

CURRICULUM VITÆ FOR THOMAS SICHERITZ-PONTÉN

Birth: 11th of January, 1967

Email: thomas@cbs.dtu.dk

Phone: +46-70 6572 471

Marital status: married, 3 children

Current address:

Konventsqatan 14

216 22 Limhamn, Sweden

Nationality: Austrian

Education and Employments

2014- Head of Section Genomic Diversity at Department of Systems Biology
2011- Professor in Metagenomics at DTU
2007- Head of the Metagenomics group at CBS/DTU
2007-2011 Associate professor in Bioinformatics, CBS/DTU
2003-2007 Assistant professor in Bioinformatics, CBS/DTU
2002-2003 Postdoctoral research, Division of Pharmacognosy - Uppsala University
2000-2002 Postdoctoral research, CBS/DTU
1996-2000 Ph.D. degree at Uppsala University (2000-2-25)
1990-1995 Master Degree in Natural Sciences at Uppsala University
1981-1984 Industrial Engineering, Techn. College of Mödling, Austria

Thomas Sicheritz-Pontén, Professor, M.Sc., fil.dr is heading the Metagenomics group at the Center for Biological Sequence Analysis (CBS) at Department of Systems Biology. He has a background in Bioinformatics and Molecular Evolution from Uppsala University, Sweden and has been working in the genome/metagenome sequencing field for over 15 years, starting 1996 when he built the bioinformatics infrastructure for the first published Scandinavian genome project. His primary interests are microbial genome analysis, metagenomics, antique systems biology, marine biotechnology, machine learning approaches and the detection and study of lateral gene transfers. TSP has co-authored 93 peer-reviewed papers - of which 12 are published in Nature and Science (5 as cover stories) and he is also co-author of the institute's most cited paper for both 2010 and 2005. He has currently an H-factor of 32 with in total 13,701 citations with an average of 147 citations per publication and is involved in several national and international research projects.

Metagenomics utilises a huge genetic reservoir of non-culturable organisms as a resource for biotechnological and medical products and processes. TSP collects different samples from all over the world and develops new tools that will address many of the unique challenges of microbial and antique systems biology. One major activity is the study of the human microbiome where his group is studying the gut and oral microbiome in relation to human health. He uses both metagenomic and metatranscriptomic analysis to relate the microbial communities and the host metadata and genome to various diseases and phenotypes. Mining of industrially relevant enzymes for bulk production and for pathway engineering is also high on the agenda in collaboration with industrial and academic centers of excellence.

Last 5 years publications:

- Palomo A et al. "Metagenomic analysis of rapid gravity sand filter microbial communities suggests novel physiology of *Nitrospira spp.*" **ISME J.** accepted March 2016
- Friis-Nielsen J et al. "Identification of Known and Novel Recurrent Viral Sequences in Data from Multiple Patients and Multiple Cancers" **Viruses** 2016 Feb
- Librado P et al. "Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments", **PNAS** 2015 Dec 15
- Saputra D et al. "Reads2Type: a web application for rapid microbial taxonomy identification", **BMC Bioinformatics** 2015 Nov 25
- Rasmussen S et al. "Early Divergent Strains of *Yersinia pestis* in Eurasia 5,000 Years Ago", **Cell** 2015 Oct 22
- Vinner L et al "Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing" **Nature Scientific Reports** 2015 Aug 19

- Nordahl Petersen T et al. "Meta-genomic analysis of toilet waste from long distance flights; a step towards global surveillance of infectious diseases and antimicrobial resistance", **Nature Scientific Reports** 2015
- Allentoft M et al. "Population genomics of Bronze Age Eurasia", **Nature**. 2015
- Jensen MK et al. "Transcriptome and genome size analysis of the Venus flytrap", **PLoS One**. 2015
- Zepeda Mendoza ML, Sicheritz-Pontén T, Gilbert MT "Environmental genes and genomes: understanding the differences and challenges in the approaches and software for their analyses", **Brief Bioinform**. 2015 Feb 11
- Kjartansdóttir KR et al. "Traces of ATCV-1 associated with laboratory component contamination", **Proc Natl Acad Sci U S A**. 2015 Mar 3
- Schubert M et al. "Prehistoric genomes reveal the genetic foundation and cost of horse domestication", **Proc Natl Acad Sci U S A**. 2014 Dec 30
- Jarvis ED et al. "Whole-genome analyses resolve early branches in the tree of life of modern birds", **Science**. 2014 Dec 12
- Malaspina AS et al. "Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil", **Curr Biol**. 2014 Nov 3
- Jónsson H et al. "Speciation with gene flow in equids despite extensive chromosomal plasticity", **Proc Natl Acad Sci U S A**. 2014 Dec 30
- Tsangaras K et al. "Hybridization capture using short PCR products enriches small genomes by capturing flanking sequences (CapFlank)", **PLoS One** 2014
- Wesolowska-Andersen et al. "Genomic profiling of thousands of candidate polymorphisms predicts risk of relapse in 778 Danish and German childhood acute lymphoblastic leukemia patients" **Leukemia** 19 June 2014
- Wesolowska-Andersen et al "Choice of bacterial DNA extraction method from fecal material influences community structure as evaluated by metagenomic analysis" **Microbiome**, 2014
- Nielsen HB et al. "Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes", **Nat Biotechnol**. 2014 Aug;3
- Spisák, S et al. "Complete Genes May Pass from Food to Human Blood", **PLoS ONE** 2013
- Orlando L et al. "Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse", **Nature**. 2013 July
- Le Chatelier et al "Richness of human gut microbial communities correlates with metabolic markers" accepted in **Nature** 26 July 2013
- UC Alsmark et al. "Patterns of prokaryotic lateral gene transfers affecting parasitic microbial eukaryotes" (2013) **Genome Biol**. 2013 Feb 25;14(2)
- Jacobsen, U.P. et al. (2012) The chemical interactome space between the human host and the genetically defined gut metatypotypes. **ISME J**.
- DB Udatha et al. "Targeted metabolic engineering guided by computational analysis of single-nucleotide polymorphisms (SNPs)" **Methods Mol Biol** 2013
- M. V. Larsen et al., "Multilocus sequence typing of total-genome-sequenced bacteria.," **J. Clin. Microbiol.**, vol. 50, no. 4, pp. 1355–1361, Apr. 2012.
- J. S. Bowman et al. "Microbial community structure of Arctic multiyear sea ice and surface seawater by 454 sequencing of the 16S RNA gene.," **ISME J**, vol. 6, no. 1, Jan. 2012.
- M. Rasmussen et al., "An Aboriginal Australian genome reveals separate human dispersals into Asia.," **Science**, vol. 334, Oct. 2011.
- A Wesolowska, et al. "Cost-effective multiplexing before capture allows screening of 25 000 clinically relevant SNPs in childhood acute lymphoblastic leukemia.," **Leukemia**, Jun. 2011.
- M. Arumugam et al "Enterotypes of the human gut microbiome" **Nature** 2011
- J. Qin et al. "A human gut microbial gene catalogue established by metagenomic sequencing.," **Nature**, Mar. 2010.
- M. Rasmussen et al. "Ancient human genome sequence of an extinct Palaeo-Eskimo.," **Nature** Feb. 2010.