



# Sonja Prohaska

## Curriculum Vitae

*“The most beautiful thing we can experience is the mysterious – it is the source of all true art and science.” -  
Albert Einstein*

### Education

- 2003–2005 **PhD, Computer Science (Bioinformatics)**, *Leipzig University*, Leipzig, Germany.  
Specialized in Bioinformatics
- 1998–2003 **MSc, Biology**, *University of Vienna*, Vienna, Austria.  
Specialized in Genetics

### Experience

#### Academic Research

- 2016–Present **Professor and Group Leader**, Computational EvoDevo, Institute of Computer Science, Leipzig University, Germany.  
Duties: independent research and teaching, supervision of PhD and MSc students, fund raising
- 2016–Present **Project Leader**, Evolution and Development, Interdisciplinary Centre for Bioinformatics, Leipzig University, Germany.  
Duties: project leadership, research, fund raising
- 2010–2016 **Junior Professor**, Computational EvoDevo, Department of Computer Science, Leipzig University, Germany.  
Duties: independent research and teaching, supervision of PhD and MSc students, fund raising
- 2008–2010 **Research Assistant**, Bioinformatics, Department of Computer Science, Leipzig University, Germany.
- 01–06/2008 **Research Fellow**, Santa Fe Institute for Complex Systems, Santa Fe NM, USA.
- 01–09/2008 **Researcher**, Theoretical Chemistry, University of Vienna, Vienna, Austria.
- 2006–2007 **Research Assistant Professional**, Biomedical Informatics, *ASU*, Tempe AZ, USA.

## Experience

### Miscellaneous

2012–2013 A serious medical issue kept me hospitalized from May 2012 to January 2013.

## Funding

- 2016 Mario Mörl, Sonja J. Prohaska. *Unusual RNA-Polymerases: Reaction Mechanism and Substrate Specificity of tRNA Nucleotidyltransferases*. DFG, 3 years, 160 kEUR
- 2010 Sonja J. Prohaska. *Evolution of Complex Translational Control Elements in the Innate Immune Response*. GIF, 1 year, 39 kEUR

## PUBLICATIONS

UNPUBLISHED

**Prohaska SJ**, Berkemer SJ, Gärtner F, Gatter T, Retzlaff N, zu Siederdisen CH, Stadler PF. *Expansion of Gene Clusters, Circular Orders, and the Shortest Hamiltonian Path Problem*. JOMB (submitted)

Indrischek H, **Prohaska SJ**, Gurevich VV, Gurevich EV, Stadler PF. *Uncovering missing pieces: Duplication and deletion history of arrestins in deuterostomes*. BMC Evol. Biol. (under revision)

Lozada-Chavez I, Stadler PF, **Prohaska SJ**. *The relationship between intron-richness and complex multicellularity has been decoupled repeatedly from genome size evolution*. NAR (submitted)

## PUBLICATIONS

2016

Krakauer D, Müller L, **Prohaska SJ**, Stadler PF. *Design specifications for cellular regulation*. Theory Biosci. 2016 Dec;135(4):231-240. Epub 2016 Nov 18.

Indrischek H, Wieseke N, Stadler PF, **Prohaska SJ**. *The paralog-to-contig assignment problem: high quality gene models from fragmented assemblies*. Algorithms Mol. Biol. 2016; 11:1.

2015

zu Siederdisen CH, **Prohaska SJ**, Stadler PF. *Algebraic Dynamic Programming over general data structures*. BMC Bioinformatics. 2015;16 Suppl 19:S2. doi: 10.1186/1471-2105-16-S19-S2. Epub 2015 Dec 16.

Laubichler M, Stadler PF, **Prohaska SJ**, Nowick K. *The Relativity of Biological Function*. Theory Biosci. 2015; 134(3-4):143-7.

Le Duc D, Renaud G, Krishnan A, Sällman Alm'en M, Huynen L, **Prohaska SJ**, Ongyerth M, Bitarello BD, Schiöth HB, Hofreiter M, Stadler PF, Prüfer K, Lambert D, Kelso J, Schöneberg T. *Kiwi genome provides insights into evolution of a nocturnal lifestyle*. Genome Biology 2015; 16:147.

Betat H, Mede T, Tretbar S, Steiner L, Stadler PF, Mörl M, **Prohaska SJ**. *Ancestral Unicellular Holozoa Acquired their CCA-Adding Enzyme from Alphaproteobacteria by Lateral Gene Transfer*. Nucl. Acids Res. 2015; pii:gkv631.

Berkemer SJ, Höner zu Siederdisen C, Amman F, Wintsche A, Will S, Hofacker IL, **Prohaska SJ**, Stadler PF. *Processed Small RNAs in Archaea and BHB Elements* GCB 2015; 1(1):e18.

- 2014 Höner zu Siederdisen, **Prohaska SJ**, Stadler PF. *Dynamic Programming for Set Data Types*. In Conference Proceedings of Brazilian Symposium on Bioinformatics BSB 14, Belo Horizonte, MG, Brazil. Lect. Notes Comp. Sci. 2014;
- Misof B, Meusemann K, von Reumont BM, Kück P, **Prohaska SJ**, Stadler PF. *A priori assessment of data quality in molecular phylogenetics*. Algorithms Mol. Biol. 2014; 9:22.
- Zeckzer D, Gerighausen D, Steiner L, **Prohaska SJ**. *Analyzing Chromatin Using Tiled Binned Scatterplot Matrices* BioVis 2014 conference proceedings. 2014;
- Lechner M, Hernandez-Rosales M, Doerr D, Wieseke N, Thévenin A, Stoye J, Hartmann RK, **Prohaska SJ**, Stadler PF. *Orthology detection combining clustering and synteny for very large datasets*. PLoS ONE 9(8): e105015. 2014;
- Müller GA, Wintsche A, Stangner K, **Prohaska SJ**, Stadler PF, Engeland K. *The CHR site: definition and genome-wide identification of a cell cycle transcriptional element*. Nucl. Acids Res. 2014; 42(16):10331-10350
- 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 SJ**, Galle J. *Transcriptional regulation by histone modifications: towards a theory of chromatin reorganization during stem cell differentiation*. Phys Biol. 2013; 10(2):026006
- Amemiya CT, Alföldi J, Lee AP, Fan S, Philippe H, MacCallum I, Braasch I, Manousaki T, Schneider I, Rohner N, **Prohaska SJ**, and others. *The African coelacanth genome provides insights into tetrapod evolution*. Nature 496.7445 (2013): 311-316.
- 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**, Fritzsich 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, Fritzsich 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, Büyükoğlu 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, Fritzsche 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 **nProhaska 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 Zool 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 Zool 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.