Curriculum vitae

Personal details

Name:	Claudia Fried
Date of Birth:	May 17th, 1978
Nationality:	Austrian

Education

2003 –	Ph.D. student, Supervisor: Prof. Peter F. Stadler, University of Leipzig, Germany
June 2003	Achieving M.Sc. (Magistra rerum naturalium), passing with distinction Diploma thesis: Discovery of Transcription Factor Binding Sites, University of Vienna, Austria
1998 – 2003	Diploma studies in Biology (Genetics)
1999	Diploma for molecular biology and gene technology
1998 – 1999	College for molecular biology and gene technology, Höhere Bundes-Lehr und Versuchsanstalt für chemische Industrie, Vienna, Austria
1999	Diploma for technical chemistry
1996 – 1998	College for technical chemistry, Höhere Bundes-Lehr und Versuchsanstalt für chemische Industrie, Vienna, Austria
1996	Matura (school leaving certificate) at BORG, Mistelbach, Austria
1992 – 1996	Highschool, BORG Mistelbach, Austria
1988 – 1992	Secondary school, Hauptschule Mistelbach
1986 – 1988	Elementary school, Volkschule Wilfersdorf

Practical experiences

07 – 09/2000	Molecular biology lab, IAEA Agriculture and Biotechnology, Seibersdorf, Austria
05 – 07/1999	Biotechnology in Plant Production, Institute for Agrobiotechnology, Tulln, Austria
07/1998	Optimization of phantom materials using polymer powder sintering under vacuum, Institute of biomedical technology and physics, University of Vienna, Austria
08/1997	Development of Newspaper-Offset Colours, SunChemical, Vienna, Austria
1998 – 2001	Archeological excavations, Schletz, Austria

Publications

[1] C. Fried, S. J. Prohaska, P. F. Stadler. **Independent Hox-Cluster Duplications in Lampreys.** J. Exp. Zool. (Mol. Dev. Evol.), 299B: 18-25, 2003.

[2] S. J. Prohaska, C. Fried, C. T. Amemiya, F. H. Ruddle, G. P. Wagner, P. F. Stadler. **The Shark HoxN cluster is homologous to the Human HoxD cluster.** J. Mol. Evol., 58(2): 212-217, 2004.

[3] S. J. Prohaska, C. Fried, C. Flamm, G. P. Wagner, P. F. Stadler. **Surveying Phylogenetic Footprints in Large Gene Clusters: Applications to Hox Cluster Duplications.** Mol. Phyl. Evol., 31(2): 581-604, 2004.

[4] C-H. Chiu, K. Dewar, G. P. Wagner, K. Takahashi, F. Ruddle, C. Ledje, P. Bartsch, J-L. Scemama, E. Stellwag, C. Fried, S. J. Prohaska, P. F. Stadler, C. T. Amemiya. **Bichir *HoxA* cluster sequence reveals surprising trends in ray-finned fish genomic evolution.** Genome Res. 14: 11-17, 2004.

[5] P. F. Stadler, C. Fried, S. J. Prohaska, W. J. Bailey, B. Y. Misof, F. H. Ruddle, G. P. Wagner. **Evidence for independent Hox gene duplications in the hagfish lineage: A PCR-based gene inventory of *Eptatretus stoutii.*** Mol. Phylog. Evol., 32: 686-694, 2004.

[6] C. Fried, S. J. Prohaska, P. F. Stadler. **Exclusion of Repetitive DNA Elements from Gnathostome Hox Clusters.** J. Exp. Zool. (Mol. Dev. Evol.), 302B: 165-173, 2004.

[7] G. P. Wagner, C. Fried, S. J. Prohaska, P. F. Stadler. **Divergence of Conserved Non-Coding Sequences: Rate Estimates and Relative Rate Tests.** Mol. Biol. Evol., 21: 2116-2121, 2004.

[8] C. Fried, W. Hordijk, S. J. Prohaska, C R. Stadler, P. F. Stadler. **The Footprint Sorting Problem.** J. Chem. Inf. Comput. Sci., 44: 332-338, 2004.

[9] A.F. Bompfünewerer, C. Flamm, C. Fried, G. Fritzsch, I.L. Hofacker, J. Lehmann, K. Missal, A. Mosig, B. Müller, S.J. Prohaska, B.M.R. Stadler, P.F. Stadler, A. Tanzer, S. Washietl, Ch. Witwer. **Evolutionary Patterns of Non-Coding RNAs.** Th. Biosci., 123: 301-369, 2005.

[10] R. R. Stocsits, I. L. Hofacker, C. Fried, P. F. Stadler. **Multiple Sequence Alignments of Partially Coding Nucleic Acid Sequences.** BMC Bioinformatics, 6: 160 [epub], 2005.

[11] G. P. Wagner, K. Takahashi, V. Lynch, S. J. Prohaska, C. Fried, P. F. Stadler, C. T. Amemiya. **Molecular Evolution of Duplicated Ray Finned Fisch HoxA Clusters: Increased synonymous substitution rate and asymmetrical co-divergence of coding and non-coding sequences.** J. Mol. Evol., 60: 665-676, 2005.

[12] J. Hertel, M. Lindemeyer, K. Missal, C. Fried, A. Tanzer, C. Flamm, I. L. Hofacker, P. F. Stadler, and The Students of Bioinformatics Computer Labs 2004 and 2005. **The Expansion of the Metazoan MicroRNA Repertoire.** BMC Genomics 2006, 7:25 [epub], 2006.

[13] A. F. Bompfünewerer, R. Backofen, S. H. Bernhart, C. Flamm, C. Fried, G. Fritzsch, J. Hackermüller, J. Hertel, I. L. Hofacker, K. Missal, A. Mosig, S. J. Prohaska, D. Rose, P. F. Stadler, A. Tanzer, S. Washietl, S.

Will. **RNAs Everywhere: Genome-Wide Annotation of Structured RNAs.** J. Exp. Zool., in Press

[14] R. Guigó, F. Denoeud, A. Reymond, P. Kapranov, J. Rozowsky, D. Zheng, R. Castelo, A. Frankish, J. Harrow, S. Ghosh, A. Sandelin, I. L. Hofacker, R. Baertsch, D. Keefe, P. Flicek, S. Dike, J. Cheng, J. Lagarde, J. F. Abril, A. Shahab, C. Flamm, C. Fried, J. Hackermüller, J. Hertel, M. Lindemeyer, K. Missal, A. Tanzer, S. Washietl, J. Korbel, O. Emanuelsson, J. S. Pedersen, N. Holroyd, R. Taylor, D. Swarbreck, N. Matthews, M. C. Dickson, D. J. Thomas, M. T. Weirauch, J. Gilbert, J. Drenkow, I. Bell, X.-D. Zhao, K.G. Srinivasan, W.-K. Sung, H. S. Ooi, K. P. Chiu, S. Foissac, T. Alioto, S. W. Choo, C. Y. Choo, C. Ucla, C. Manzano, C. Wyss, E. Cheung, T. Clarke, J. B. Brown, M. Ganesh, S. Patel, H. Tammana, J. Chrast, C. N. Henrichsen, C. Kai, J. Kawai, U. Nagalakshmi, J. Wu, Z. Lian, J. Lian, P. Newburger, X. Zhang, P. Bickel, J. S. Mattick, P. Carninci, Y. Hayashizaki, S. M. Weissman, E. Dermitzakis, E. H. Margulies, T. Hubbard, R. M. Myers, J. Rogers, P. F. Stadler, T. M. Lowe, C.-L. Wei, Y. Ruan, M. Snyder, E. Birney, M. Gerstein, S. E. Antonarakis, T. R. Gingeras. **Distance and Global Transcription Networks Characterize ENCODE Regions.** submitted

[15] C. Fried, P. F. Stadler, P. Ahnert. **Genome-Wide Analysis of Single Nucleotide Polymorphisms in Evolutionary Conserved DNA.** submitted

[16] S. Washietl, J. S. Pedersen, J. O. Korbel, C. Fried, A. R. Gruber, J. Hackermüller, J. Hertel, M. Lindenmayer, K. Missal, A. Tanzer, C. Ucla, S. E. Antonarakis, A. Reymond, F. Denoeud, J. Lagarde, J. Drenkow, P. Kapranov, T. R. Gingeras, M. Snyder, M. B. Gerstein, I. L. Hofacker, P. F. Stadler. **Structured RNAs in the ENCODE Selected Regions of the Human Genome.** submitted

Presentations

Talk	**Transcription Factor Target Detection in Comparative Genomics.** MATH/CHEM/COMP 2005, Dubrovnik, 20.06.-25.06.2005
Poster	**Distribution of Single Nucleotide Polymorphisms in Genes, Phylogenetic Footprints, and Non-Coding Regions of the Genome.** Researchfestival, Leipzig 10.12.2004
Poster	**Distribution of Single Nucleotide Polymorphisms in Genes, Phylogenetic Footprints, and Non-Coding Regions of the Genome.** GCB 2004, Bielefeld, 4-6.10.2004
Poster	**Distribution of SNPs in Genes, Phylogenetic Footprints, and Non-Coding Regions.** MATH/CHEM/COMP 2004, Dubrovnik, 21-26.06.2004
Poster	**Surveys of Phylogenetic Footprints in Large Gene Clusters.** 3.Biotechnologie-Tag 2004, Leipzig 19.05.2004
Poster	**Correlation of SNPs with Phylogenetic Footprints.** GCB 2003, Munich, 12-14.10.2003
Poster	**Surveys of Phylogenetic Footprints in Large Gene Clusters.** ECCB 2003, Paris, 27-30.09.2003
Talk	**Surveying phylogenetic footprints: an efficient method and an application to vertebrate Hox clusters.** Computational Biology in Saxony 2003, Dresden 14.03.2003
Poster	**Detection of phylogenetic footprints in large gene clusters.** 2.Biotechnologie-Tag 2003, Leipzig 21.05.2003
Poster	**The Footprint Sorting Problem.** MATH/CHEM/COMP 2003, Dubrovnik, 21.06.-28.06.2003