

# Resume

## Erik Arner

MSc, PhD



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

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**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:**

2015 – present: Unit Leader, CLST, RIKEN, Yokohama

2014 – present: Senior Research Scientist, CLST, DGT, RIKEN, Yokohama

2013 – 2014: Research Scientist, CLST, DGT, RIKEN, Yokohama

2008 – 2013: Research Scientist, OSC, RIKEN, Yokohama

2007 – 2008: Research Scientist, GERG, GSC, RIKEN, Yokohama

2007 – present: Affiliated, Department of Medicine (H7), Karolinska Institutet

**Grants received:**

1. RIKEN Single Cell Project (Japan), 22 500 000 JPY awarded for 2015 – 2017 to Erik Arner

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

3. Åke Wiberg's Foundation (Sweden), 100 000 SEK (~1 360 000 JPY) awarded for 2011 to Erik Arner.

4. Gun och Bertil Stohne's Foundation (Sweden), 20 000 SEK (~270 000 JPY) awarded for 2011 to Erik Arner.

5. Magnus Bergvall's Foundation (Sweden), 50 000 SEK (~680 000 JPY) awarded for 2011 to Erik Arner.

### **Bibliometric data past five years (Google Scholar)**

Number of publications since 2013: **33**

Number of first name publications since 2013 (including shared): **3**

Number of senior author publications since 2013 (including shared): **3**

Citations since 2013: **4933**                      h-index since 2013: **24**                      i10-index since 2013: **35**

### **Talks at international conferences:**

Human Cell Atlas Asia Meeting, Okinawa 2017; Life Science Frontiers in Health, Disease and Aging, Kobe 2017; Frontiers in Life Science Technologies – Decoding Health and Disease, Stockholm 2016; IMGC 2015, Yokohama; BMB 2014, Yokohama; New Era of Life Science Symposium 2014, Stockholm; Science Seminar (Applied Biosystems) 2008, Tokyo; Sequencing Expert Panel (Illumina) 2007, Washington D.C.; Workshop on Genomics 2005, Singapore; RECOMB Satellite 2004, Stanford; RECOMB Satellite 2003, Stanford; RECOMB Satellite 2002, Stanford; AGBT 2002, Marco Island

### **Teaching:**

Epigenomics: Methods, Mechanisms and Application to Disease and Development, RIKEN – KI 2015

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 Institute 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 Institute 2009

Bioinformatics for Cell Biologists, Karolinska Institute 2008

Introduction to Bioinformatics, Karolinska Institute 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), Japanese (Intermediate), German (Intermediate), Spanish (Basic)

### **Software:**

DNPtrapper: <http://dnptrapper.sourceforge.net>

NGSView: <http://ngsview.sourceforge.net>

## List of publications

\*: First author      #: Corresponding author

### Peer reviewed articles:

Zhang P, Dimont E, Ha T, Swanson DJ, Itoh M, Kawaji H, Lassmann T, Daub CO, Arner E; FANTOM Consortium, Carninci P, Hayashizaki Y, Forrest ARR, Hide W, Goldowitz D. Correction to: Relatively frequent switching of transcription start sites during cerebellar development. *BMC Genomics*. 2018; **19**(1):39.

Zhang PGY, Yeung J, Gupta I, Ramirez M, Ha T, Swanson DJ, Nagao-Sato S, Itoh M, Kawaji H, Lassmann T, Daub CO, **Arner E**, de Hoon M; FANTOM consortium, Carninci P, Forrest ARR, Hayashizaki Y, Goldowitz D. Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. *Cerebellum*. 2018; doi: 10.1007/s12311-017-0912-3.

Qin XY, Hara M, **Arner E**, Kawaguchi Y, Inoue I, Tatsukawa H, Furutani Y, Nagatsuma K, Matsuura T, Wei F, Kikuchi J, Sone H, Daub C, Kawaji H, Lassmann T, Itoh M, Suzuki H, Carninci P, Hayashizaki Y; FANTOM consortium, Kokudo N, Forrest ARR, Kojima S. Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. *EBioMedicine*. 2017; **24**:257-266.

Lizio M, Deviatiiarov R, Nagai H, Galan L, **Arner E**, Itoh M, Lassmann T, Kasukawa T, Hasegawa A, Ros MA, Hayashizaki Y, Carninci P, Forrest ARR, Kawaji H, Gusev O, Sheng G. Systematic analysis of transcription start sites in avian development. *PLoS Biol*. 2017; **15**(9):e2002887.

Noguchi S, Arakawa T, Fukuda S, Furuno M, Hasegawa A, [...], **Arner E**, Harshbarger J, Kondo A, Lassmann T, Lizio M, Sahin S, Sengstag T, Severin J, Shimoji H, Suzuki M, Suzuki H, Kawai J, Kondo N, Itoh M, Daub CO, Kasukawa T, Kawaji H, Carninci P, Forrest ARR, Hayashizaki Y. FANTOM5 CAGE profiles of human and mouse samples. *Sci Data*. 2017; **4**:170112.

Rapakoulia T, Gao X, Huang Y, de Hoon M, Okada-Hatakeyama M, Suzuki H, **#Arner E**. Genome-scale regression analysis reveals a linear relationship for promoters and enhancers after combinatorial drug treatment. *Bioinformatics* 2017; **33**(23):3696-3700.

de Rie D, Abugessaisa I, Alam T, **Arner E** et al. An integrated expression atlas of miRNAs and their promoters in human and mouse. *Nat Biotechnol.* 2017; **35**(9):872-878.

Andersson DP, **Arner E**, Hogling DE, Rydén M, Arner P. Abdominal subcutaneous adipose tissue cellularity in men and women. *Int J Obes (Lond).* 2017; **41**(10):1564-1569.

Baillie JK, **Arner E**, Daub C, De Hoon M, Itoh M, Kawaji H, Lassmann T, Carninci P, Forrest AR, Hayashizaki Y, FANTOM Consortium, Faulkner GJ, Wells CA, Rehli M, Pavli P, Summers KM, Hume DA. Analysis of the human monocyte-derived macrophage transcriptome and response to lipopolysaccharide provides new insights into genetic aetiology of inflammatory bowel disease. *PLoS Genet.* 2017; **13**(3):e1006641.

Hon CC, Ramilowski JA, Harshbarger J, Bertin N, Rackham OJ, Gough J, Denisenko E, Schmeier S, Poulsen TM, Severin J, Lizio M, Kawaji H, Kasukawa T, Itoh M, Burroughs AM, Noma S, Djebali S, Alam T, Medvedeva YA, Testa AC, Lipovich L, Yip CW, Abugessaisa I, Mendez M, Hasegawa A, Tang D, Lassmann T, Heutink P, Babina M, Wells CA, Kojima S, Nakamura Y, Suzuki H, Daub CO, de Hoon MJ, **Arner E**, Hayashizaki Y, Carninci P, Forrest AR. An atlas of human long non-coding RNAs with accurate 5' ends. *Nature.* 2017; doi: 10.1038/nature21374.

Ehrlund A, Mejhert N, Björk C, Andersson R, Kulyté A, Åström G, Itoh M, Kawaji H, Lassmann T, Daub CO, Carninci P, Forrest AR, Hayashizaki Y, Sandelin A, Ingelsson E, FANTOM Consortium, Rydén M, Laurencikiene J, Arner P, **#Arner E**. Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. *Diabetes.* 2017; **66**(1):218-230.

Kleftogiannis D, Kalnis P, **Arner E**, Bajic VB. Discriminative identification of transcriptional responses of promoters and enhancers after stimulus. *Nucleic Acids Res.* 2017; **45**(4):e25.

Davis MR, **Arner E**, Duffy CR, De Sousa PA, Dahlman I, Arner P, Summers KM. Datasets of genes coexpressed with FBN1 in mouse adipose tissue and during human adipogenesis. *Data Brief.* 2016; **8**:851-7.

Davis MR, **Arner E**, Duffy CR, De Sousa PA, Dahlman I, Arner P, Summers KM. Expression of FBN1 during adipogenesis: Relevance to the lipodystrophy phenotype in Marfan syndrome and related conditions. *Mol Genet Metab.* 2016; **119**(1-2):174-85.

Klein S, Dieterich LC, Mathelier A, Chong C, Sliwa-Primorac A, Hong YK, Shin JW, Lizio M, Itoh M, Kawaji H, Lassmann T, Daub CO, **Arner E**, FANTOM consortium, Carninci P, Hayashizaki Y, Forrest AR, Wasserman WW, Detmar M. DeepCAGE transcriptomics identify HOXD10 as a transcription factor regulating lymphatic endothelial responses to VEGF-C. *J Cell Sci.* 2016; **129**(13):2573-85.

St Laurent GS, Vyatkin Y, Antonets D, Ri M, Qi Y, Saik O, Shtokalo D, de Hoon MJ, Kawaji H, Itoh M, Lassmann T, **Arner E**, Forrest AR, FANTOM consortium, Nicolas E, McCaffrey TA, Carninci P, Hayashizaki Y, Wahlestedt C, Kapranov P. Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. *Nucleic Acids Res.* 2016; **44**(7):3233-52.

Lennartsson A, \***Arner E**, Fagiolini M, Saxena A, Andersson R, Takahashi H, Noro Y, Sng J, Sandelin A, Hensch TK, Carninci P. Remodeling of retrotransposon elements during epigenetic induction of adult visual cortical plasticity by HDAC inhibitors. *Epigenetics Chromatin.* 2015; **8**:55.

Carbajo D, Magi S, Itoh M, Kawaji H, Lassmann T, **Arner E**, Forrest AR, Carninci P, Hayashizaki Y, Daub CO, FANTOM consortium, Okada-Hatakeyama M, Mar JC. Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. *PLoS One.* 2015; **10**(12):e0144176.

Dieterich LC, Klein S, Mathelier A, Sliwa-Primorac A, Ma Q, Hong YK, Shin JW, Hamada M, Lizio M, Itoh M, Kawaji H, Lassmann T, Daub CO, **Arner E**, Carninci P, Hayashizaki Y, Forrest AR, Wasserman WW, Detmar M. DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. *Cell Rep.* 2015; **13**(7):1493-504.

Rydén M, Uzunel M, Hård JL, Borgström E, Mold JE, **Arner E**, Mejhert N, Andersson DP, Widlund Y, Hassan M, Jones CV, Spalding KL, Svahn BM, Ahmadian A, Frisén J, Bernard S, Mattsson J, Arner P. Transplanted Bone Marrow-Derived Cells Contribute to Human Adipogenesis. *Cell Metab.* 2015; **22**(3):408-17.

Mina M, Magi S, Jurman G, Itoh M, Kawaji H, Lassmann T, **Arner E**, Forrest AR, Carninci P, Hayashizaki Y, Daub CO, FANTOM Consortium, Okada-Hatakeyama M, Furlanello C. Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. *Sci Rep.* 2015; **5**:11999.

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Aitken S, Magi S, Alhendi AM, Itoh M, Kawaji H, Lassmann T, Daub CO, **Arner E**, Carninci P, Forrest AR, Hayashizaki Y, FANTOM Consortium, Khachigian LM, Okada-Hatakeyama M, Semple CA. Transcriptional dynamics reveal critical roles for non-coding RNAs in the immediate-early response. *PLoS Comput Biol.* 2015; **11**(4):e1004217.

\***Arner E**, Daub CO, Vitting-Seerup K, Andersson R et al. Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. *Science.* 2015; **347**(6225):1010-4.

Lizio M, Harshbarger J, Shimoji H, Severin J, Kasukawa T, Sahin S, Abugessaisa I, Fukuda S, Hori F, Ishikawa-Kato S, Mungall CJ, **Arner E** et al. Gateways to the FANTOM5 promoter level mammalian expression atlas. *Genome Biology.* 2015; **16**:22.

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; **507**(7493):455-61.

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, Dimont E, **Arner E** et al. A promoter level mammalian expression atlas. *Nature.* 2014; **507**(7493):462-70.

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.* 2014; **123**(17):e79-89.

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.* 2014; **123**(17):e46-57.

\*#**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*. 2014; **9**(3):e80274.

Andersson DP, Eriksson Hogling D, Thorell A, Toft E, Qvisth V, Näslund E, Thörne A, Wirén M, Löfgren P, Hoffstedt J, Dahlman I, Mejhert N, Rydén M, **Arner E**, Arner P. Changes in subcutaneous fat cell volume and insulin sensitivity after weight loss. *Diabetes Care*. 2014; **37**(7):1831-6.

Gao H, Mejhert N, Fretz JA, **Arner E**, Lorente-Cebrián S, Ehrlund A, Dahlman-Wright K, Gong X, Strömblad S, Douagi I, Laurencikiene J, Dahlman I, Daub CO, Rydén M, Horowitz MC, Arner P. Early B cell factor 1 regulates adipocyte morphology and lipolysis in white adipose tissue. *Cell Metab*. 2014; **19**(6):981-92.

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*. 2014; **63**(4):1248-58.

\***Arner E**, Mejhert N, Kulyté A, Balwiercz 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.

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.

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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.

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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. Letter in *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.