

Timo Lassmann

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/2460674/timo-lassmann-publications-by-year.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	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
111	Functional validation of variants of unknown significance using CRISPR gene editing and transcriptomics: A Kleefstra syndrome case study.. <i>Gene</i> , 2022 , 821, 146287	3.8	0
110	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
109	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
108	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
107	Bilateral murine tumor models for characterizing the response to immune checkpoint blockade. <i>Nature Protocols</i> , 2020 , 15, 1628-1648	18.8	6
106	Rhinovirus Infection Drives Complex Host Airway Molecular Responses in Children With Cystic Fibrosis. <i>Frontiers in Immunology</i> , 2020 , 11, 1327	8.4	6
105	Reference exome data for Australian Aboriginal populations to support health-based research. <i>Scientific Data</i> , 2020 , 7, 129	8.2	
104	Comparative transcriptomics of primary cells in vertebrates. <i>Genome Research</i> , 2020 , 30, 951-961	9.7	12
103	Reference exome data for a Northern Brazilian population. <i>Scientific Data</i> , 2020 , 7, 360	8.2	
102	A flexible computational pipeline for research analyses of unsolved clinical exome cases. <i>Npj Genomic Medicine</i> , 2020 , 5, 54	6.2	1
101	Identification of novel cerebellar developmental transcriptional regulators with motif activity analysis. <i>BMC Genomics</i> , 2019 , 20, 718	4.5	3
100	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019 , 10, 360	17.4	45
99	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
98	A Diagnosis for All Rare Genetic Diseases: The Horizon and the Next Frontiers. <i>Cell</i> , 2019 , 177, 32-37	56.2	53
97	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
96	Kalign 3: multiple sequence alignment of large data sets. <i>Bioinformatics</i> , 2019 ,	7.2	17

95	Expression Levels of Therapeutic Targets as Indicators of Sensitivity to Targeted Therapeutics. <i>Molecular Cancer Therapeutics</i> , 2019 , 18, 2480-2489	6.1	3
94	Personalised analytics for rare disease diagnostics. <i>Nature Communications</i> , 2019 , 10, 5274	17.4	9
93	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , 2019 , 56, 5392-5415	6.2	15
92	A phenotype centric benchmark of variant prioritisation tools. <i>Npj Genomic Medicine</i> , 2018 , 3, 5	6.2	24
91	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
90	Transcriptional landscape of Mycobacterium tuberculosis infection in macrophages. <i>Scientific Reports</i> , 2018 , 8, 6758	4.9	41
89	Arylsulphatase A Pseudodeficiency (ARSA-PD), hypertension and chronic renal disease in Aboriginal Australians. <i>Scientific Reports</i> , 2018 , 8, 10912	4.9	3
88	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
87	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
86	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
85	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
84	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017 , 543, 199-204	50.4	581
83	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , 2017 , 4, 170147	8.2	10
82	Transcriptome Analysis Uncovers a Growth-Promoting Activity of Orosomucoid-1 on Hepatocytes. <i>EBioMedicine</i> , 2017 , 24, 257-266	8.8	13
81	Systematic analysis of transcription start sites in avian development. <i>PLoS Biology</i> , 2017 , 15, e2002887	9.7	22
80	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
79	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017 , 35, 872-878	44.5	282
78	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017 , 4, 170112	8.2	88

77	Monitoring transcription initiation activities in rat and dog. <i>Scientific Data</i> , 2017 , 4, 170173	8.2	4
76	Integrative CAGE and DNA Methylation Profiling Identify Epigenetically Regulated Genes in NSCLC. <i>Molecular Cancer Research</i> , 2017 , 15, 1354-1365	6.6	20
75	Transcriptional Dynamics During Human Adipogenesis and Its Link to Adipose Morphology and Distribution. <i>Diabetes</i> , 2017 , 66, 218-230	0.9	19
74	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
73	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
72	Reference genotype and exome data from an Australian Aboriginal population for health-based research. <i>Scientific Data</i> , 2016 , 3, 160023	8.2	18
71	CAGEd-oPOSSUM: motif enrichment analysis from CAGE-derived TSSs. <i>Bioinformatics</i> , 2016 , 32, 2858-60	7.2	11
70	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
69	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
68	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
67	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
66	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
65	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
64	Gateways to the FANTOM5 promoter level mammalian expression atlas. <i>Genome Biology</i> , 2015 , 16, 22	18.3	443
63	The frequent evolutionary birth and death of functional promoters in mouse and human. <i>Genome Research</i> , 2015 , 25, 1546-57	9.7	33
62	Telomerase reverse transcriptase regulates microRNAs. <i>International Journal of Molecular Sciences</i> , 2015 , 16, 1192-208	6.3	15
61	Transcriptional dynamics reveal critical roles for non-coding RNAs in the immediate-early response. <i>PLoS Computational Biology</i> , 2015 , 11, e1004217	5	15
60	TagDust2: a generic method to extract reads from sequencing data. <i>BMC Bioinformatics</i> , 2015 , 16, 24	3.6	44

59	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
58	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
57	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
56	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
55	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
54	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
53	Transcribed enhancers lead waves of coordinated transcription in transitioning mammalian cells. <i>Science</i> , 2015 , 347, 1010-4	33.3	384
52	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
51	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014 , 507, 455-461	50.4	1595
50	The enhancer and promoter landscape of human regulatory and conventional T-cell subpopulations. <i>Blood</i> , 2014 , 123, e68-78	2.2	58
49	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
48	Transcription and enhancer profiling in human monocyte subsets. <i>Blood</i> , 2014 , 123, e90-9	2.2	101
47	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
46	MOIRAI: a compact workflow system for CAGE analysis. <i>BMC Bioinformatics</i> , 2014 , 15, 144	3.6	49
45	Effects of cytosine methylation on transcription factor binding sites. <i>BMC Genomics</i> , 2014 , 15, 119	4.5	156
44	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
43	High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. <i>Blood</i> , 2014 , 123, e46-57	2.2	19
42	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. <i>BMC Genomics</i> , 2014 , 15, 1177	4.5	7

41	Redefinition of the human mast cell transcriptome by deep-CAGE sequencing. <i>Blood</i> , 2014 , 123, e58-67	2.2	126
40	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
39	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
38	Digital expression profiling of the compartmentalized transcriptome of Purkinje neurons. <i>Genome Research</i> , 2014 , 24, 1396-410	9.7	39
37	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
36	5Uend-centered expression profiling using cap-analysis gene expression and next-generation sequencing. <i>Nature Protocols</i> , 2012 , 7, 542-61	18.8	182
35	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
34	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
33	Understanding transcriptional regulation by integrative analysis of transcription factor binding data. <i>Genome Research</i> , 2012 , 22, 1658-67	9.7	133
32	Landscape of transcription in human cells. <i>Nature</i> , 2012 , 489, 101-8	50.4	3544
31	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
30	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
29	Unamplified cap analysis of gene expression on a single-molecule sequencer. <i>Genome Research</i> , 2011 , 21, 1150-9	9.7	143
28	SAMStat: monitoring biases in next generation sequencing data. <i>Bioinformatics</i> , 2011 , 27, 130-1	7.2	130
27	Genome-wide analysis of promoter architecture in <i>Drosophila melanogaster</i> . <i>Genome Research</i> , 2011 , 21, 182-92	9.7	178
26	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
25	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010 , 7, 528-34	21.6	123
24	Building promoter aware transcriptional regulatory networks using siRNA perturbation and deepCAGE. <i>Nucleic Acids Research</i> , 2010 , 38, 8141-8	20.1	11

23	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
22	An atlas of combinatorial transcriptional regulation in mouse and man. <i>Cell</i> , 2010 , 140, 744-52	56.2	555
21	An Atlas of Combinatorial Transcriptional Regulation in Mouse and Man. <i>Cell</i> , 2010 , 141, 369	56.2	3
20	TagDust--a program to eliminate artifacts from next generation sequencing data. <i>Bioinformatics</i> , 2009 , 25, 2839-40	7.2	173
19	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
18	An RNA-dependent RNA polymerase formed by TERT and the RMRP RNA. <i>Nature</i> , 2009 , 461, 230-5	50.4	287
17	Tiny RNAs associated with transcription start sites in animals. <i>Nature Genetics</i> , 2009 , 41, 572-8	36.3	302
16	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009 , 41, 563-71	36.3	601
15	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
14	Small RNAs derived from snoRNAs. <i>Rna</i> , 2009 , 15, 1233-40	5.8	325
13	FANTOM4 EdgeExpressDB: an integrated database of promoters, genes, microRNAs, expression dynamics and regulatory interactions. <i>Genome Biology</i> , 2009 , 10, R39	18.3	56
12	Automatic extraction of reliable regions from multiple sequence alignments. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 5, S9	3.6	4
11	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
10	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
9	Kalign, Kalignvu and Mumsa: web servers for multiple sequence alignment. <i>Nucleic Acids Research</i> , 2006 , 34, W596-9	20.1	79
8	Pfam: clans, web tools and services. <i>Nucleic Acids Research</i> , 2006 , 34, D247-51	20.1	1784
7	Automatic assessment of alignment quality. <i>Nucleic Acids Research</i> , 2005 , 33, 7120-8	20.1	102
6	Kalign--an accurate and fast multiple sequence alignment algorithm. <i>BMC Bioinformatics</i> , 2005 , 6, 298	3.6	476

5	Quality assessment of multiple alignment programs. <i>FEBS Letters</i> , 2002 , 529, 126-30	3.8	95
4	Single-cell transcriptomes of fluorescent, ubiquitination-based cell cycle indicator cells		4
3	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease		2
2	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution		1
1	Systematic assessment of tissue dissociation and storage biases in single-cell and single-nucleus RNA-seq workflows		9