Konrad **Rudolph**

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Wellcome Trust/Cancer Research UK Gurdon Institute
Tennis Court Road
Cambridge CB2 1QN, UK

DEGREES

UNIVERSITY OF CAMBRIDGE

PhD 2016
Bioinformatics
St Edmund's College

FREIE UNIVERSITÄT BERLIN

Master of Science 2011
Bioinformatics

Bachelor 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 & WELLCOME TRUST SANGER INSTITUTE

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 (organiser, presenter) 2011–2015
Bash scripting · Unix · Git · R · LaTeX

FREIE UNIVERSITÄT BERLIN 2008–2011

Algorithms 101 · Algorithms 102 · Algorithms in bioinformatics · Database systems · C++

ACTIVEVB

ActiveVB workshop (organiser, presenter) 2005–2007
Visual Basic 8 · Regular expressions · Algorithms and data structures

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 Berkyurek, 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/EMB0-4 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.

*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.

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.

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).