

# Sven Findeiß



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BIRTH                    Zwickau/Saxony (Germany), September 16, 1982

## EDUCATION

### **February 2008 - April 2011**

PhD student at the Bioinformatics Group,  
Head of Group: Peter F. Stadler,  
focusing on bacterial non-coding RNAs  
University Leipzig, Germany

### **September 2002 - February 2008**

Diploma studies in Computer Science,  
focused on Bioinformatics,  
University Leipzig, Germany

### **August 1993 - June 2001**

Grammar School,  
finished with Abitur (general qualification for university entrance),  
Gerhart-Hauptmann Gymnasium, Zwickau, Germany

### **September 1989 - June 1993**

Elementary school,  
Sigmund-Jähn Grundschule, Zwickau, Germany

WORK  
EXPERIENCE

*University assistant  
Bioinformatics*

**University of Vienna**  
**Austria**  
**Mai 2011 - now**

*Part-time research assistant  
Bioinformatics*

**University Leipzig**  
**Germany**  
**February 2008 - April 2011**

*Expanding the repertoire of bacterial (non-)coding RNAs*

From housekeeping to group specific non-coding RNAs. The results of biological experiments (e.g. 454 sequencing) and computational approaches (e.g. RNAz, RNACode) were used to detect and analyze these functional transcripts.

*Diploma Thesis  
Bioinformatics*

**University Leipzig**  
**Germany**  
**May 2007 - January 2008**

*Ultra-Conserved Regions – Analyzing the Tip of the Iceberg*

Genome-wide detection of ultra-conserved regions (UCRs). Within this thesis the hypothesis that UCRs result from cases of multiple, overlapping sequence features has been addressed.

*Undergraduate Assistant  
Bioinformatics*

**University Leipzig**  
**Germany**  
**November 2006 – March 2007**

Prediction and analysis of non-coding RNAs (ncRNAs) in different bacterial species like *Pseudomonas aeruginosa* and *Xanthomonas campestris*.

*Intern at Laboratory of Evolutionary  
Functional Genomics (EFG)*

**Arizona State University**  
**USA**  
**August 2006 – November 2006**

Task 1: Software development for evolution of orthologous non-coding, gene-flanking sequences in a large number of whole genomes, based on a list of gene/protein sequences.

Task 2: Timing of divergence among drosophilids based on genomic mutation sites.

*Undergraduate Assistant  
Bioinformatics*

**University Leipzig  
Germany**  
**November 2005 – May 2006**

Motif detection and discovery with common programs like MEME and implementations of different algorithms. Study of the regulation of gene expression especially focused on the gene-family CD97.

**ADDITIONAL  
EXPERIENCE**

*Organization of the Bioinformatics  
Herbstseminar  
(02.10.2012 - 07.10.2012)  
Doubice (Decin), Czech republic*

**University Leipzig  
Germany**  
**October 2012**

*Organization of the Bioinformatics  
Herbstseminar  
(29.09.2011 - 04.10.2011)  
Vysoka Lipa (Decin), Czech republic*

**University Leipzig  
Germany**  
**October 2011**

*Organization of the Symposium on  
Molecular Systems: From Chemistry to  
Evolution dedicated to Peter K.  
Schuster  
(07.10.2011 - 08.10.2011)  
Vienna, Austria*

**University of Vienna  
Austria**  
**October 2011**

*Organization of the Bioinformatics  
Herbstseminar  
(05.10.2010 - 10.10.2010)  
Vysoka Lipa (Decin), Czech republic*

**University Leipzig  
Germany**  
**October 2010**

*Organization of the Bioinformatics  
Herbstseminar  
(21.10.2009 - 25.10.2009)  
Vysoka Lipa (Decin), Czech republic*

**University Leipzig  
Germany**  
**October 2009**

**SKILLS**

- Languages: German (native); English (fluent); Latin (basic knowledge)
- Operating System: Linux
- Programming/Scripting: Perl, JAVA (basics), HTML, PHP, Postscript  
Command-line based scripting (e.g. awk, sed, cut)
- Bioinformatic tools: advanced knowledge of RNA secondary structure prediction and comparison programs comprised in the Vienna RNA Package; development of software tools which use algorithmic details of these programs
- Advanced knowledge of the professional typesetting package L<sup>A</sup>T<sub>E</sub>X

SUBMITTED  
PUBLICATIONS

Doose G, Kirsch R, Alexis M, Findeiß S, Langenberger D, Machné R, Hoffmann S, Mörl M, Stadler PF. *Unusual Transcripts in Prokaryotic Transcriptome Sequencing Data*

PUBLICATIONS

**2013**

Müller SA, Findeiß S, Pernitzsch SR, Wissenbach DK, Stadler PF, Hofacker IL, von Bergen M, Kalkhof S. *Identification of new protein coding sequences and signal peptidase cleavage sites of Helicobacter pylori strain 26695 by proteogenomics*, Journal of Proteomics [accepted].

Wachsmuth M, Findeiß S, Weissheimer N, Stadler PF, Mörl M. *De novo design of a synthetic riboswitch that regulates transcription termination*. Nucleic Acids Res. 2013 Feb 1;41(4):2541-51.

**2012**

Schmidtke C, Findeiß S, Sharma CM, Kuhfuß J, Hoffmann S, Vogel J, Stadler PF and Bonas U. *Genome-wide automated differential transcriptome analysis of the plant pathogen Xanthomonas identifies sRNAs with putative virulence functions*. Nucleic Acids Res. 2012 Mar;40(5):2020-31.

**2011**

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 Jul 31.

Lechner M, Findeiß S, Steiner L, Marz M, Stadler PF, Prohaska SJ. *Proteinortho: detection of (co-)orthologs in large-scale analysis*. BMC Bioinformatics. 2011 Apr 28;12:124.

Washietl S, Findeiß S, Müller S, Kalkhof S, von Bergen M, Hofacker IL, Stadler PF and Goldman N. *RNAcode: robust discrimination of coding and noncoding regions in comparative sequence data*. RNA. 2011 Apr;17(4):578-94.

Findeiß S, Langenberger D, Stadler PF and Hoffmann S. *Traces of Post-Transcriptional RNA Modifications in Deep Sequencing Data*. Biol. Chem., 2011 Apr; 392(4):305-13.

**2010**

Müller SA, Kohajda T, Findeiß S, Stadler PF, Washietl S, Kellis M, von Bergen M and Kalkhof S. *Optimization of Parameters for Coverage of Low Molecular Weight Proteins*. Analytical and Bioanalytical Chemistry, 2010 Dec; 398(7-8):2867-81.

Schilling D, Findeiß S, Richter AS, Taylor JA and Gerischer U. *The small RNA Aar in Acinetobacter baylyi: a putative regulator of amino acid metabolism.* Arch Microbiol, 2010 Sep; 192(9): 691-702.

Sharma CM, Hoffmann S, Darfeuille F, Reignier J, Findeiß S, Sittka A, Chabas S, Reiche K, Hackermüller J, Reinhardt R, Stadler PF and Vogel J. *The primary transcriptome of the major human pathogen Helicobacter pylori.* Nature, 2010 Mar; 464(7286): 250-5.

Donath A, Findeiß S, Hertel J, Marz M, Otto W, Schulz C, Stadler PF and Wirth S. *Noncoding RNA. In Evolutionary Genomics and Systems Biology.* Editor Gustavo Caetano-Anollés; Wiley-Blackwell, Hoboken; 2010; 251-283.

Findeiß S, Schubert C, Stadler PF and Bonas U. *A novel family of plasmid-transferred anti-sense ncRNAs.* RNA Biol, 2010 Mar 8;7(2).

Gruber AR, Findeiß S, Washietl S, Hofacker IL and Stadler PF. *RNAZ 2.0: IMPROVED NONCODING RNA DETECTION.* Pac Symp Biocomput, 2010 Jan; 15:69-79.

## 2009

Hiller M, Findeiß S, Lein S, Marz M, Nickel C, Rose D, Schulz C, Backofen R, Prohaska SJ, Reuter G and Stadler PF. *Conserved introns reveal novel transcripts in Drosophila melanogaster.* Genome Res, 2009 Jul; 19(7): 1289-300.

## 2008

Sonnleitner E, Sorger-Domenigg T, Madej MJ, Findeiß S, Hackermüller J, Hüttenhofer A, Stadler PF, Bläsi U and Moll I. *Detection of small RNAs in Pseudomonas aeruginosa by RNomics and structure-based bioinformatic tools.* Microbiology, 2008 Oct; 154(10): 3175-3187.

Wobus M, Wandel E, Prohaska SJ, Findeiß, Tschöp K and Aust G. *Transcriptional regulation of the human CD97 promoter by Sp1/Sp3 in smooth muscle cells.* Gene, 2008 Apr; 413(1-2): 67-75.

## 2007

Rose D, Hackermüller J, Washietl S, Reiche K, Hertel J, Findeiß S, Stadler PF and Prohaska SJ. *Computational RNomics of drosophilids.* BMC Genomics, 2007 Nov; 8:406.

Drosophila 12 Genomes Consortium. *Evolution of genes and genomes on the Drosophila phylogeny.* Nature 2007, Nov; 450(7167) :203-18.

## 2006

Hertel J, Lindemeyer M, Missal K, Fried C, Tanzer A, Flamm C, Hofacker IL, Stadler PF and Students of Bioinformatics Computer Labs 2004 and 2005. *The expansion of the metazoan microRNA repertoire.* BMC Genomics, 2006 Feb; 7:25.

PRESENTATIONS

**2012**

Findeiß S, *Rational Transcription Regulator Design*, 4th Bioinformatics Round Table, Vienna, Austria, 8 November 2012. Talk.

Findeiß S, *Rational Transcription Regulator Design*, Young Investigator Day, Vienna, Austria, 19 April 2012. Talk.

Findeiß S, *Theo Controls Stop and Go*, 27th TBI Winterseminar, Bled, Slovenia, 12 - 19 February, 2012. Talk.

**2011**

Findeiß S, *How time consuming is (self) organization?*, 9. Herbstseminar, Vysoka Lipa, Czech Republic, 29th September - 4th October, 2011. Talk.

Findeiß S, *Expanding the repertoire of bacterial (non-)coding RNAs*, Defensio Talk, Leipzig, Germany, 7th March, 2011. Talk.

**2010**

Findeiß S, Hoffmann S and Stadler PF, *Towards Automated Transcription Start Site Annotation*, SPP1258 Meeting Kassel, Germany, July 1, 2010. Talk.

Findeiß S, *How to assess (non)coding potential?!*, Mini workshop on Genome exploration, Copenhagen, Denmark, March 23, 2010. Talk.

Findeiß S, *Transcript analysis using RNA-seq; What others call transcriptomics?!*, 25th TBI Winterseminar, Bled, Slovenia, February 20, 2010. Talk.

Findeiß S, *Transcriptomics in Prokaryotes; Deep sequencing-based discovery of the Chlamydia trachomatis transcriptome*, Transcriptomics Journal Club, Leipzig, Germany, January 29, 2010. Talk.

**2009**

Findeiß S, Schubert C, Stadler PF and Bonas U, *Jumping Anti-Sense RNA found in Xanthomonas campestris pv. vesicatoria*, ProkaGENOMICS 2009, Göttingen, Germany, October 4-7, 2009. Poster.

Gruber AR, Findeiß S, Washietl S, Hofacker IL and Stadler PF *RNAz 2.0: improved noncoding RNA detection*, German Conference on Bioinformatics, Halle, Germany, September 28-30, 2009. Poster.

Findeiß S, Schubert C, Stadler PF and Bonas U, *Jumping Anti-Sense RNA found in Xanthomonas campestris pv. vesicatoria*, ProRNA 2009, Berlin, Germany, June 03-06, 2009. Poster.

Findeiß S, *YELLOW Sticks, STRUCTURED RNAs and BLACK Spots Small regulatory RNAs in Xanthomonas campestris pv. vesicatoria*, BBZ Doktoranden-Kolloquium, Leipzig, Germany, April 1, 2009. Talk.

Findeiß S, *Yellow Sticks Listen To Jazz; Anti Sense RNAs Small regulatory RNAs in Xanthomonas campestris pv. vesicatoria*, 24th TBI Winterseminar, Bled, Slovenia, February 21, 2009. **Talk**.

## 2008

Findeiß S, Schubert C, Stadler PF and Bonas U, *Small regulatory RNAs with a function in the virulence of Xanthomonas campestris pv. vesicatoria*, Bioinformatics Herbstseminar, Studeny, Czech republic, November 2, 2008. **Talk**.

Findeiß S, *Small regulatory RNAs with a function in the virulence of Xanthomonas campestris pv. vesicatoria*, Symposium on Gene Regulation in Prokaryotes, Jugendburg, Germany, October 9, 2008. **Talk**.

Findeiß S, Schubert C, Stadler PF and Bonas U, *Small regulatory RNAs with a function in the virulence of Xanthomonas campestris pv. vesicatoria*, 5th Meeting of the GBM study section RNA-Biochemistry, Kassel, Germany, September 18-21, 2008. **Poster**.

Findeiß S, Schubert C, Stadler PF and Bonas U, *Small regulatory RNAs with a function in the virulence of Xanthomonas campestris pv. vesicatoria*, SPP1258 Meeting, Kassel, Germany, September 16-18, 2008. **Poster**.

## 2007

Findeiß S, Hernandez Rosales M and Stadler PF, *BioInformatic approaches to detect and verify ncRNAs*, Kickoff meeting SPP1258, Bochum, Germany, September 5-7, 2007, **Poster**.

Findeiß S, *Trip into the Desert Drosophila melanogaster & Co*, 22th TBI Winterseminar, Bled, Slovenia, February 19, 2007, **Talk**.

## 2006

Findeiß S, *Barrier Trees, The (Bio)Informatics View*, Seminar 'parallel algorithms and complex systems', Leipzig, Germany, June 23, 2006. **Talk**.

Findeiß S, Prohaska SJ, *The CD97 Promoter - conserved elements*. 3rd EGF-TM7 Workshop, Amsterdam, Netherlands. March 23, 2006. **Talk**.

## 2005

Prohaska SJ, Findeiß S and Jöris J, *The jungle of motif detection Searching for binding sites in CD97 promotor*, Bioinformatics Herbstseminar, Chribska, Czech republic, October 2005. **Talk**.