

CURRICULUM VITAE

Name Finn Sverre Drabløs
Year of birth 1957
Nationality Norwegian
Position Professor (bioinformatics)
Department of Cancer Research and Molecular Medicine
Faculty of Medicine, NTNU

Education Cand. scient., University of Bergen, Dept. of Organic Chemistry, 1983.
Dr.scient., University of Bergen, 1992.

Experience

1983-1984	Research Assistant, Dept. of Chemistry, University of Bergen
1984-1987	Research Fellow, NTNF funds
1987	Research Assistant, Dept. of Chemistry, University of Bergen
1988-1996	Research Scientist, Computer Admin, SINTEF Unimed MR Center
1996-1997	Research Scientist, Computer Admin, SINTEF Unimed Biotech
1997-1998	Research Scientist, SINTEF Unimed MR Center
1998-2002	Senior Scientist, SINTEF Unimed MR Center
2001-2002	Førsteamanuensis II, Dep. of Cancer Research and Mol. Biol., NTNU
2002-2004	Research Scientist, Dep. of Cancer Research and Mol. Medicine, NTNU
2004-	Professor, Dep. of Cancer Research and Mol. Medicine, NTNU

Main fields of competence

- Bioinformatics
- Protein structure
- Protein and DNA sequence analysis
- Protein electrostatics
- Computational chemistry
- Computer programming and administration
- Chemometrics
- Organic chemistry

Professional memberships

- International Network of Protein Engineering Centres (INPEC) – Member, former Norwegian representative
- Nordic Bioinformatic Society (SocBiN) – Member, former Norwegian representative
- Norwegian Biochemical Society – Member
- Society for Molecular Biology and Evolution – Member
- Molecular Graphics and Modelling Society – Member
- International Society for Computational Biology – Member

Publications

- 33 book chapters or accepted papers in international journals
- 26 oral presentations and 8 posters at national and international meetings
- 14 SINTEF reports
- 9 other publications

Pedagogical experience

- Lecturing at NTNU courses in protein structure and bioinformatics
- Lecturing at specialist courses in molecular modelling and bioinformatics
- Supervision of students on student projects
- Supervision of students on master/diploma projects
- Supervision of students on doctoral degree projects
- Extensive experience from examinations

19. Grimholt U, Drabløs F, Jørgensen SM, Høyheim B, Stet RJM. *The major histocompatibility class I locus in Atlantic salmon (Salmo salar L.): polymorphism, linkage analysis and protein modelling*. Immunogenetics, 54, 570-581, 2002.
20. Krokan H, Drabløs F, Slupphaug G. *Uracil in DNA - occurrence, consequences and repair*. Oncogene, 21, 8935-8948, 2002.
21. Tøndel K, Anderssen E, Drabløs F. *Protein alpha shape similarity analysis (PASSA): A new method for mapping protein binding sites. Application in the design of a selective inhibitor of Tyrosine kinase 2*. J. Comput.-Assist. Mol. Des. 16, 831-840, 2002
22. Wieman H, Tøndel K, Anderssen E, Drabløs F. *Homology-based modelling of targets for rational drug design* (Review). Mini-Reviews in Medicinal Chemistry 4, 793-804, 2004
23. Bjerkan TM, Bender CL, Ertesvåg H, Drabløs F, Fakhr MK, Preston LA, Skjåk-Bræk G, Valla S. *The Pseudomonas syringae genome encodes a combined mannuronan C-5-epimerase and O-acetyl hydrolase, which strongly enhances the predicted gel-forming properties of alginates*. J. Biol. Chem. 279, 28920-28929, 2004.
24. Drabløs F, Feyzi E, Aas PA, Vaagbø CB, Kavli B, Bratlie MS, Diaz JP, Otterlei M, Slupphaug G, Krokan HE. *Alkylation damage in DNA and RNA – repair mechanisms and medical significance*. DNA Repair 3, 1389-1407, 2004.
25. Bratlie MS, Drabløs F. *Bioinformatic mapping of AlkB homology domains in viruses*. BMC Genomics 6, 1, 2005.
26. Sandve GK, Drabløs F. *Generalized Composite Motif Discovery*. Lecture Notes in Computer Science 3683, 763-769, 2005.
27. Tøndel K, Drabløs F. *Design of selective inhibitors of Tyrosine Kinase 2*. Letters in Drug Design & Discovery 2, 507-515, 2005.
28. Sandve GK, Drabløs F. *A survey of motif discovery methods in an integrated framework*. Biology Direct 1, 11, 2006.
29. Tøndel K, Anderssen E, Drabløs F. *Protein Alpha Shape (PAS) Dock: A new gaussian-based score function suitable for docking in homology modelled protein structures*. J. Comput. Aided Mol. Design 20(3),131-144, 2006.
30. Sundheim O, Vågbo CB, Bjørås M, de Sousa M, Talstad V, Aas PA, Drabløs F, Krokan HE, Tainer JA, Slupphaug G. *Crystal structure and role of key residues in hABH3 DNA/RNA demethylase*. EMBO J. 25(14), 3389-3397, 2006.
31. Abul O, Sandve GK, Drabløs F. *A methodology for motif discovery employing iterated cluster re-assignment*. Series on Advances in Bioinformatics and Computational Biology 4, 257-268, 2006.
32. Sandve GK, Nedland M, Syrstad ØB, Eidsheim LA, Abul O, Drabløs F. *Accelerating motif discovery: Motif matching on parallel hardware*. Lecture Notes in Computer Science 4175, 197-206, 2006.
33. Abul O, Sandve GK, Drabløs F. *TScan: A two-step de novo motif discovery method*. Proceedings of RECOMB Gene Regulation Satellite Meeting. Accepted.
34. Abul O, Sandve GK, Drabløs F. *False discovery rates in identifying functional DNA motifs*. Accepted.
35. Nesse LL, Drabløs F, Flodgaard LR, Olsaker L, Djønne B. *Variations in the luxR-homologue sdiA of different salmonella wild type strains*. Submitted.

36. Mjaaland S, Drabløs F, Syvertsen BL, Nguyen-Doan VC, GjØen T. *Recombinant protein expression and 3D homology analysis shows that infectious salmon anaemia virus genomic segment 6 encodes a hemagglutinin-esterase*. Submitted.
37. Sandve GK, Abul O, Walseng V, Drabløs F. *Improved benchmarks for computational motif discovery*. Submitted.
38. Klepper K, Sandve GK, Abul O, Johansen J, Drabløs F. *Assessment of composite discovery methods*. In preparation.

Oral presentations

20. Drabløs F. *Identification of protein folds by consensus methods*. Biochemical Contact Meeting - Norwegian Biochemical Society, BeitostØlen, January 18-21, 2001.
21. Drabløs F., Amundsen H.L. *Identification of unique properties in multiple alignments of protein sequences*. Biochemical Contact Meeting - Norwegian Biochemical Society, RØros, January 17-20, 2002.
22. Drabløs F. *From novel genes to old structures*. Bioinformatics 2002, Bergen, April 4-7, 2002.
23. Drabløs F. *Identification of remote homologues*. Bioinformatics – Sequence and structure, Trondheim, September 16, 2003.
24. Drabløs F. *Homology modelling of potential drug targets*. Norwegian Bioinformatics Forum Meeting, Oslo, May 2-3, 2004.
25. Drabløs F, Bratlie MS. *Bioinformatic mapping of viral AlkB-domains*. Biochemical Contact Meeting - Norwegian Biochemical Society, TromsØ, January 13-16, 2005.
26. Sandve GK, Stenersen K, Walseng V, Lekang Ø, Klepper K, Abul O, Hveem TS, Bratlie MS, Drabløs F. *An integrated approach to motif discovery in DNA sequences*. Biochemical Contact Meeting - Norwegian Biochemical Society, Storefjell, January 19-22, 2006.

Posters

8. Drabløs F, Wieman HL. *Molecular modeling of the 1918 'Spanish' influenza hemagglutinin protein*. Bioinformatics 2002, Bergen, April 4-7, 2002.

SINTEF Reports

14. Sunde LM, Heide MA, Brakstad OG, Salvesen I, Drabløs F, Knudsen OØ. *Begroing i havbruk. Informasjonsgrunnlag og strategier for SINTEF-gruppen*. April 2002. STF80 I024012.

Other publications

7. Drabløs, F. *Gener inn i skolen!* NBS-nytt 25(3), 24, 2001.
8. Drabløs, F. *Norge som forskningsnasjon*, Adresseavisen, January 16, 2002.
9. Drabløs F, Fjelstad S, *Bioinformatics in the Fast Lane*, ERCIM News 60, 43-44, 2005.