature Communications 11(1):3363
- Cain AK#, **Barquist L**, Goodman AL, Paulsen IT, Parkhill J, van Opijnen T# (2020)
A decade of advances in transposon-insertion sequencing
Nature Reviews Genetics 21(9):526-540
- Wheeler NE#, Gardner PP, **Barquist L**# (2018)
*Machine learning identifies signatures of host adaptation in the bacterial pathogen *Salmonella enterica**
PLoS Genetics 14(5):e1007333
- **Barquist L**, Mayho M, Cummins C, Cain AK, Boinett CJ, Page AJ, Langridge GC, Quail MA, Keane JA, Parkhill J (2016)
The TraDIS toolkit: sequencing and analysis for dense transposon mutant libraries
Bioinformatics 32(7):1109-1111