

CV - Erik Sandelin

1 Personal Information

Name: Erik Sandelin
Date of birth: 28th of Dec. 1972
Citizenship: Swedish

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2 Positions and Degrees

- **March 2003 - .** Research position at Stockholm Bioinformatics Center (SBC). The position is funded by the Knut and Alice Wallenberg foundation as part of my postdoc grant.
- **Dec. 2000 - Dec. 2002.** Postdoctoral studies in professor Michael Levitt's group in computational structural biology at Stanford University, California, USA.
- **20 Oct. 2000.** Ph.D. in Theoretical Physics at Lund University. My Ph.D. work was carried out in the Complex Systems Division at the Department of Theoretical Physics with Professor Anders Irbäck as thesis advisor. The thesis titled *Thermodynamics of Protein Folding and Design* can be downloaded at <http://www.sbc.su.se/~erik/ms/thesis.pdf>.
- **Sep. 1996 - Dec. 2000.** Ph.D. position at the Department of Theoretical Physics at Lund University. The position was part of the NGSSC program (National Graduate School in Scientific Computing).
- **Sep 1996.** Fil.Mag. (M.Sc.), Lund University. Major: Physics Minor: Mathematics.

3 Awards

- **March 2000.** Postdoctoral grant in bioinformatics from the Knut and Alice Wallenberg foundation.

4 Research interests

- Protein folding
 - Monte Carlo simulations of lattice and off-lattice protein models
 - Exact enumeration of lattice protein models
 - Protein sequence analysis
 - Protein design
 - Hydrophobicity

- Bioinformatics
 - Monte Carlo methods for sequence assembly
 - Structural alignments
 - MSA - Multiple sequence and structural alignments
 - Homology modelling
 - Sequence diversity

5 Publications

All publications can be accessed at <http://www.sbc.su.se/~erik/papers.html>.

- E. Sandelin. 2004. On Hydrophobicity and Conformational Specificity in Proteins. *Biophys. J.* 86:23-30.
- E. Sandelin. 2000. Thermodynamics of Protein Folding and Design (Ph.D. Thesis). Date of issue: 2000-09-08, ISBN 91-628-4305-2

- E. Sandelin. 2000. A Monte Carlo Approach to Sequence Assembly. LU TP 00-32 <http://www.sbc.su.se/erik/ms/shotgun.pdf>.
- A. Irbäck and E. Sandelin. 2000. On Hydrophobicity Correlations in Protein Chains. *Biophys. J.* 79:2252-2258.
- A. Irbäck and E. Sandelin. 1999. Monte Carlo Study of the Phase Structure of Compact Polymer Chains. *J. Chem. Phys.* 110:12256-12262.
- A. Irbäck, C. Peterson, F. Potthast and E. Sandelin. 1999. Design of Sequences with Good Folding Properties in Coarse-Grained Protein Models. *Structure with Folding & Design* 7:347-360.
- A. Irbäck, C. Peterson, F. Potthast and E. Sandelin. 1998. Monte Carlo Procedure for Protein Design. *Phys. Rev. E* 58:R5249-R5252.
- A. Irbäck and E. Sandelin. 1998. Local Interactions and Protein Folding: A Model Study on the Square and Triangular Lattices. *J. Chem. Phys.* 108:2245-2250.

6 Referee Assignments

- Bioinformatics

7 Presentations

7.1 Talks

- *On Hydrophobicity, Stability and Conformational Specificity in Proteins*, presented at SBC/CGB meeting September 10 2003, Karolinska Institutet, Stockholm, Sweden.
- *Monte Carlo study of the phase structure of compact polymer chains*, presented at Stat-Mech network meeting on life, order and disorder, November 20-21 1998, Niels Bohr Institute, Copenhagen, Denmark.
- *Non-randomness of sequences of good folders in a simple lattice model for protein folding*, presented at Protein folding workshop, May 12-13 1998, Lund University, Sweden.

7.2 Posters

- *Monte Carlo study of the phase structure of compact polymer chains* presented at The 5th International Conference on Computational Physics, October 11-13 1999, Kanazawa, Japan.
- *A Novel Monte Carlo Procedure for Protein Design* presented at Slow Dynamics in Complex Systems, November 9-14 1998, Fukuoka, Japan.
- *A Novel Monte Carlo Procedure for Protein Design* Statistical Mechanics of Biocomplexity, XV Conference on Statistical Mechanics, June 8-12 1998, Sitges, Barcelona, Spain.

8 Teaching

- *Current State of the Art in Protein Structure Prediction course.* Developing and responsible for this graduate course to start at Stockholm Bioinformatics Center January 2004.
- Laboratory teaching assistant (10%, Sep. 1996 - Dec. 2000). Supervision and development of computer exercises.

9 Programming

- C
- Perl
- Fortran
- HTML
- MPI for parallel programming

10 References

Please do not hesitate to contact:

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- *Head of Computational Structural Biology at Stanford University:*

Michael Levitt
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- *Thesis Advisor:*

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