

# Konrad Rudolph

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Tennis Court Road  
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## 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

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. “The helicase Aquarius/EMB-4 is required to overcome intronic barriers to allow nuclear RNAi pathways to heritably silence transcription.” *Developmental Cell* (Aug 2017), DOI: 10.1016/j.devcel.2017.07.002.

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. “TlnA (T-Invariant Analysis): a tool box for exploring pathways in biochemical systems at steady state.” *Abstract book of CGB 2009* (Sep 2009).