

# Erik A Arner

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/7767569/erik-a-arner-publications-by-year.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

77  
papers

10,520  
citations

33  
h-index

80  
g-index

80  
ext. papers

13,013  
ext. citations

12.9  
avg, IF

4.87  
L-index

#	Paper	IF	Citations
77	DeepCellState: An autoencoder-based framework for predicting cell type specific transcriptional states induced by drug treatment. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009465	5	2
76	Automatic identification of small molecules that promote cell conversion and reprogramming. <i>Stem Cell Reports</i> , <b>2021</b> , 16, 1381-1390	8	3
75	Development of p53 knockout U87MG cell line for unbiased drug delivery testing system using CRISPR-Cas9 and transcriptomic analysis. <i>Journal of Biotechnology</i> , <b>2021</b> , 332, 72-82	3.7	
74	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , <b>2021</b> , 12, 3297	17.4	3
73	ReFeaFi: Genome-wide prediction of regulatory elements driving transcription initiation. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009376	5	2
72	Analysis of Enhancer-Promoter Interactions using CAGE and RADICL-Seq Technologies. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2351, 201-210	1.4	2
71	The Transcriptional Network That Controls Growth Arrest and Macrophage Differentiation in the Human Myeloid Leukemia Cell Line THP-1. <i>Frontiers in Cell and Developmental Biology</i> , <b>2020</b> , 8, 498	5.7	10
70	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , <b>2020</b> , 30, 1060-1072	9.7	41
69	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , <b>2020</b> , 30, 951-961	9.7	12
68	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , <b>2019</b> , 20, 718	4.5	3
67	Detailed Functional Characterization of a Waist-Hip Ratio Locus in 7p15.2 Defines an Enhancer Controlling Adipocyte Differentiation. <i>IScience</i> , <b>2019</b> , 20, 42-59	6.1	2
66	MicroRNA-27a/b-3p and PPARG regulate SCAMP3 through a feed-forward loop during adipogenesis. <i>Scientific Reports</i> , <b>2019</b> , 9, 13891	4.9	12
65	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , <b>2019</b> , 10, 360	17.4	45
64	A framework for identification of on- and off-target transcriptional responses to drug treatment. <i>Scientific Reports</i> , <b>2019</b> , 9, 17603	4.9	13
63	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. <i>Cerebellum</i> , <b>2018</b> , 17, 308-325	4.3	1
62	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , <b>2018</b> , 8, 6758	4.9	41
61	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. <i>Open Biology</i> , <b>2018</b> , 8,	7	3

60	Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1 <i>Scientific Reports</i> , <b>2018</b> , 8, 13164	4.9	6
59	An atlas of human long non-coding RNAs with accurate 5aends. <i>Nature</i> , <b>2017</b> , 543, 199-204	50.4	581
58	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , <b>2017</b> , 24, 257-266	8.8	13
57	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , <b>2017</b> , 15, e2002887	9.7	22
56	Analysis of the human monocyte-derived macrophage transcriptome and response to lipopolysaccharide provides new insights into genetic aetiology of inflammatory bowel disease. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006641	6	64
55	Discriminative identification of transcriptional responses of promoters and enhancers after stimulus. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e25	20.1	2
54	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 872-878	44.5	282
53	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , <b>2017</b> , 4, 170112	8.2	88
52	Genome-scale regression analysis reveals a linear relationship for promoters and enhancers after combinatorial drug treatment. <i>Bioinformatics</i> , <b>2017</b> , 33, 3696-3700	7.2	6
51	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , <b>2017</b> , 66, 218-230	0.9	19
50	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 3233-52	20.1	21
49	DeepCAGE transcriptomics identify HOXD10 as a transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , <b>2016</b> , 129, 2573-85	5.3	11
48	Expression of FBN1 during adipogenesis: Relevance to the lipodystrophy phenotype in Marfan syndrome and related conditions. <i>Molecular Genetics and Metabolism</i> , <b>2016</b> , 119, 174-85	3.7	15
47	Datasets of genes coexpressed with FBN1 in mouse adipose tissue and during human adipogenesis. <i>Data in Brief</i> , <b>2016</b> , 8, 851-7	1.2	2
46	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , <b>2015</b> , 16, 22	18.3	443
45	Transplanted Bone Marrow-Derived Cells Contribute to Human Adipogenesis. <i>Cell Metabolism</i> , <b>2015</b> , 22, 408-17	24.6	61
44	Transcriptional dynamics reveal critical roles for non-coding RNAs in the immediate-early response. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004217	5	15
43	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 6969-82	20.1	38

42	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. <i>Scientific Reports</i> , <b>2015</b> , 5, 11999	4.9	24
41	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , <b>2015</b> , 13, 1493-1504	10.6	25
40	Remodeling of retrotransposon elements during epigenetic induction of adult visual cortical plasticity by HDAC inhibitors. <i>Epigenetics and Chromatin</i> , <b>2015</b> , 8, 55	5.8	27
39	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. <i>PLoS ONE</i> , <b>2015</b> , 10, e0144176	3.7	1
38	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , <b>2015</b> , 347, 1010-4	33.3	384
37	Adipose tissue morphology predicts improved insulin sensitivity following moderate or pronounced weight loss. <i>International Journal of Obesity</i> , <b>2015</b> , 39, 893-8	5.5	49
36	A promoter-level mammalian expression atlas. <i>Nature</i> , <b>2014</b> , 507, 462-70	50.4	1301
35	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , <b>2014</b> , 507, 455-461	50.4	1595
34	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , <b>2014</b> , 123, e79-89	2.2	59
33	High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. <i>Blood</i> , <b>2014</b> , 123, e46-57	2.2	19
32	Early B cell factor 1 regulates adipocyte morphology and lipolysis in white adipose tissue. <i>Cell Metabolism</i> , <b>2014</b> , 19, 981-92	24.6	72
31	Ceruloplasmin is a novel adipokine which is overexpressed in adipose tissue of obese subjects and in obesity-associated cancer cells. <i>PLoS ONE</i> , <b>2014</b> , 9, e80274	3.7	36
30	Additive effects of microRNAs and transcription factors on CCL2 production in human white adipose tissue. <i>Diabetes</i> , <b>2014</b> , 63, 1248-58	0.9	35
29	Changes in subcutaneous fat cell volume and insulin sensitivity after weight loss. <i>Diabetes Care</i> , <b>2014</b> , 37, 1831-6	14.6	70
28	Health and obesity: not just skin deep. <i>Science</i> , <b>2013</b> , 342, 558-9	33.3	7
27	Adipose tissue microRNAs as regulators of CCL2 production in human obesity. <i>Diabetes</i> , <b>2012</b> , 61, 1986-93	3.9	217
26	Dynamics of human adipose lipid turnover in health and metabolic disease. <i>Nature</i> , <b>2011</b> , 478, 110-3	50.4	259
25	Genetic predisposition for Type 2 diabetes, but not for overweight/obesity, is associated with a restricted adipogenesis. <i>PLoS ONE</i> , <b>2011</b> , 6, e18284	3.7	98

24	Optimization of turn-back primers in isothermal amplification. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, e59	20.1	54
23	The short non-coding transcriptome of the protozoan parasite <i>Trypanosoma cruzi</i> . <i>PLoS Neglected Tropical Diseases</i> , <b>2011</b> , 5, e1283	4.8	29
22	Tumor necrosis factor alpha and regulation of adipose tissue. <i>New England Journal of Medicine</i> , <b>2010</b> , 362, 1151-3	59.2	39
21	NGSView: an extensible open source editor for next-generation sequencing data. <i>Bioinformatics</i> , <b>2010</b> , 26, 125-6	7.2	8
20	Adipocyte turnover: relevance to human adipose tissue morphology. <i>Diabetes</i> , <b>2010</b> , 59, 105-9	0.9	414
19	Regional impact of adipose tissue morphology on the metabolic profile in morbid obesity. <i>Diabetologia</i> , <b>2010</b> , 53, 2496-503	10.3	159
18	The combination of gene perturbation assay and CHIP-chip reveals functional direct target genes for IRF8 in THP-1 cells. <i>Molecular Immunology</i> , <b>2010</b> , 47, 2295-302	4.3	25
17	Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns. <i>BMC Genomics</i> , <b>2010</b> , 11, 257	4.5	24
16	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , <b>2009</b> , 41, 553-62	36.3	356
15	Genome-wide investigation of in vivo EGR-1 binding sites in monocytic differentiation. <i>Genome Biology</i> , <b>2009</b> , 10, R41	18.3	55
14	Transcriptional features of genomic regulatory blocks. <i>Genome Biology</i> , <b>2009</b> , 10, R38	18.3	77
13	Dynamics of fat cell turnover in humans. <i>Nature</i> , <b>2008</b> , 453, 783-7	50.4	1612
12	Database of <i>Trypanosoma cruzi</i> repeated genes: 20,000 additional gene variants. <i>BMC Genomics</i> , <b>2007</b> , 8, 391	4.5	43
11	GRAT--genome-scale rapid alignment tool. <i>Computer Methods and Programs in Biomedicine</i> , <b>2007</b> , 86, 87-92	6.9	1
10	DNPtrapper: an assembly editing tool for finishing and analysis of complex repeat regions. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 155	3.6	12
9	The genome sequence of <i>Trypanosoma cruzi</i> , etiologic agent of Chagas disease. <i>Science</i> , <b>2005</b> , 309, 409-15	35.3	1085
8	Adipocyte lipases and defect of lipolysis in human obesity. <i>Diabetes</i> , <b>2005</b> , 54, 3190-7	0.9	293
7	ReDiT: Repeat Discrepancy Tagger--a shotgun assembly finishing aid. <i>Bioinformatics</i> , <b>2004</b> , 20, 803-4	7.2	4

6	TRAP: Tandem Repeat Assembly Program produces improved shotgun assemblies of repetitive sequences. <i>Computer Methods and Programs in Biomedicine</i> , <b>2003</b> , 70, 47-59	6.9	9
5	Correcting errors in shotgun sequences. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 4663-72	20.1	31
4	Separation of nearly identical repeats in shotgun assemblies using defined nucleotide positions, DNPs. <i>Bioinformatics</i> , <b>2002</b> , 18, 379-88	7.2	20
3	Automatic identification of small molecules that promote cell conversion and reprogramming		1
2	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution		1
1	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6