

Dr. Sonja J. Prohaska

Junior Professor
Dr. Sonja J. Prohaska
Computational EvoDevo
Institute of Computer Science
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BIRTH Waidhofen/Thaya (Austria), December 25th, 1979

EDUCATION 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 Stadler
Academic degree: *Doctor rerum naturalium*
University of Leipzig, Germany

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

Research Assistant
Bioinformatics

University of Leipzig
Germany
since October 2008

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.

AWARDS

University of Vienna, Faculty of Sciences and Mathematics,
award for brilliant achievement, 2001

FUNDING

Sudhir Kumar, Sethuraman Panchanathan, Sonja Prohaska, et al. Comparative
gene expression image analysis, NSF; submitted November 2006 (Co-PI 5%
annual effort) – granted

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PUBLICATIONS

- 2011 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
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- 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, Fritzscht 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, Fritzscht 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, Bıyıkođlu 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.

Bompfünewerer AF, Backofen R, Bernhart SH, Flamm C, Fried C, Fritzscht 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 Zool 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.
- Bompfünnewerer 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.
- Prohaska SJ. *Mordfall*. Literatur- und Kulturzeitschrift Mondstaub. 2005; ISSN:1612-7943, 3:20-21.
- 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.

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

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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.

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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.