

Erik A Arner

List of Publications by Citations

Source: <https://exaly.com/author-pdf/7767569/erik-a-arner-publications-by-citations.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	Dynamics of fat cell turnover in humans. <i>Nature</i> , 2008 , 453, 783-7	50.4	1612
76	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014 , 507, 455-461	50.4	1595
75	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
74	The genome sequence of <i>Trypanosoma cruzi</i> , etiologic agent of Chagas disease. <i>Science</i> , 2005 , 309, 409-413	35.3	1085
73	An atlas of human long non-coding RNAs with accurate 5aends. <i>Nature</i> , 2017 , 543, 199-204	50.4	581
72	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015 , 16, 22	18.3	443
71	Adipocyte turnover: relevance to human adipose tissue morphology. <i>Diabetes</i> , 2010 , 59, 105-9	0.9	414
70	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015 , 347, 1010-4	33.3	384
69	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009 , 41, 553-62	36.3	356
68	Adipocyte lipases and defect of lipolysis in human obesity. <i>Diabetes</i> , 2005 , 54, 3190-7	0.9	293
67	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017 , 35, 872-878	44.5	282
66	Dynamics of human adipose lipid turnover in health and metabolic disease. <i>Nature</i> , 2011 , 478, 110-3	50.4	259
65	Adipose tissue microRNAs as regulators of CCL2 production in human obesity. <i>Diabetes</i> , 2012 , 61, 1986-939	3.9	217
64	Regional impact of adipose tissue morphology on the metabolic profile in morbid obesity. <i>Diabetologia</i> , 2010 , 53, 2496-503	10.3	159
63	Genetic predisposition for Type 2 diabetes, but not for overweight/obesity, is associated with a restricted adipogenesis. <i>PLoS ONE</i> , 2011 , 6, e18284	3.7	98
62	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017 , 4, 170112	8.2	88
61	Transcriptional features of genomic regulatory blocks. <i>Genome Biology</i> , 2009 , 10, R38	18.3	77

60	Early B cell factor 1 regulates adipocyte morphology and lipolysis in white adipose tissue. <i>Cell Metabolism</i> , 2014 , 19, 981-92	24.6	72
59	Changes in subcutaneous fat cell volume and insulin sensitivity after weight loss. <i>Diabetes Care</i> , 2014 , 37, 1831-6	14.6	70
58	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> , 2017 , 13, e1006641	6	64
57	Transplanted Bone Marrow-Derived Cells Contribute to Human Adipogenesis. <i>Cell Metabolism</i> , 2015 , 22, 408-17	24.6	61
56	Analysis of the DNA methylome and transcriptome in granulopoiesis reveals timed changes and dynamic enhancer methylation. <i>Blood</i> , 2014 , 123, e79-89	2.2	59
55	Genome-wide investigation of in vivo EGR-1 binding sites in monocytic differentiation. <i>Genome Biology</i> , 2009 , 10, R41	18.3	55
54	Optimization of turn-back primers in isothermal amplification. <i>Nucleic Acids Research</i> , 2011 , 39, e59	20.1	54
53	Adipose tissue morphology predicts improved insulin sensitivity following moderate or pronounced weight loss. <i>International Journal of Obesity</i> , 2015 , 39, 893-8	5.5	49
52	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019 , 10, 360	17.4	45
51	Database of Trypanosoma cruzi repeated genes: 20,000 additional gene variants. <i>BMC Genomics</i> , 2007 , 8, 391	4.5	43
50	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , 2018 , 8, 6758	4.9	41
49	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020 , 30, 1060-1072	9.7	41
48	Tumor necrosis factor alpha and regulation of adipose tissue. <i>New England Journal of Medicine</i> , 2010 , 362, 1151-3	59.2	39
47	Redefining the transcriptional regulatory dynamics of classically and alternatively activated macrophages by deepCAGE transcriptomics. <i>Nucleic Acids Research</i> , 2015 , 43, 6969-82	20.1	38
46	Ceruloplasmin is a novel adipokine which is overexpressed in adipose tissue of obese subjects and in obesity-associated cancer cells. <i>PLoS ONE</i> , 2014 , 9, e80274	3.7	36
45	Additive effects of microRNAs and transcription factors on CCL2 production in human white adipose tissue. <i>Diabetes</i> , 2014 , 63, 1248-58	0.9	35
44	Correcting errors in shotgun sequences. <i>Nucleic Acids Research</i> , 2003 , 31, 4663-72	20.1	31
43	The short non-coding transcriptome of the protozoan parasite Trypanosoma cruzi. <i>PLoS Neglected Tropical Diseases</i> , 2011 , 5, e1283	4.8	29

42	Remodeling of retrotransposon elements during epigenetic induction of adult visual cortical plasticity by HDAC inhibitors. <i>Epigenetics and Chromatin</i> , 2015 , 8, 55	5.8	27
41	DeepCAGE Transcriptomics Reveal an Important Role of the Transcription Factor MAFB in the Lymphatic Endothelium. <i>Cell Reports</i> , 2015 , 13, 1493-1504	10.6	25
40	The combination of gene perturbation assay and ChIP-chip reveals functional direct target genes for IRF8 in THP-1 cells. <i>Molecular Immunology</i> , 2010 , 47, 2295-302	4.3	25
39	Promoter-level expression clustering identifies time development of transcriptional regulatory cascades initiated by ErbB receptors in breast cancer cells. <i>Scientific Reports</i> , 2015 , 5, 11999	4.9	24
38	Core promoter structure and genomic context reflect histone 3 lysine 9 acetylation patterns. <i>BMC Genomics</i> , 2010 , 11, 257	4.5	24
37	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , 2017 , 15, e2002887	9.7	22
36	Functional annotation of the vlinc class of non-coding RNAs using systems biology approach. <i>Nucleic Acids Research</i> , 2016 , 44, 3233-52	20.1	21
35	Separation of nearly identical repeats in shotgun assemblies using defined nucleotide positions, DNPs. <i>Bioinformatics</i> , 2002 , 18, 379-88	7.2	20
34	High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. <i>Blood</i> , 2014 , 123, e46-57	2.2	19
33	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017 , 66, 218-230	0.9	19
32	Transcriptional dynamics reveal critical roles for non-coding RNAs in the immediate-early response. <i>PLoS Computational Biology</i> , 2015 , 11, e1004217	5	15
31	Expression of FBN1 during adipogenesis: Relevance to the lipodystrophy phenotype in Marfan syndrome and related conditions. <i>Molecular Genetics and Metabolism</i> , 2016 , 119, 174-85	3.7	15
30	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017 , 24, 257-266	8.8	13
29	A framework for identification of on- and off-target transcriptional responses to drug treatment. <i>Scientific Reports</i> , 2019 , 9, 17603	4.9	13
28	MicroRNA-27a/b-3p and PPARG regulate SCAMP3 through a feed-forward loop during adipogenesis. <i>Scientific Reports</i> , 2019 , 9, 13891	4.9	12
27	DNPtrapper: an assembly editing tool for finishing and analysis of complex repeat regions. <i>BMC Bioinformatics</i> , 2006 , 7, 155	3.6	12
26	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020 , 30, 951-961	9.7	12
25	DeepCAGE transcriptomics identify HOXD10 as a transcription factor regulating lymphatic endothelial responses to VEGF-C. <i>Journal of Cell Science</i> , 2016 , 129, 2573-85	5.3	11

24	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> , 2020 , 8, 498	5.7	10
23	TRAP: Tandem Repeat Assembly Program produces improved shotgun assemblies of repetitive sequences. <i>Computer Methods and Programs in Biomedicine</i> , 2003 , 70, 47-59	6.9	9
22	NGSView: an extensible open source editor for next-generation sequencing data. <i>Bioinformatics</i> , 2010 , 26, 125-6	7.2	8
21	Health and obesity: not just skin deep. <i>Science</i> , 2013 , 342, 558-9	33.3	7
20	Genome-scale regression analysis reveals a linear relationship for promoters and enhancers after combinatorial drug treatment. <i>Bioinformatics</i> , 2017 , 33, 3696-3700	7.2	6
19	Functional Annotation of Human Long Non-Coding RNAs via Molecular Phenotyping		6
18	Promoter Usage and Dynamics in Vascular Smooth Muscle Cells Exposed to Fibroblast Growth Factor-2 or Interleukin-1. <i>Scientific Reports</i> , 2018 , 8, 13164	4.9	6
17	ReDiT: Repeat Discrepancy Tagger—a shotgun assembly finishing aid. <i>Bioinformatics</i> , 2004 , 20, 803-4	7.2	4
16	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , 2019 , 20, 718	4.5	3
15	Automatic identification of small molecules that promote cell conversion and reprogramming. <i>Stem Cell Reports</i> , 2021 , 16, 1381-1390	8	3
14	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021 , 12, 3297	17.4	3
13	Conserved temporal ordering of promoter activation implicates common mechanisms governing the immediate early response across cell types and stimuli. <i>Open Biology</i> , 2018 , 8,	7	3
12	Detailed Functional Characterization of a Waist-Hip Ratio Locus in 7p15.2 Defines an Enhancer Controlling Adipocyte Differentiation. <i>iScience</i> , 2019 , 20, 42-59	6.1	2
11	Discriminative identification of transcriptional responses of promoters and enhancers after stimulus. <i>Nucleic Acids Research</i> , 2017 , 45, e25	20.1	2
10	DeepCellState: An autoencoder-based framework for predicting cell type specific transcriptional states induced by drug treatment. <i>PLoS Computational Biology</i> , 2021 , 17, e1009465	5	2
9	Datasets of genes coexpressed with FBN1 in mouse adipose tissue and during human adipogenesis. <i>Data in Brief</i> , 2016 , 8, 851-7	1.2	2
8	ReFeaFi: Genome-wide prediction of regulatory elements driving transcription initiation. <i>PLoS Computational Biology</i> , 2021 , 17, e1009376	5	2
7	Analysis of Enhancer-Promoter Interactions using CAGE and RADICL-Seq Technologies. <i>Methods in Molecular Biology</i> , 2021 , 2351, 201-210	1.4	2

6	Discovery of Transcription Factors Novel to Mouse Cerebellar Granule Cell Development Through Laser-Capture Microdissection. <i>Cerebellum</i> , 2018 , 17, 308-325	4.3	1
5	Application of Gene Expression Trajectories Initiated from ErbB Receptor Activation Highlights the Dynamics of Divergent Promoter Usage. <i>PLoS ONE</i> , 2015 , 10, e0144176	3.7	1
4	GRAT--genome-scale rapid alignment tool. <i>Computer Methods and Programs in Biomedicine</i> , 2007 , 86, 87-92	6.9	1
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	Development of p53 knockout U87MG cell line for unbiased drug delivery testing system using CRISPR-Cas9 and transcriptomic analysis. <i>Journal of Biotechnology</i> , 2021 , 332, 72-82	3.7	