

## Curriculum Vitae

Name: Dr. rer. nat. Kristian Mikael Rother  
Date of Birth: 11. 4. 1977 in Berlin  
Nationality: Finnish/German  
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## Academic Degrees and Positions

- 2009-now** DAAD Fellowship at the Adam Mickiewicz University, Poznań, Poland. Mentor and coach for a group 20 young scientists.
- 2006-2009** Marie Curie Postdoc at the International Institute of Molecular and Cell Biology Warsaw, Poland ([www.genesilico.pl](http://www.genesilico.pl)).
- 2002-2006** **Doctoral degree** in Biology, Humboldt Universität Berlin; Doctoral thesis: *Efficient use of a Protein Structure Annotation Database* (magna cum laude).
- 1996-2002** **Diploma of Biochemistry** at the Freie Universität Berlin; Diploma thesis: *Packing density and packing defects in protein structures* (sehr gut).
- 2001-2002** Web administrator at the Neuroinformatics Group, Institute of Biology, Humboldt Universität Berlin.
- 1996** **University entrance diploma** at the Gymnasium Steglitz Berlin (average 1.3).

## Languages

German (native)  
Finnish (native)  
English (advanced; TOEFL 117/120 points in 2009)  
Polish (fluent)  
Latin (9 school years)  
Chinese/Mandarin (basic)

## Selected skills

### IT Skills

Professional SCRUM Master I Certificate (2011)  
Programming in Python (since 2000)  
Web frameworks (Django, TurboGears, Zope)  
Testing frameworks: unittest, doctest, django.test, Webtest  
Test-Driven-Development  
Engineering with User Stories, code reviews, CRC cards, etc.  
Version control with SVN, Mercurial, GIT  
Relational databases (PosGreSQL, MySQL)  
IBM DB2 User Certificate  
Basic knowledge of Fortran, Java, and C

### Training & moderation

techniques for communicating in groups  
(brainstorming, Metaplan, feedback)  
techniques for training and active teaching  
TMI programme for leadership and mentoring ([www.toastmasters.org](http://www.toastmasters.org))  
TMI programme for public speaking ([www.toastmasters.org](http://www.toastmasters.org))

### Project management

formal project planning, supervision and review  
GANTT/PERT charts  
time management  
Kanban  
Professional SCRUM Master I Certificate

### Bioinformatics

Creation and curation of biological databases  
RNA 3D modeling  
RNA 2D structure prediction

## Grants & Awards

**DAAD fellowship “Modern applications of biotechnology” (2009-2011).**

**“20 Characters” - Awarded 1st prize**, Visual Reflections on Science, ISMB/ECCB, Stockholm (2009).

**“Lightweight Techniques for developing Bioinformatics Software” - Best Poster award** at the German conference of bioinformatics (GCB) 2010.

## **Selected Training Topics**

### **Train the trainer**

Techniques for systematic preparation of teaching units and for creating interesting tutorials, seminars, and lectures.

### **Design patterns in Python**

Creating advanced object-oriented architectures in Python.

### **Analyzing biological data with Python**

Using the Python programming language to manage biological data for beginners and advanced programmers. Includes plotting of results, retrieving sequences and literature from the web etc.

### **Software development techniques**

Basic tools like repositories, User Stories, and Unit Testing that help develop reliable software in an agile or non-agile development process.

### **Introduction to Linux**

First steps on Linux operating systems, using the console, useful programs, basics of system administration.

### **Scientific writing**

How to write a paper or thesis. Includes drafting an outline, creating print-quality figures, managing references with EndNote etc.

### **Management of scientific projects**

Basics that help young scientists to keep their project under control. Covers written project plans, time management, and charts usable in grant applications.

### **Molecular visualization**

Creating publication-quality images of 3D molecules (proteins, DNA, RNA, drugs) with the PyMOL program.

## Memberships

**Faculty advisor** for the **ISCB-SC Regional Student Group Poland**

Co-founder of the **Bioinformatics Training Network** ([www.biotnet.org](http://www.biotnet.org)).

Member of the **ISCB Education Council** ([www.iscb.org](http://www.iscb.org)).

Member of the **Polish Society for Bioinformatics** ([ptbi.org.pl](http://ptbi.org.pl)).

Treasurer of the English Toastmasters club in Poznań ([www.toastmasters.org](http://www.toastmasters.org)).

## Scientific papers

### 2011

**Rother K**, Potrzebowski W, Puton T, Rother M, Wywiał E, Bujnicki JM. A toolbox for developing bioinformatics software. Briefings in Bioinformatics (in press).

Rother M, **Rother K**, Puton T, Bujnicki JM. ModeRNA: A tool for comparative modeling of RNA 3D structure. Nucleic Acids Res. 2011 Feb 7.

**Rother K**, Rother M, Boniecki M, Puton T, Bujnicki JM. RNA and protein 3D structure modeling: similarities and differences. J Mol Model. 2011 Jan 22.

Milanowska K, Krwawicz J, Papaj G, Kosiński J, Poleszak K, Lesiak J, Osińska E, **Rother K**, Bujnicki JM. REPAIRtoire—a database of DNA repair pathways. Nucleic Acids Res. 2011 Jan;39 (Database issue):D788-92. Epub 2010 Nov 4.

### 2010

Holzthütter HG, Gille C, Boelling C, Hoppe A, Bulik S, Hoffmann S, Hübner K, Karlstädt A, Ganeshan R, König M, **Rother K**, Weidlich M, Behre J. HEPATONET1: A comprehensive metabolic network of the human hepatocyte. Molecular Systems Biology 2010; 6:411; doi:10.1038/msb.2010.62.

**Rother K**, Rother M, Pleus A, Upmeyer zu Belzen A, Multi-Stage Learning Aids applied to hands-on software training. Brief Bioinform 2010; doi: 10.1093/bib/bbq024.

Musielak M, **Rother K**, Puton T, Bujnicki JM. ModeRNA builds RNA 3D Models from Template Structures. ERCIM News 82. Jul 2010.

Schneider MV, Watson J, Attwood T, **Rother K**, Budd A, McDowall J, Via A, Fernandes F, Nyronen T, Blicher T, Jones P, Blatter MC, De Las Rivas J, Judge DP, van der Gool W, Brooksbank C. Bioinformatics training: a review of challenges, actions and support requirements. Brief Bioinform, Advance Access published on June 18, 2010; doi: doi:10.1093/bib/bbq021.

**Rother K**, Hoffmann S, Bulik S, Hoppe A, Gasteiger J, Holzthütter HG. IGERS: inferring Gibbs energy changes of biochemical reactions from reaction similarities. Biophys J. 2010. 98: 2478-2486.

### 2009

Bauer R, **Rother K**, Moor P, Bujnicki JM, Preissner R. Fast structural alignment of biomolecules using a hash table, n-grams and string descriptors. Algorithms 2009, 2(2), 692-709.

Czerwoniec A, Dunin-Horkawicz S, Purta E, Kaminska KH, Kasprzak J, Bujnicki JM, Grosjean H, **Rother K**. MODOMICS: A database of RNA modification pathways. 2008 update. Nucleic Acids Res. 2009 Jan;37 (Database issue):D118-21. Epub 2008 Oct 14.

**2008**

**Rother K**, Hildebrand PW, Goede A, Gruening B, Preissner R. Voronoia: Analyzing packing in protein structures. *Nucleic Acids Res.* 2009 Jan;37(Database issue):D393-5. Epub 2008 Oct 23.

Bauer RA, **Rother K**, Bujnicki JM, Preissner R. Suffix techniques as a rapid method for RNA substructure search. *Genome Informatics.* 2008. 20, pp. 183-198.

Smit S, **Rother K**, Heringa J, Knight R (2008). From knotted to nested RNA structures: a variety of computational methods for pseudoknot removal, *RNA.* 2008 Mar;14(3):410-6.

**2007**

Hodis E, Schreiber G, **Rother K**, Sussman JL. eMovie: a storyboard-based tool for making molecular movies. *Trends Biochem Sci.* 2007 May;32(5):199-204. Epub 2007 Apr 19.

Zbilut JP, Chua GH, Krishnan A, Bossa C, **Rother K**, Webber CL Jr, Giuliani A. A topologically related singularity suggests a maximum preferred size for protein domains. *Proteins.* 2007 Feb 15;66(3):621-9.

**2006**

Günther S, Hempel D, Dunkel M, **Rother K**, Preissner R. SuperHapten: a comprehensive database for small immunogenic compounds. *Nucleic Acids Res.* 2007 Jan;35(Database issue):D906-10. Epub 2006 Nov 7.

Günther S, **Rother K**, Frömmel C. Molecular flexibility in protein-DNA-interactions. *Biosystems* 2006 Aug;85(2):126-36. Epub Feb 20.

**Rother K**, Dunkel M, Michalsky E, Trissl S, Goede A, Leser U, Preißner R. A structural keystone for drug design. *Journal of Integrative Bioinformatics.* 2006 Jan 19; 0019. Online Journal.

**2000-2005**

**Rother K**, Michalsky E, Leser U. How well are protein structures annotated in secondary databases? *Proteins.* 2005 Sep 1; 60(4):571-576.

Trissl S, **Rother K**, Müller H, Steinke T, Koch I, Preißner R, Frömmel C, Leser U. Columba: an integrated database of proteins, structures, and annotations. *BMC Bioinformatics* 2005, Mar 31;6(81).

Hildebrandt P, **Rother K**, Preißner R, Goede A, Frömmel C. Packing density and packing defects in helical membrane proteins. *Biophys J* 2005, 88;1970-1977.

**Rother K**, Müller H, Trissl S, Koch I, Steinke T, Preißner R, Frömmel C, Leser, U. Columba: Multidimensional data integration of protein annotations. *DILS conference on databases in life sciences* 2004, 2994, 156-171.

**Rother K**, Preißner R, Goede A, Frömmel C. Inhomogeneous molecular density: reference packing densities and distribution of cavities within proteins. *Bioinformatics.* 2003 Nov 1;19(16):2112-2121.

Preißner R, Goede A, **Rother K**, Osterkamp F, Koert U, Frömmel C. Matching organic libraries with protein-substructures. *J Comput Aided Mol Des.* 2001 Sep;15(9):811-817.

Gille C, Goede A, Preißner R, **Rother K**, Frömmel C. Conservation of substructures in proteins: interfaces of secondary structural elements in proteasomal subunits. *J Mol Biol.* 2000 Jun 16;299(4):1147-1154.

## Book Contributions

Czerwoniec A, Kasprzak JM, Kaminska KH, **Rother K**, Bujnicki JM. Folds and functions of domains in RNA modification enzymes. In „DNA and RNA Enzymes“ edited by Henri Grosjean. Landes Bioscience 2009. ISBN-13/EAN: 9781587063299.

**Rother K**, Czerwoniec A, Bujnicki JM, Grosjean H. Chemical Structures, classification of modified nucleosides in RNA and the MODOMICS database concerning the corresponding RNA modification enzymes. In „DNA and RNA Enzymes“ edited by Henri Grosjean. Landes Bioscience 2009. ISBN-13/EAN: 9781587063299.

**Rother K**, Papaj G, Bujnicki JM. Databases of DNA Modifications. In „DNA and RNA Enzymes“ edited by Henri Grosjean. Landes Bioscience 2009. ISBN-13/EAN: 9781587063299.

**Rother K**. Zwanzig Zeichen. In „Ein Entscheidender Teil fehlt“ edited by Käthe Wenzel, Lisa Glauer and Tatjana Fell . Mensch & Buch Verlag Berlin, 208 pages.

Knapp W, Wenzel K, Frömmel C, Schnalke T (Ed.): The Missing Link. Art meets Biomedicine. Public understanding of art and sciences. Berlin 2005. ISBN 3-89462-133.

## Exhibitions & Art

**Fashion & mug collection** in cooperation with the ISCB Student Council, [www.cafepress.com/iscb](http://www.cafepress.com/iscb) (2010).

**Oszillogramme** - Re-Linking art and sciences, 2B Galéria und Goethe Institut, Budapest (2009).

**Visual Reflections on Science**, ISMB/ECCB 2009, Stockholm (2009). **Awarded 1st prize.**

**Proteinkalligraphie**, Institute of Biochemistry, FU Berlin (2006).

**Missing Link** - Art Meets Biomedicine, The Rubelle & Norman Schafler Gallery, Brooklyn, N.Y. (2006).

**arts & science in vitro** - Der seltsame Tanz der sozialen Amöbe. With Jan Saam, Sasha Waltz and Guests. Institute of Biochemistry, Charité Berlin (2006).

**The Missing Link** – Communication in Science and Arts. Berliner Medizinhistorisches Museum, Charité (2005).