

Scientific papers

2011

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.

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.

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

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.

Musiela 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.

Teaching & Training

Applied Didactics. Two-day workshop. Nov 2011, Giessen.

Organizer of the RuPy 2011 conference. Three days. 2011, Poznan, Poland.

Methodology of Experimental work. 10h course for biotechnology students. 2011, UAM Poznan.

Python Basics at www.nobleprog.com. 32h training. 2011, Poznan.

Career skills for scientists. 20h tutorial series. 2010-2011, UAM Poznan.

Applied Didactics. Two-day workshop. March 2011, Giessen.

Train the Trainer – Computer tutorials. One-day workshop. 2011, VIB Belgium.

Organizer of the Python & Friends programming workshop. Three days. 2010, Karpacz, Poland.

Project Management Basics. One-day workshop. 2010, UAM Poznan.

Advanced Python programming. 60h course for bioinformatics students. 2007-2010, UAM Poznan.

Python Basics at www.nobleprog.com. 40h training. 2010, London.

Organizer of the IRTG Bioinformatics Workshop. Four days. 2009, UAM Poznan.

Introduction to RNA Bioinformatics. 20h course for PhD students. 2009, UAM Poznan.

Applied didactics workshop. One-day workshop. 2009, UAM Poznan.

Structural biology of nucleic acids. 10h course course for bioinformatics students. 2009, IMIM, Barcelona.

Introduction to Python programming. One-day workshop. 2008, IIMCB Warsaw.

Bioinformatics Applications in Python. 15h course for PhD students. 2008, UAM Poznan.

Applied bioinformatics. 6 ECTS course for bioinformatics students. 2003, 2005 and 2006, FU Berlin.

Homology modeling of aaRS proteins. 40h course for bioinformatics students. 2005, FU Berlin.

Basic Chemistry. 40h seminar and lab course for medical students. 2005 (2x) and 2006, Charité Berlin.

Basic Biochemistry. 20h seminar for medical students. 2004, Charité Berlin.

Molecular modeling. 40h course for biology students. 2001-2004, HU Berlin.

Exhibitions

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