

Dr. Roland Keller



Background (*Curriculum Vitae*)

- 1995 - 2004: Hans-Purrmann-Gymnasium Speyer
- 2004 - 2010: Studies of bioinformatics (*Studium der Bioinformatik*), Universität Tübingen
- 2007 - 2008: Exchange student (*Auslandsstudium*), University of Massachusetts, Amherst, USA
- 02/2011 - : Research assistant (*Wissenschaftlicher Assistent*), ZBIT (Zentrum für Bioinformatik Tübingen)

Research Interests (*Wissenschaftliche Interessen*)

- Systems Biology (*Systembiologie*)
- Gene expression (*Genexpression*)

Current Projects (*Aktuelle Projekte*)

- Virtual Liver (*Virtuelle Leber*)


Diploma thesis (*Diplomarbeit*)

- "Statistische Anreicherungsmethoden von unabhängigen und abhängigen Gengruppen", Universität Tübingen, 2010

Publications (*Publikationen*)

- [1] Roland Keller, Marcus Klein, Maria Thomas, Andreas Dräger, Ute Metzger, Markus F. Templin, Thomas O. Joos, Wolfgang E. Thasler, Andreas Zell, and Ulrich M. Zanger. Coordinating role of RXR α in downregulating hepatic detoxification during inflammation revealed by fuzzy-logic modeling. *PLoS Computational Biology*, 12(1):e1004431, January 2016. [[DOI](#) | [link](#)]
- [2] Andreas Dräger, Daniel C. Zielinski, Roland Keller, Matthias Rall, Johannes Eichner, Bernhard O. Palsson, and Andreas Zell. SBMLsqueezer 2: Context-sensitive creation of kinetic equations in biochemical networks. *BMC Systems Biology*, 9(1):1-17, September 2015. [[DOI](#) | [link](#) | [pdf](#)]
- [3] Nicolas Rodriguez, Alex Thomas, Leandro Watanabe, Ibrahim Y. Vazirabad, Victor Kofia, Harold F. Gómez, Florian Mittag, Jakob Matthes, Jan D. Rudolph, Finja Wrzodek, Eugen Netz, Alexander Diamantikos, Johannes Eichner, Roland Keller, Clemens Wrzodek, Sebastian Fröhlich, Nathan E. Lewis, Chris J. Myers, Nicolas Le Novère, Bernhard Ø. Palsson, Michael Hucka, and Andreas Dräger. JSBML 1.0: providing a smorgasbord of options to encode systems biology models. *Bioinformatics*, June 2015. [[DOI](#) | [arXiv](#) | [link](#) | [pdf](#)]
- [4] Alexander Dörr, Roland Keller, Andreas Zell, and Andreas Dräger. SBMLsimulator: a Java tool for model simulation and parameter estimation in systems biology. *Computation*, 2(4):246-257, December 2014. [[DOI](#) | [link](#) | [link](#)]
- [5] Finja Büchel, Nicolas Rodriguez, Neil Swainston, Clemens Wrzodek, Tobias Czauderna, Roland Keller, Florian Mittag, Michael Schubert, Mihai Glont, Martin Golebiewski, Martijn van Iersel, Sarah M. Keating, Matthias Rall, Michael Wybrow, Henning Hermjakob, Michael Hucka, Douglas B Kell, Wolfgang Müller, Pedro Mendes, Andreas Zell, Claudine Chaouiya, Julio Saez-Rodriguez, Falk Schreiber, Camille Laibe, Andreas Dräger, and Nicolas Le

- Novère. Path2Models: large-scale generation of computational models from biochemical pathway maps. *BMC Systems Biology*, 7(1):116, November 2013. [[DOI](#) | [link](#) | [pdf](#)]
- [6] Roland Keller, Alexander Dörr, Akito Tabira, Akira Funahashi, Michael J. Ziller, Richard Adams, Nicolas Rodriguez, Nicolas Le Novère, Noriko Hiroi, Hannes Planatscher, Andreas Zell, and Andreas Dräger. The systems biology simulation core algorithm. *BMC Systems Biology*, 7:55, July 2013. [[DOI](#) | [link](#) | [pdf](#)]

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