

Timo Lassmann

List of Publications by Citations

Source: <https://exaly.com/author-pdf/2460674/timo-lassmann-publications-by-citations.pdf>

Version: 2024-04-23

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.

112
papers

33,301
citations

47
h-index

119
g-index

119
ext. papers

40,637
ext. citations

13.1
avg. IF

8.22
L-index

#	Paper	IF	Citations
112	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
111	Landscape of transcription in human cells. <i>Nature</i> , 2012 , 489, 101-8	50.4	3544
110	The GENCODE v7 catalog of human long noncoding RNAs: analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012 , 22, 1775-89	9.7	3408
109	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006 , 34, D247-51	20.1	1784
108	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014 , 507, 455-461	50.4	1595
107	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
106	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
105	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009 , 41, 563-71	36.3	601
104	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017 , 543, 199-204	50.4	581
103	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , 2010 , 140, 744-52	56.2	555
102	Myogenic gene expression signature establishes that brown and white adipocytes originate from distinct cell lineages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 4401-6	11.5	550
101	Kalign--an accurate and fast multiple sequence alignment algorithm. <i>BMC Bioinformatics</i> , 2005 , 6, 298	3.6	476
100	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015 , 16, 22	18.3	443
99	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015 , 347, 1010-4	33.3	384
98	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
97	Small RNAs derived from snoRNAs. <i>Rna</i> , 2009 , 15, 1233-40	5.8	325
96	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009 , 41, 572-8	36.3	302

95	An RNA-dependent RNA polymerase formed by TERT and the RMRP RNA. <i>Nature</i> , 2009 , 461, 230-5	50.4	287
94	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017 , 35, 872-878	44.5	282
93	Kalign2: high-performance multiple alignment of protein and nucleotide sequences allowing external features. <i>Nucleic Acids Research</i> , 2009 , 37, 858-65	20.1	214
92	Induction of microRNAs, mir-155, mir-222, mir-424 and mir-503, promotes monocytic differentiation through combinatorial regulation. <i>Leukemia</i> , 2010 , 24, 460-6	10.7	205
91	5Uend-centered expression profiling using cap-analysis gene expression and next-generation sequencing. <i>Nature Protocols</i> , 2012 , 7, 542-61	18.8	182
90	Genome-wide analysis of promoter architecture in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2011 , 21, 182-92	9.7	178
89	TagDust--a program to eliminate artifacts from next generation sequencing data. <i>Bioinformatics</i> , 2009 , 25, 2839-40	7.2	173
88	Effects of cytosine methylation on transcription factor binding sites. <i>BMC Genomics</i> , 2014 , 15, 119	4.5	156
87	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011 , 21, 1150-9	9.7	143
86	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012 , 22, 1658-67	9.7	133
85	SAMStat: monitoring biases in next generation sequencing data. <i>Bioinformatics</i> , 2011 , 27, 130-1	7.2	130
84	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014 , 123, e58-67	2.2	126
83	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010 , 7, 528-34	21.6	123
82	Systematic assessment of tissue dissociation and storage biases in single-cell and single-nucleus RNA-seq workflows. <i>Genome Biology</i> , 2020 , 21, 130	18.3	117
81	Cross-mapping and the identification of editing sites in mature microRNAs in high-throughput sequencing libraries. <i>Genome Research</i> , 2010 , 20, 257-64	9.7	105
80	The human PINK1 locus is regulated in vivo by a non-coding natural antisense RNA during modulation of mitochondrial function. <i>BMC Genomics</i> , 2007 , 8, 74	4.5	104
79	Automatic assessment of alignment quality. <i>Nucleic Acids Research</i> , 2005 , 33, 7120-8	20.1	102
78	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014 , 123, e90-9	2.2	101

77	Quality assessment of multiple alignment programs. <i>FEBS Letters</i> , 2002 , 529, 126-30	3.8	95
76	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017 , 4, 170112	8.2	88
75	Differential roles of epigenetic changes and Foxp3 expression in regulatory T cell-specific transcriptional regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5289-94	11.5	85
74	Sensitization to immune checkpoint blockade through activation of a STAT1/NK axis in the tumor microenvironment. <i>Science Translational Medicine</i> , 2019 , 11,	17.5	83
73	Kalign, Kalignvu and Mumsa: web servers for multiple sequence alignment. <i>Nucleic Acids Research</i> , 2006 , 34, W596-9	20.1	79
72	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
71	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
70	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014 , 123, e68-78	2.2	58
69	Transcriptome Analysis of Recurrently Deregulated Genes across Multiple Cancers Identifies New Pan-Cancer Biomarkers. <i>Cancer Research</i> , 2016 , 76, 216-26	10.1	56
68	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009 , 10, R39	18.3	56
67	A Diagnosis for All Rare Genetic Diseases: The Horizon and the Next Frontiers. <i>Cell</i> , 2019 , 177, 32-37	56.2	53
66	MOIRAI: a compact workflow system for CAGE analysis. <i>BMC Bioinformatics</i> , 2014 , 15, 144	3.6	49
65	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019 , 10, 360	17.4	45
64	TagDust2: a generic method to extract reads from sequencing data. <i>BMC Bioinformatics</i> , 2015 , 16, 24	3.6	44
63	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , 2018 , 8, 6758	4.9	41
62	Digital expression profiling of the compartmentalized transcriptome of Purkinje neurons. <i>Genome Research</i> , 2014 , 24, 1396-410	9.7	39
61	The rare and undiagnosed diseases diagnostic service - application of massively parallel sequencing in a state-wide clinical service. <i>Orphanet Journal of Rare Diseases</i> , 2016 , 11, 77	4.2	39
60	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

59	RECLU: a pipeline to discover reproducible transcriptional start sites and their alternative regulation using capped analysis of gene expression (CAGE). <i>BMC Genomics</i> , 2014 , 15, 269	4.5	37
58	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
57	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , 2015 , 25, 1546-57	9.7	33
56	Integration of genetics and miRNA-target gene network identified disease biology implicated in tissue specificity. <i>Nucleic Acids Research</i> , 2018 , 46, 11898-11909	20.1	26
55	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
54	A phenotype centric benchmark of variant prioritisation tools. <i>Npj Genomic Medicine</i> , 2018 , 3, 5	6.2	24
53	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
52	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , 2017 , 15, e2002887	9.7	22
51	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
50	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , 2017 , 15, 1354-1365	6.6	20
49	High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. <i>Blood</i> , 2014 , 123, e46-57	2.2	19
48	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017 , 66, 218-230	0.9	19
47	Reference genotype and exome data from an Australian Aboriginal population for health-based research. <i>Scientific Data</i> , 2016 , 3, 160023	8.2	18
46	Automated workflow for preparation of cDNA for cap analysis of gene expression on a single molecule sequencer. <i>PLoS ONE</i> , 2012 , 7, e30809	3.7	18
45	Technical Advance: Transcription factor, promoter, and enhancer utilization in human myeloid cells. <i>Journal of Leukocyte Biology</i> , 2015 , 97, 985-995	6.5	17
44	Kalign 3: multiple sequence alignment of large data sets. <i>Bioinformatics</i> , 2019 ,	7.2	17
43	YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. <i>Scientific Reports</i> , 2016 , 6, 37324	4.9	16
42	Telomerase reverse transcriptase regulates microRNAs. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 1192-208	6.3	15

41	Transcriptional dynamics reveal critical roles for non-coding RNAs in the immediate-early response. <i>PLoS Computational Biology</i> , 2015 , 11, e1004217	5	15
40	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , 2019 , 56, 5392-5415	6.2	15
39	Specific mesothelial signature marks the heterogeneity of mesenchymal stem cells from high-grade serous ovarian cancer. <i>Stem Cells</i> , 2014 , 32, 2998-3011	5.8	14
38	Transcriptome analysis of periodontitis-associated fibroblasts by CAGE sequencing identified DLX5 and RUNX2 long variant as novel regulators involved in periodontitis. <i>Scientific Reports</i> , 2016 , 6, 33666	4.9	14
37	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017 , 24, 257-266	8.8	13
36	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020 , 30, 951-961	9.7	12
35	On-the-fly selection of cell-specific enhancers, genes, miRNAs and proteins across the human body using SlideBase. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	12
34	CAGEd-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. <i>Bioinformatics</i> , 2016 , 32, 2858-60	7.2	11
33	Mapping Mammalian Cell-type-specific Transcriptional Regulatory Networks Using KD-CAGE and CHIP-seq Data in the TC-YIK Cell Line. <i>Frontiers in Genetics</i> , 2015 , 6, 331	4.5	11
32	Off-target effect of endogenous siRNA derived from RMRP in human cells. <i>International Journal of Molecular Sciences</i> , 2013 , 14, 9305-18	6.3	11
31	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. <i>Nucleic Acids Research</i> , 2010 , 38, 8141-8	20.1	11
30	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
29	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , 2017 , 4, 170147	8.2	10
28	Systematic assessment of tissue dissociation and storage biases in single-cell and single-nucleus RNA-seq workflows		9
27	Personalised analytics for rare disease diagnostics. <i>Nature Communications</i> , 2019 , 10, 5274	17.4	9
26	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , 2018 , 14, e1005934	5	8
25	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. <i>BMC Genomics</i> , 2014 , 15, 1177	4.5	7
24	Bilateral murine tumor models for characterizing the response to immune checkpoint blockade. <i>Nature Protocols</i> , 2020 , 15, 1628-1648	18.8	6

23	Rhinovirus Infection Drives Complex Host Airway Molecular Responses in Children With Cystic Fibrosis. <i>Frontiers in Immunology</i> , 2020 , 11, 1327	8.4	6
22	Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , 2017 , 4, 170173	8.2	4
21	Automatic extraction of reliable regions from multiple sequence alignments. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 5, S9	3.6	4
20	Single-cell transcriptomes of fluorescent, ubiquitination-based cell cycle indicator cells		4
19	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , 2019 , 20, 718	4.5	3
18	Arylsulphatase A Pseudodeficiency (ARSA-PD), hypertension and chronic renal disease in Aboriginal Australians. <i>Scientific Reports</i> , 2018 , 8, 10912	4.9	3
17	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010 , 141, 369	56.2	3
16	Expression Levels of Therapeutic Targets as Indicators of Sensitivity to Targeted Therapeutics. <i>Molecular Cancer Therapeutics</i> , 2019 , 18, 2480-2489	6.1	3
15	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
14	Functional genomics in cancer immunotherapy: computational approaches for biomarker and drug discovery. <i>Molecular Systems Design and Engineering</i> , 2019 , 4, 689-700	4.6	2
13	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. <i>Scientific Data</i> , 2017 , 4, 170163	8.2	2
12	CRISPR single base editing, neuronal disease modelling and functional genomics for genetic variant analysis: pipeline validation using Kleefstra syndrome EHMT1 haploinsufficiency.. <i>Stem Cell Research and Therapy</i> , 2022 , 13, 69	8.3	2
11	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease		2
10	Zika Virus Changes Methylation of Genes Involved in Immune Response and Neural Development in Brazilian Babies Born With Congenital Microcephaly. <i>Journal of Infectious Diseases</i> , 2021 , 223, 435-440	7	2
9	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
8	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
7	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution		1
6	A flexible computational pipeline for research analyses of unsolved clinical exome cases. <i>Npj Genomic Medicine</i> , 2020 , 5, 54	6.2	1

5	Elucidating the Interaction of CF Airway Epithelial Cells and Rhinovirus: Using the Host-Pathogen Relationship to Identify Future Therapeutic Strategies. <i>Frontiers in Pharmacology</i> , 2018 , 9, 1270	5.6	1
4	Common and Rare Genetic Variants That Could Contribute to Severe Otitis Media in an Australian Aboriginal Population. <i>Clinical Infectious Diseases</i> , 2021 , 73, 1860-1870	11.6	0
3	Functional validation of variants of unknown significance using CRISPR gene editing and transcriptomics: A Kleeftstra syndrome case study.. <i>Gene</i> , 2022 , 821, 146287	3.8	0
2	Reference exome data for Australian Aboriginal populations to support health-based research. <i>Scientific Data</i> , 2020 , 7, 129	8.2	
1	Reference exome data for a Northern Brazilian population. <i>Scientific Data</i> , 2020 , 7, 360	8.2	