

Curriculum Vitae

name: Dr. rer. nat. Kristian Mikael Rother
date of birth: 11. 4. 1977 in Berlin
nationality: German/Finnish
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Career

2011- **Freelance trainer for scientists.**
www.academis.eu

2009-2011 **Technical leader for 20 bioinformaticians.**
DAAD-Fellowship at the Adam Mickiewicz University,
Poznań, Poland.

2006-2009 **Software development for RNA 3D structure modeling.**
Marie Curie Postdoc at the International Institute of Molecular
and Cell Biology Warsaw, Poland (www.genesilico.pl).

Education

2006 **Doctoral degree in biology**, Humboldt Universität Berlin
with Prof. Cornelius Frömmel. Thesis:
[Efficient use of a Protein Structure Annotation Database](#)
(*magna cum laude*).

2002 **Diploma in biochemistry**, Freien Universität Berlin
(degree: *sehr gut*).

1996 **University entrance diploma**, Gymnasium Steglitz Berlin
(average 1.3).

Languages

German (native)
Finnish (native)
English (advanced; TOEFL 113/120 points in 2009)
Polish (fluent)
Latin (9 school years)

Key skills

Interactive teaching & moderation methods

Python software development

Django web framework

Agile best practices (User Stories, Iterations, Kanban etc.)

SQL databases (PosgreSQL, MySQL, SQLite)

HTML/CSS

Certificates

Professional SCRUM Master I Certificate

Toastmasters Competent Communicator Certificate

IBM DB2 User Certificate

Social activities

Founding member of the [Bioinformatics Training Network](#).

Faculty advisor of the [ISCB-SC Regional Student Group Poland](#).

Treasurer of [Spreeredner Berlin](#).

Treasurer of [Verbal Victory Toastmasters Poznan](#).

Awards

“20 Characters” 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 2010.

Publications

2012

Ramrath DJ, Yamamoto H, **Rother K**, Wittek D, Pech M, Mielke T, Loerke J, Scheerer P, Ivanov P, Teraoka Y, Shpanchenko O, Nierhaus KH, Spahn CM. The complex of tmRNA-SmpB and EF-G on translocating ribosomes. *Nature*. 2012 May 6;485(7399):526-9.

Cruz JA, Blanchet MF, Boniecki M, Bujnicki JM, Chen SJ, Cao S, Das R, Ding F, Dokholyan NV, Flores SC, Huang L, Lavender CA, Lisi V, Major F, Mikolajczak K, Patel DJ, Philips A, Puton T, Santalucia J, Sijen F, Hermann T, **Rother K**, Rother M, Serganov A, Skorupski M, Soltysinski T, Sripakdeevong P, Tuszyńska I, Weeks KM, Waldsich C, Wildauer M, Leontis NB, Westhof E. RNA-Puzzles: A CASP-like evaluation of RNA three-dimensional structure prediction. *RNA*. 2012 Apr;18(4):610-25. Epub 2012 Feb 23.

2011

Rother K, Potrzebowski W, Puton T, Rother M, Wywiał E, Bujnicki JM. A toolbox for developing bioinformatics software. *Briefings in Bioinformatics* 2011; doi: 10.1093/bib/bbr035.

Philips A, Milanowska K, Lach G, Boniecki M, **Rother K**, Bujnicki JM. MetalionRNA: computational predictor of metal-binding sites in RNA structures. *Bioinformatics*. 2011 Nov 21.

Schneider MV, Walter P, Blatter MC, Watson J, Brazas MD, **Rother K**, Budd A, Via A, van Gelder CW, Jacob J, Fernandes P, Nyrönen TH, De Las Rivas J, Blicher T, Jimenez RC, Loveland J, McDowall J, Jones P, Vaughan BW, Lopez R, Attwood TK, Brooksbank C. Bioinformatics Training Network (BTN): a community resource for bioinformatics trainers. *Brief Bioinform*. 2011 Nov 22.

Puton T, Kozłowski L, Tuszyńska I, **Rother K**, Bujnicki JM. Computational methods for prediction of protein-RNA interactions. *J Struct Biol*. 2011 Oct 12.

Rother M, **Rother K**, Puton T, Bujnicki JM. RNA tertiary structure prediction with ModeRNA. *Brief Bioinform*. 2011 Nov;12(6):601-13. Epub 2011 Sep 6.

Rother M, Milanowska K, Puton T, Jeleniewicz J, **Rother K**, Bujnicki JM. ModeRNA server: an online tool for modeling RNA 3D structures. *Bioinformatics*. 2011 Sep 1;27(17):2441-2. Epub 2011 Jul 4.

Milanowska K, **Rother K**, Bujnicki JM. Databases and Bioinformatics Tools for the Study of DNA Repair. *Molecular Biology International* 2011, Article ID 475718, 9 pages; doi:10.4061/2011/475718.

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

Holzhütter 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, Holzhutter 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.

Czerwonec 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.

Czerwonec 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, Czerwonec 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.

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.

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

2000-2005

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.

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.

Exhibitions

Fashion & mug collection in cooperation with the ISCB Student Council, www.cafepress.com/iscbsc (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 Schafner 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).