

DEGREES

UNIVERSITY OF CAMBRIDGE

PhD 2016
Bioinformatics

FREIE UNIVERSITÄT BERLIN

Master of Science 2011
BioinformaticsBachelor of Science 2008
Major: bioinformatics
Minor: physics

AWARDS

EMBL PhD fellowship

Awarded 4 year funded PhD fellowship

SKILLS

LANGUAGES

Fluency in written & spoken English, German, and French

ANALYSIS

Data exploration · data visualisation · statistical modelling · RNA-seq · ChIP-seq · motif analysis

PROGRAMMING

C++ · C · R · Python · Perl · Bash · Make · C# · Java · PHP · VB · JavaScript · Ruby · ...

TOOLS

Version control · unit testing · reproducible research · literate programming · lexical/semantic analysis · Unix · Windows · macOS

MANAGEMENT

Software development team lead · EMBL PhD Symposium organising committee · EMBL Bioinformatics Workshop coordination

PRESENTATIONS

INVITED TALKS

Cambridge Epigenetics Symposium 2014

PROFILES

GITHUB

klmr

ORCID

0000-0002-9866-7051

STACK OVERFLOW

Konrad Rudolph

EXPERIENCE

UNIVERSITY OF CAMBRIDGE

Postdoctoral research associate May 2016–
Gene regulation by non-coding RNA · Nuclear RNAi · RNA modifications · transposable elements · trans-generational epigenetic inheritance
Group leader: Prof Dr Eric Miska

EMBL-EBI

Postdoctoral fellow Oct 2015–Mar 2016
Group leader: Dr John Marioni

Predoctoral fellow

Oct 2011–Sep 2015
Link between tRNA and mRNA abundance in mammals via codon–anticodon pairing
Group leader: Dr John Marioni

INDEPENDENT CONSULTANCY

Developer Jun 2011–Aug 2011
Integration of FPGA kernel with C++ library

ILLUMINA INC.

Research associate (intern) Oct 2008–Jan 2009
Implementation of short-read mapping on GPGPUs with Nvidia CUDA

FREIE UNIVERSITÄT BERLIN

Master project student 2010–2011

Thesis: Generic parallelisation of a sequence analysis library

Group leader: Prof Dr Knut Reinert

Tutor

2008–2011

Bachelor project student

2008
Thesis: Implementation of a read mapping tool based on the pigeon-hole principle
Group leader: Prof Dr Knut Reinert

ITOSA

Full stack developer Jan 2007–Dec 2007
C# Windows application; PHP/JavaScript/HTML web application & database frontend

TEACHING

UNIVERSITY OF CAMBRIDGE

smallRNA sequencing 2017

NST Part II BBS Bioinformatics minor 2017

Next generation sequencing (focus on RNA-seq & ChIP-seq) 2013–2015

EMBL-EBI

Bioinformatics workshop 2011–2015

Bash scripting · Unix · Git · R · \LaTeX

FREIE UNIVERSITÄT BERLIN

2008–2011
Algorithms 101 · Algorithms 102 · Algorithms in bioinformatics · Database systems · C++

PUBLICATIONS

Katharina Gapp, Gretchen van Steenwyck, Wayo Matsushima, Konrad L M Rudolph, Francesca Manuella, Grégoire Vernaz, Tanay Gosh, Pawel Pelzcar, Isabelle M Mansuy, Eric A Miska. "A sperm long RNA fraction transmits effects of early life traumatic stress." (submitted).

Alper Akay, Tomás Di Domenico, Kin M Suen, Amena Nabih, Guillermo E Parada, Mark Larance, Ragini Medhi, Ahmet C Berkurek, Xinlian Zhang, Christopher J Wedeles, Konrad L M Rudolph, Jan Engelhardt, Martin Hemberg, Ping Ma, Angus I Lamond, Julie M Claycomb, Eric A Miska. "Small RNA pathways require the helicase Aquarius/EMBO-4 to heritably silence transcription." *Developmental Cell* (accepted).Pieter van Delft, Alper Akay, Sabrina M Huber, Christoph Bueschl, Konrad L M Rudolph, Tomás Di Domenico, Rainer Schuhmacher, Eric A Miska, Shankar Balasubramanian. "The profile and dynamics of RNA modifications in animals." *ChemBioChem* (Apr 2017), DOI: 10.1002/cbic.201700093.Bianca M Schmitt*, Konrad L M Rudolph*, Panagiota Karagianni, Nuno A Fonseca, Robert J White, Iannis Talianidis, Duncan T Odom, John C Marioni, Claudia Kutter. "High-resolution mapping of transcriptional dynamics across tissue development reveals a stable mRNA–tRNA interface." *Genome Research* (Aug 2014), DOI: 10.1101/gr.176784.114.Konrad L M Rudolph*, Bianca M Schmitt*, Diego Villar, Robert J White, John C Marioni, Claudia Kutter, Duncan T Odom. "Codon-driven translational efficiency is stable across diverse mammalian cell states." *PLOS Genetics* (May 2016), DOI: 10.1371/journal.pgen.1006024.Anja Thormann, Konrad L M Rudolph, Ina Koch. "TinA (T-Invariant Analysis): a tool box for exploring pathways in biochemical systems at steady state." *Abstract book of CGB 2009* (Sep 2009).