Curriculum Vitae

Erik Arner

MSc, PhD

Date of birth: July 20, 1973, Stockholm Sweden.

Nationality: Swedish

Email: arner@gsc.riken.jp

Academic history:

2002 – 2006: PhD Student, CMB/GB, Karolinska Institutet

2001: Project student, Dept. of Genetics and Pathology, Uppsala University

1994 – 1995, 1997 – 2000, 2004: Molecular biotechnology engineering program, Uppsala University

1993 – 1994: German, Uppsala University

1992 – 1993: History of science and ideas, Uppsala University

Professional history:

2013 – present: Researcher, CLST, DGT, RIKEN, Yokohama

2008 – 2013: Researcher, OSC, RIKEN, Yokohama

2007 – 2008: Researcher, GERG, GSC, RIKEN, Yokohama

2000: Project work, Dept. of Genetics and Pathology, Uppsala University

Grants received:

1. KAKENHI (Japan), Grant-in-aid for Young Scientists A, 8 000 000 JPY awarded for 2011 and 2012 to Erik Arner.

2. Åke Wiberg's Foundation (Sweden), 100000 SEK (~1 200 000 JPY) awarded for 2011 to Erik Arner.

3. Gun och Bertil Stohne's Foundation (Sweden), 20 000 SEK (~250 000 JPY) awarded for 2011 to Erik Arner.

4. Magnus Bergvall's Foundation (Sweden), 50 000 SEK (~625 000 JPY) awarded for 2011 to Erik Arner.

Conferences:

BMB 2013, Kobe: Poster; Keystone Obesity Conference 2011: Poster; BMB 2010, Kobe: Poster; Japan Society of Breeding 2010, Kyoto: Poster; Science Seminar (Applied Biosystems) 2008, Tokyo: Talk; Sequencing Expert Panel (Illumina) 2007, Washington D.C.: Talk; Workshop on Genomics 2005, Singapore: Talk; RECOMB Satellite 2004, Stanford: Talk; RECOMB Satellite 2003, Stanford: Talk; RECOMB Satellite 2002, Stanford: Talk; AGBT 2002, Marco Island: Talk; ISMB 2001, Copenhagen: Poster.

Teaching/ supervision:

Epigenomics: methods and applications to disease and development, RIKEN – KI 2013

Functional regulation in development and disease, RIKEN – KI 2012

Omics Informatics, Tokyo Medical and Dental University 2011

Bioinformatics for Cell Biologists, Karolinska Institutet 2011

Omics Informatics, Tokyo Medical and Dental University 2010

Functional Architecture of the Cell Nucleus, RIKEN – KI 2010

Omics Informatics, Tokyo Medical and Dental University 2009

Bioinformatics for Cell Biologists, Karolinska Institutet 2009

Bioinformatics for Cell Biologists, Karolinska Institutet 2008

Introduction to Bioinformatics, Karolinska Institutet 2004

Scientific Computing, Uppsala University 2002

Scientific Computing, Uppsala University 2001:1

Scientific Computing, Uppsala University 2001:2

Neural Networks and Complex Adaptive Systems, Uppsala University 2000

Programming and computer skills: C++, Perl, MySQL, Berkeley DB, Unix, R, Matlab

Languages: Swedish (fluent), English (fluent), German (Intermediate), Japanese (Intermediate)

Software:

DNPTrapper: http://dnptrapper.sourceforge.net

NGSView: http://ngsview.sourceforge.net

Erik Arner: List of publications

*: Shared first author   #: Corresponding author

Peer reviewed articles:

Forrest ARR, Kawaji H, Rehli M, Baillie JK, de Hoon MJL, Haberle V, Lassmann T, Kulakovskiy IV, Lizio M, Itoh M, Andersson R, Mungall CJ, Meehan TF, Schmeier S, Bertin N, Jørgensen M, DimontE, **Arner E** et al. A promoter level mammalian expression atlas. *Nature*. 2014, in press.

Andersson R, Gebhard C, Miguel-Escalada I, Hoof I, Bornholdt J, Boyd M, Chen Y, Zhao X, Schmidl C, Suzuki T, Ntini E, **Arner E** et al. An atlas of active enhancers across human cell types and tissues. *Nature*. 2014, in press.

Kulyté A, Belarbi Y, Lorente-Cebrián S, Bambace C, **Arner E**, Daub CO, Hedén P, Rydén M, Mejhert N, Arner P. Additive effects of miRNAs and transcription factors on CCL2 production in human white adipose tissue. *Diabetes*. 2013, in press.

Rönnerblad M, Andersson R, Olofsson T, Douagi I, Karimi M, Lehmann S, Hoof I, Sandelin A, de Hoon M, Itoh M, Nago-Sato S, Kawaji H, Lassmann T, Carninci P, Hayashizaki Y, Forrest ARR, Ekwall K, **#Arner E**, Lennartsson A. Analysis of the DNA methylome and transcriptome in granulopoiesis reveal timed changes and dynamic enhancer methylation. *Blood*. 2013, in press.

#Arner E, Forrest ARR, Ehrlund A, Mejhert N, Itoh M, Kawaji H, Lassmann T, Laurencikiene J, Rydén M, Arner P. Ceruloplasmin is a novel adipokine which is overexpressed in adipose tissue of obese subjects and in obesity-associated cancer cells. *PLOS ONE*. 2013, in press.

Prasad P, Rönnerblad M, **Arner E**, Itoh M, Kawaji H, Lassmann T, Daub C, Forrest ARR, Lennartsson A, Ekwall K. High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. *Blood*. 2013, in press.

Arner E, Mejhert N, Kulyté A, Balwierz PJ, Pachkov M, Cormont M, Lorente-Cebrián S, Ehrlund A, Laurencikiene J, Hedén P, Dahlman-Wright K, Tanti JF, Hayashizaki Y, Rydén M, Dahlman I, van Nimwegen E, Daub CO, Arner P. Adipose tissue microRNAs as regulators of CCL2 production in human obesity. *Diabetes*. 2012; **61**(8):1986-93.

Arner P, Bernard S, Salehpour M, Possnert G, Liebl J, Steier P, Buchholz BA, Eriksson M, **Arner E**, Hauner H, Skurk T, Rydén M, Frayn KN, Spalding KL. Dynamics of human adipose lipid turnover in health and metabolic disease. *Nature*. 2011; **478**(7367):110-3.

Franzén O, ***Arner E***, Ferella M, Nilsson D, Respuela P, Carninci P, Hayashizaki Y, Aslund L, Andersson B, Daub CO. The short non-coding transcriptome of the protozoan parasite Trypanosoma cruzi. *PLoS Negl Trop Dis*. 2011; **5**(8):e1283.

Arner P, **Arner E**, Hammarstedt A, Smith U. Genetic predisposition for Type 2 diabetes, but not for overweight/obesity, is associated with a restricted adipogenesis. *PLoS One*. 2011; **6**(4):e18284.

Kimura Y, de Hoon MJ, Aoki S, Ishizu Y, Kawai Y, Kogo Y, Daub CO, Lezhava A, **Arner E**, Hayashizaki Y. Optimization of turn-back primers in isothermal amplification. *Nucleic Acids Res*. 2011; **39**(9):e59.

Hoffstedt J, **Arner E**, Wahrenberg H, Andersson DP, Qvisth V, Löfgren P, Rydén M, Thörne A, Wirén M, Palmér M, Thorell A, Toft E, Arner P. Regional impact of adipose tissue morphology on the metabolic profile in morbid obesity. *Diabetologia*. 2010; **53**(12):2496-503.

Kubosaki A, Lindgren G, Tagami M, Simon C, Tomaru Y, Miura H, Suzuki T, **Arner E**, Forrest AR, Irvine KM, Schroder K, Hasegawa Y, Kanamori-Katayama M, Rehli M, Hume DA, Kawai J, Suzuki M, Suzuki H, Hayashizaki Y. The combination of gene perturbation assay and ChIP-chip reveals functional direct target genes for IRF8 in THP-1 cells. *Mol Immunol*. 2010; **47**(14):2295-302.

Kratz A, **#Arner E**, Saito R, Kubosaki A, Kawai J, Suzuki H, Carninci P, Arakawa T, Tomita M, Hayashizaki Y, Daub CO. Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns. *BMC Genomics*. 2010; **11**:257.

Arner E, Rydén M, Arner P. Tumor necrosis factor alpha and regulation of adipose tissue. *N Engl J Med*. 2010; **362**(12):1151-3.

Arner E, Hayashizaki Y, Daub CO. NGSView: an extensible open source editor for next-generation sequencing data. *Bioinformatics*. 2010; **26**(1):125-6.

Arner E, Westermark PO, Spalding KL, Britton T, Rydén M, Frisén J, Bernard S, Arner P. Adipocyte turnover: relevance to human adipose tissue morphology. *Diabetes*. 2010; **59**(1):105-9.

FANTOM Consortium, Suzuki H, Forrest AR, van Nimwegen E, Daub CO, Balwierz PJ, Irvine KM, Lassmann T, Ravasi T, Hasegawa Y, de Hoon MJ, Katayama S, Schroder K, Carninci P, Tomaru Y, Kanamori-Katayama M, Kubosaki A, Akalin A, Ando Y, **Arner E** et al. The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. *Nat Genet*. 2009; **41**(5):553-62.

Kubosaki A, Tomaru Y, Tagami M, **Arner E**, Miura H, Suzuki T, Suzuki M, Suzuki H, Hayashizaki Y. Genome-wide investigation of in vivo EGR-1 binding sites in monocytic differentiation. *Genome Biol*. 2009; **10**(4):R41.

Akalin A, Fredman D, **Arner E**, Dong X, Bryne JC, Suzuki H, Daub CO, Hayashizaki Y, Lenhard B. Transcriptional features of genomic regulatory blocks. *Genome Biol*. 2009; **10**(4):R38.

Spalding KL, **Arner E**, Westermark PO, Bernard S, Buchholz BA, Bergmann O, Blomqvist L, Hoffstedt J, Näslund E, Britton T, Concha H, Hassan M, Rydén M, Frisén J, Arner P. Dynamics of fat cell turnover in humans. *Nature*. 2008; **453**(7196):783-7.

Arner E, Kindlund E, Nilsson D, Farzana F, Ferella M, Tammi MT, Andersson B. Database of Trypanosoma cruzi repeated genes: 20,000 additional gene variants. *BMC Genomics*. 2007; **8**:391.

Kindlund E, Tammi MT, **Arner E**, Nilsson D, Andersson B. GRAT--genome-scale rapid alignment tool. *Comput Methods Programs Biomed*. 2007; **86**(1):87-92.

Arner E, Tammi MT, Tran AN, Kindlund E, Andersson B. DNPTrapper: an assembly editing tool for finishing and analysis of complex repeat regions. *BMC Bioinformatics*. 2006; **7**:155.

Langin D, Dicker A, Tavernier G, Hoffstedt J, Mairal A, Rydén M, **Arner E**, Sicard A, Jenkins CM, Viguerie N, van Harmelen V, Gross RW, Holm C, Arner P. Adipocyte lipases and defect of lipolysis in human obesity. *Diabetes*. 2005; **54**(11):3190-7.

El-Sayed NM, Myler PJ, Bartholomeu DC, Nilsson D, Aggarwal G, Tran AN, Ghedin E, Worthey EA, Delcher AL, Blandin G, Westenberger SJ, Caler E, Cerqueira GC, Branche C, Haas B, Anupama A, **Arner E** et al. The genome sequence of Trypanosoma cruzi, etiologic agent of Chagas disease. *Science*. 2005; **309**(5733):409-15.

Tammi MT, **Arner E**, Kindlund E, Andersson B. ReDiT: Repeat Discrepancy Tagger--a shotgun assembly finishing aid. *Bioinformatics*. 2004; **20**(5):803-4.

Tammi MT, **Arner E**, Kindlund E, Andersson B. Correcting errors in shotgun sequences. *Nucleic Acids Res*. 2003; **31**(15):4663-72.

Tammi MT, **Arner E**, Andersson B. TRAP: Tandem Repeat Assembly Program produces improved shotgun assemblies of repetitive sequences. *Comput Methods Programs Biomed*. 2003; **70**(1):47-59.

Tammi MT, **Arner E**, Britton T, Andersson B. Separation of nearly identical repeats in shotgun assemblies using defined nucleotide positions, DNPs. *Bioinformatics*. 2002; **18**(3):379-88.

Other publications:

#Arner E and Arner P. Health and obesity: not just skin deep. *Science*. 2013; **342**(6158):558-9.

CAP-ANALYSIS GENE EXPRESSION (CAGE) The Science of Decoding Gene Transcription (2009). Co-author on chapter "From Sequencing Output to CAGE Tags: A Chapter on the Extraction of CAGE Tags from the Raw Output of the Sequencing Machine". ISBN 9814241342.