

Junior Professor
Dr. Sonja J. Prohaska
Computational EvoDevo
Institute of Computer Science
University of Leipzig
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EDUCATION Postdoctoral research with Prof. Peter F. Stadler, July 2008 - November 2010
University of Leipzig, Germany

Postdoctoral research with Prof. David Krakauer, January - June 2008
Santa Fe Institute, Santa Fe, NM

Postdoctoral research with Prof. Sudhir Kumar, January 2006 - December 2007
Arizona State University, Tempe, AZ

PhD, Bioinformatics, graduated with honors, December 2005
Thesis: *Evolution of Conserved Non-Coding Sequences*
Supervisor: Prof. Peter F. Stadler
Academic degree: *Doctor rerum naturalium*
University of Leipzig, Germany

MSc, Genetics, 2nd diploma with honors, July 2003
Thesis: *Picking Up the Trail of Phylogenetic Footprints*
Supervisor: Prof. Peter F. Stadler
Academic degree: *Magistra rerum naturalium*
University of Vienna, Austria

Biology, 1st diploma with honors, June 2001
University of Vienna, Austria

Matura with honors, June 1998
High school, Horn, Austria

CSE with honors, June 1994
Secondary school, Groß-Siegharts, Austria
Elementary school, Dietmanns, Austria

RESEARCH AND
EXPERIENCE

Juniorprofessor
Computational EvoDevo

University of Leipzig
Germany
since December 2010

Research topics range from the origin of regulation to modelling of chromatin dynamics, and detection of protein-binding RNA motifs.
Positive mid-term evaluation in summer 2013.

Research Assistant
Bioinformatics

University of Leipzig
Germany
October 2008 – November 2010

Functional role and evolutionary implications of chromatin regulation and the link to structured RNAs. Initiation of a Working Group on “Computational EvoDevo”. Application for funding. Supervision of graduate and undergraduate students. Teaching.

Researcher
Theoretical Chemistry

University of Vienna
Austria
January 2008 – September 2008

Involvement of RNAs and RNA structures in gene regulatory mechanisms.

Research Fellow
Evolutionary/Theoretical Biology

Santa Fe Institute
Santa Fe, NM
January 2008 – June 2008

Examination and modelling of the evolution of gene regulation. Regulatory mechanisms, with focus on chromatin regulation, were traced back to their evolutionary origin.

Research Assistant Professional
Biomedical Informatics

Arizona State University
Tempe, AZ
January 2006 – December 2007

Bioinformatics approaches to study gene regulation. Postdoctoral Research. Application for funding at NIH and NSF. Supervision of undergraduates. Scientific mentor: Sudhir Kumar.

Research Assistant
Bioinformatics

University of Leipzig
Germany
July 2003 – December 2005

Investigation of phylogenetic footprints and their evolutionary changes. Research and dissertation. Supervision of undergraduates at bioinformatics courses. Supervisor: Peter Stadler.

PUBLICATIONS

- 2013 Arnold C, Stadler PF, Prohaska SJ. *Chromatin Computation: Epigenetic Inheritance as a Pattern Reconstruction Problem*. J Theor Biol. 2013; 336:61-74
- Binder H, Steiner L, Przybilla J, Rohlf T, Prohaska S, Galle J. *Transcriptional regulation by histone modifications: towards a theory of chromatin re-organization during stem cell differentiation*. Phys Biol. 2013; 10(2):026006
- 2012 Steiner L, Hopp L, Wirth H, Galle J, Binder H, Prohaska SJ, Rohlf T. *A global genome segmentation method for exploration of epigenetic patterns*. PLoS One 2012; 7(10):e46811
- Rohlf T, Steiner L, Przybilla J, Prohaska S, Binder H, Galle J. *Modeling the dynamic epigenome: from histone modifications towards self-organizing chromatin*. Epigenomics. 2012; 4(2):205-19
- 2011 Lechner M, Findeiss S, Steiner L, Marz M, Stadler PF, Prohaska SJ. *Proteinortho: Detection of (Co-)Orthologs in Large-Scale Analysis*. BMC Bioinformatics 2011; 12:124
- Findeiss S, Engelhardt J, Prohaska SJ, Stadler PF. *Protein-Coding Structured RNAs A Computational Survey of Conserved RNA Secondary Structures Overlapping Coding Regions in Drosophilids*. Biochimie 2011; 93(11):2019-23
- Lozada-Chávez I, Stadler PF, Prohaska SJ. *Hypothesis for the modern RNA world': a pervasive non-coding RNA-based genetic regulation is a prerequisite for the emergence of multicellular complexity*. Orig Life Evol Biosph. 2011; 41:587-607
- Krakauer DC, Collins JP, Erwin D, Flack JC, Fontana W, Laubichler MD, Prohaska SJ, West GB, Stadler PF. *The challenges and scope of theoretical biology*. J.Theor.Biol. 2011
- 2010 Parikesit AA, Stadler PF, Prohaska SJ. *Quantitative Comparison of Genomic-Wide Protein Domain Distributions*. GCB2010 conference proceeding. 2010; P-173:93-102
- Prohaska SJ, Stadler PF, Krakauer DC. *Innovation in Gene Regulation: The Case of Chromatin Computation*. J.Theor.Biol. 2010; 265:27-44
- Bermudez-Santana C, Stephan-Otto Attolini C, Kirsten T, Engelhardt J, Prohaska SJ, Steigele S, Stadler PF. *Genomic Organization of Eukaryotic tRNAs*. BMC Genomics 2010; 11:270

- Amemiya CT, Powers TP, Prohaska SJ, Grimwood J, Schmutz J, Dickson M, Miyake T, Schoenborn MA, Myers RM, Ruddle FH, Stadler PF, . *Complete HOX cluster characterization of the coelacanth provides further evidence for slow evolution of its genome*. PNAS 2010; 107(8):3622-3627
- 2009 Stadler PF, Prohaska SJ, Forst CV, Krakauer DC. *Defining genes: a computational framework*. Theory Biosci. 2009; 128(3):165-70
- Stadler PF, Chen JJ, Hackermüller J, Hoffmann S, Horn F, Khaitovich P, Kretzschmar A, Mosig A, Prohaska SJ, Qi X, Schutt K, Ullmann K. *Evolution of vault RNAs* Mol Biol Evol. 2009; 26(9):1975-91
- Ingalls T, Martius G, Hellmuth M, Marz M, Prohaska SJ. *Converting DNA to Music: ComposAlign*. Proceedings of the German Conference on Bioinformatics 2009, LNI. 2009; P-157:93-103.
- Hiller M, Findeiß S, Nickel C, Lein S, Marz M, Rose D, Schulz C, Backofen R, Prohaska SJ, Reuter G, Stadler PF. *Conserved Introns Reveal Novel Transcripts in Drosophila melanogaster*. Genome Res. 2009; 19(7):1289-300
- 2008 Heffel A, Stadler PF, Prohaska SJ, Kauer G, Kuska J-P. *Process Flow for Classification and Clustering of Fruit Fly Gene Expression Patterns*. Proceedings of the 15'th IEEE International Conference on Image Processing, ICIP 2008. IEEE CD Proceedings ICIP'08, 721-724.
- Lehmann J, Stadler PF, Prohaska SJ. *SynBlast: Assisting the Analysis of Conserved Synteny Information*. BMC Bioinformatics 2008. 9:351.
- Prohaska SJ, Stadler PF. *A Story of Growing Confusion: Genes and Their Regulation*. In: Rubem P. Mondaini, Rui Dilo Biomat 2007 - International Symposium on Mathematical and Computational Biology , World Scientific, Singapore 2008; 325-345
- Prohaska SJ, Fritsch G, Stadler PF. *Rate Variations, Phylogenetics, and Partial Orders*. In: Proceedings of the Fifth International Workshop on Computational Systems Biology, WCSB 2008. 375-391.
- Dress AWM, Flamm Ch, Fritsch G, Grünewald St, Kruspe M, Prohaska SJ, Stadler PF. *Noisy: identification of problematic columns in multiple sequence alignments*. Alg. Mol. Biol. 3:7
- Filipski A, Prohaska SJ, Kumar S. *Detecting molecular signatures of adaptive evolution*. In "Evolutionary Genomics and Proteomics" edited by Pagel M and Pomiankowski A. Sinauer Press, Massachusetts; 241-254.
- Prohaska SJ, Stadler PF. *"Genes"*. Theory Biosci. 2008; 127(3):215-221.

- Amemiya CT, Prohaska SJ, Hill-Force A, Cooke A, Wasserscheid J, Ferrier D, Anaya JP, Garcia-Fernández J, Dewar K, Stadler PF. *The Amphioxus Hox Cluster: Characterization, Comparative Genomics, and Evolution*. J Exp Zool part B Mol Dev Evol. 2008; 310B:465-477.
- Mosig A, Bıyıkoglu T, Prohaska SJ, Stadler PF. *Discovering Cis-Regulatory Modules by Optimizing Barbecues*. Discr.Appl.Math; 2009; 157:2458-2468
- Wobus M, Wandel E, Prohaska SJ, Findeiß S, Tschöp K, Aust G. *Transcriptional regulation of the human CD97 promoter by Sp1/Sp3 in smooth muscle cells*. Gene. 2008; 413(1-2):67-75
- 2007 Rose D, Hackermüller J, Washietl S, Findeiß S, Reiche K, Hertel J, Stadler PF, Prohaska SJ. *Computational RNomics of Drosophilids*. BMC Genomics. 2007; 8:406.
- Prohaska SJ, Mosig A, Stadler PF. *Regulatory Signals in Genomic Sequences*. In "Networks: From Biology to Theory" edited by Feng, Jianfeng Juergen Jost and Qian Minping. 2007; p191-220.
- Drosophila 12 Genomes Consortium. *Evolution of genes and genomes on the Drosophila phylogeny*. Nature. 2007; 450(7167):203-218.
- Bompfünnewerer AF, Backofen R, Bernhart SH, Flamm C, Fried C, Fritsch G, Hackermüller J, Hertel J, Hofacker IL, Missal K, Mosig A, Prohaska SJ, Rose D, Stadler PF, Tanzer A, Washietl S and Will S. *RNAs Everywhere: Genome-Wide Annotation of Structured RNAs*. J Exp Zoolog part B Mol Dev Evol. 2007; 308B:1-25.
- Prohaska SJ. *Hotelnacht*. Literatur- und Kulturzeitschrift Mondstaub. 2007; ISSN:1612-7943, 8:31-33.
- 2006 Prohaska SJ, Stadler PF, Wagner GP. *Evolutionary Genomics of Hox Gene Clusters*. In: HOX Gene Expression, S. Papageorgiou, Landes Bioscience & Springer, 2006;
- Prohaska SJ, Stadler PF. *Evolution of the Vertebrate Parahox Clusters*. J Exp Zoolog Part B Mol Dev Evol. 2006; 306(5):481-487.
- Morgenstern B, Prohaska SJ, Pohler D, Stadler PF. *Multiple sequence alignment with user-defined anchor points*. Alg.Mol.Biol. 2006; 1:6. (update from the article with the same title, published in conference proceedings, GCB 2004)
- 2005 Wagner GP, Takahashi K, Lynch V, Prohaska SJ, Fried C, Stadler PF, Amemiya CT. *Molecular Evolution of Duplicated Ray Finned Fish HoxA Clusters: Increased synonymous substitution rate and asymmetrical co-divergence of coding and non-coding sequences*. J Mol Evol. 2005 May ; 60(5): 665-76.

Bompiünnewerer AF, Flamm C, Fied C, Fritzsche G, Hofacker IL, Lehmann J, Missal K, Mosig A, Müller B, Prohaska SJ, Stadler BMR, Stadler PF, Tanzer A, Washietl S, Witwer C. *Evolutionary Patterns of Non-Coding RNAs*. Th.Biosci. 2005; 123(4):301-369.

Morgenstern B, Werner N, Prohaska SJ, Steinkamp R, Schneider I, Subramanian AR, Stadler PF, Weyer-Menkhoff J. *Multiple sequence alignment with user-defined constraints @ GOBICS*. Bioinformatics. 2005; 21:1271-1273.

2004

Prohaska SJ, Stadler PF. *The Duplication of the Hox Gene Clusters in Teleost Fishes*. Th Biosci. 2004; 123(1):89-110

Morgenstern B, Prohaska SJ, Werner N, Weyer-Menkhoff J, Schneider I, Subramanian AR, Stadler PF. *Multiple sequence alignment with user-defined constraints*. Proceedings of the German Conference on Bioinformatics 2004, LNI. 2004; P-53, 25-36.

Wagner GP, Fried C, Prohaska SJ, Stadler PF. *Divergence of Conserved Non-Coding Sequences: Rate Estimates and Relative Rate Tests*. Mol Biol Evol. 2004; 21(11):2116-2121.

Fried C, Prohaska SJ, Stadler PF. *Exclusion of repetitive DNA elements from gnathostome Hox clusters*. J Exp Zoolog Part B Mol Dev Evol. 2004; 302(2):165-73.

Stadler PF, Fried C, Prohaska SJ, Bailey WJ, Misof BY, Ruddle FH, Wagner GP. *Evidence for independent Hox gene duplications in the hagfish lineage: a PCR-based gene inventory of Eptatretus stoutii*. Mol Phylogenet Evol. 2004; 32(3):686-94.

Fried C, Hordijk W, Prohaska SJ, Stadler CR, Stadler PF. *The footprint sorting problem*. J Chem Inf Comput Sci. 2004; 44(2):332-8.

Chiu CH, Dewar K, Wagner GP, Takahashi K, Ruddle F, Ledje C, Bartsch P, Scemama JL, Stellwag E, Fried C, Prohaska SJ, Stadler PF, Amemiya CT. *Bichir HoxA cluster sequence reveals surprising trends in ray-finned fish genomic evolution*. Genome Res. 2004; 14(1):11-7.

Prohaska SJ, Fried C, Amemiya CT, Ruddle FH, Wagner GP, Stadler PF. *The shark HoxN cluster is homologous to the human HoxD cluster*. J Mol Evol. 2004; 58(2):212-7.

Prohaska SJ, Fried C, Flamm C, Wagner GP, Stadler PF. *Surveying phylogenetic footprints in large gene clusters: applications to Hox cluster duplications*. Mol Phylogenet Evol. 2004; 31(2):581-604.

2003

Fried C, Prohaska SJ, Stadler PF. *Independent Hox-cluster duplications in lampreys*. J Exp Zool Part B Mol Dev Evol. 2003 Oct 15; 299(1):18-25.