

Tarjei S Mikkelsen

List of Publications by Citations

Source: <https://exaly.com/author-pdf/6287577/tarjei-s-mikkelsen-publications-by-citations.pdf>

Version: 2024-04-26

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.

88

papers

70,703

citations

59

h-index

90

g-index

90

ext. papers

83,986

ext. citations

25.5

avg, IF

8.43

L-index

#	Paper	IF	Citations
88	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366
87	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
86	A bivalent chromatin structure marks key developmental genes in embryonic stem cells. <i>Cell</i> , 2006 , 125, 315-26	56.2	4097
85	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. <i>Nature</i> , 2007 , 448, 553-60	50.4	3296
84	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , 2009 , 458, 223-7	50.4	3230
83	Genome-scale CRISPR-Cas9 knockout screening in human cells. <i>Science</i> , 2014 , 343, 84-87	33.3	3080
82	The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells. <i>Nature Biotechnology</i> , 2014 , 32, 381-386	44.5	2466
81	Massively parallel digital transcriptional profiling of single cells. <i>Nature Communications</i> , 2017 , 8, 14049	17.4	2276
80	Mapping and analysis of chromatin state dynamics in nine human cell types. <i>Nature</i> , 2011 , 473, 43-9	50.4	2153
79	Genome-scale DNA methylation maps of pluripotent and differentiated cells. <i>Nature</i> , 2008 , 454, 766-70	50.4	1999
78	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005 , 437, 69-87	50.4	1828
77	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005 , 438, 803-19	50.4	1809
76	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004 , 306, 636-40	33.3	1692
75	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010 , 28, 1045-8	44.5	1284
74	Dissecting direct reprogramming through integrative genomic analysis. <i>Nature</i> , 2008 , 454, 49-55	50.4	1205
73	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
72	Positive natural selection in the human lineage. <i>Science</i> , 2006 , 312, 1614-20	33.3	833

71	Genomewide analysis of PRC1 and PRC2 occupancy identifies two classes of bivalent domains. <i>PLoS Genetics</i> , 2008 , 4, e1000242	6	746
70	A unique regulatory phase of DNA methylation in the early mammalian embryo. <i>Nature</i> , 2012 , 484, 339-44	56.4	723
69	Perturbation of m6A writers reveals two distinct classes of mRNA methylation at internal and 5T sites. <i>Cell Reports</i> , 2014 , 8, 284-96	10.6	700
68	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007 , 447, 167-77	50.4	577
67	Systematic dissection and optimization of inducible enhancers in human cells using a massively parallel reporter assay. <i>Nature Biotechnology</i> , 2012 , 30, 271-7	44.5	431
66	High-resolution mapping reveals a conserved, widespread, dynamic mRNA methylation program in yeast meiosis. <i>Cell</i> , 2013 , 155, 1409-21	56.2	415
65	Comparative epigenomic analysis of murine and human adipogenesis. <i>Cell</i> , 2010 , 143, 156-69	56.2	402
64	Cellular source and mechanisms of high transcriptome complexity in the mammalian testis. <i>Cell Reports</i> , 2013 , 3, 2179-90	10.6	334
63	Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. <i>Nature Methods</i> , 2010 , 7, 133-6	21.6	258
62	A second fatty acid amide hydrolase with variable distribution among placental mammals. <i>Journal of Biological Chemistry</i> , 2006 , 281, 36569-78	5.4	257
61	Systematic discovery of regulatory motifs in conserved regions of the human genome, including thousands of CTCF insulator sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 7145-50	11.5	242
60	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , 2016 , 165, 1519-1529	56.2	228
59	Non-equivalence of Wnt and R-spondin ligands during Lgr5 intestinal stem-cell self-renewal. <i>Nature</i> , 2017 , 545, 238-242	50.4	209
58	Systematic Functional Dissection of Common Genetic Variation Affecting Red Blood Cell Traits. <i>Cell</i> , 2016 , 165, 1530-1545	56.2	204
57	Intestinal Enteroendocrine Lineage Cells Possess Homeostatic and Injury-Inducible Stem Cell Activity. <i>Cell Stem Cell</i> , 2017 , 21, 78-90.e6	18	203
56	LIN28 Regulates Stem Cell Metabolism and Conversion to Primed Pluripotency. <i>Cell Stem Cell</i> , 2016 , 19, 66-80	18	192
55	Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. <i>Genome Research</i> , 2013 , 23, 800-11	9.7	191
54	Defining the human C2H2 zinc finger degrome targeted by thalidomide analogs through CRBN. <i>Science</i> , 2018 , 362,	33.3	171

53	The case for selection at CCR5-Delta32. <i>PLoS Biology</i> , 2005 , 3, e378	9.7	153
52	Prospective functional classification of all possible missense variants in PPARG. <i>Nature Genetics</i> , 2016 , 48, 1570-1575	36.3	149
51	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. <i>Cell</i> , 2015 , 162, 412-424	56.2	148
50	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015 , 518, 355-359	50.4	140
49	Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. <i>Genes and Development</i> , 2012 , 26, 2802-16	12.6	124
48	ZBED6, a novel transcription factor derived from a domesticated DNA transposon regulates IGF2 expression and muscle growth. <i>PLoS Biology</i> , 2009 , 7, e1000256	9.7	124
47	Characterization of directed differentiation by high-throughput single-cell RNA-Seq		111
46	Comprehensive mutational scanning of a kinase in vivo reveals substrate-dependent fitness landscapes. <i>Nucleic Acids Research</i> , 2014 , 42, e112	20.1	109
45	Progenitor identification and SARS-CoV-2 infection in human distal lung organoids. <i>Nature</i> , 2020 , 588, 670-675	50.4	103
44	Large, Diverse Population Cohorts of hiPSCs and Derived Hepatocyte-like Cells Reveal Functional Genetic Variation at Blood Lipid-Associated Loci. <i>Cell Stem Cell</i> , 2017 , 20, 558-570.e10	18	102
43	Enhanced methods for unbiased deep sequencing of Lassa and Ebola RNA viruses from clinical and biological samples. <i>Genome Biology</i> , 2014 , 15, 519	18.3	97
42	microRNA-140 targets RALA and regulates chondrogenic differentiation of human mesenchymal stem cells by translational enhancement of SOX9 and ACAN. <i>Stem Cells and Development</i> , 2014 , 23, 290-304	44	95
41	A human-specific gene in microglia. <i>Science</i> , 2005 , 309, 1693	33.3	94
40	Systematic dissection of genomic features determining transcription factor binding and enhancer function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E1291-E1300	11.5	88
39	Dynamics of lineage commitment revealed by single-cell transcriptomics of differentiating embryonic stem cells. <i>Nature Communications</i> , 2017 , 8, 1096	17.4	92
38	DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006 , 439, 331-5	50.4	86
37	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. <i>Nature Biotechnology</i> , 2020 , 38, 954-961	44.5	85
36	Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. <i>Nature Biotechnology</i> , 2016 , 34, 1180-1190	44.5	85

35	Phenotypic Characterization of a Comprehensive Set of MAPK1/ERK2 Missense Mutants. <i>Cell Reports</i> , 2016 , 17, 1171-1183	10.6	78
34	The regulatory landscape of osteogenic differentiation. <i>Stem Cells</i> , 2014 , 32, 2780-93	5.8	72
33	Parallel derivation of isogenic human primed and naive induced pluripotent stem cells. <i>Nature Communications</i> , 2018 , 9, 360	17.4	70
32	The DAILY (Daily Automated Intensive Log for Youth) trial: a wireless, portable system to improve adherence and glycemic control in youth with diabetes. <i>Diabetes Technology and Therapeutics</i> , 2004 , 6, 445-53	8.1	67
31	Integrative genomics identifies the corepressor SMRT as a gatekeeper of adipogenesis through the transcription factors C/EBP β and KAISO. <i>Molecular Cell</i> , 2012 , 46, 335-50	17.6	62
30	Genome-wide map of quantified epigenetic changes during in vitro chondrogenic differentiation of primary human mesenchymal stem cells. <i>BMC Genomics</i> , 2013 , 14, 105	4.5	61
29	A distant trophoblast-specific enhancer controls HLA-G expression at the maternal-fetal interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 5364-9	11.5	55
28	FOSL2 promotes leptin gene expression in human and mouse adipocytes. <i>Journal of Clinical Investigation</i> , 2012 , 122, 1010-21	15.9	54
27	Organism-Level Analysis of Vaccination Reveals Networks of Protection across Tissues. <i>Cell</i> , 2017 , 171, 398-413.e21	56.2	50
26	Identification of nuclear hormone receptor pathways causing insulin resistance by transcriptional and epigenomic analysis. <i>Nature Cell Biology</i> , 2015 , 17, 44-56	23.4	49
25	System-wide genomic and biochemical comparisons of sialic acid biology among primates and rodents: Evidence for two modes of rapid evolution. <i>Journal of Biological Chemistry</i> , 2006 , 281, 25689-7024	5.4	46
24	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005 , 437, 551-5	50.4	45
23	Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome. <i>Cell Systems</i> , 2018 , 7, 258-268.e3	10.6	40
22	Altered chromatin occupancy of master regulators underlies evolutionary divergence in the transcriptional landscape of erythroid differentiation. <i>PLoS Genetics</i> , 2014 , 10, e1004890	6	33
21	Massively parallel reporter assays in cultured mammalian cells. <i>Journal of Visualized Experiments</i> , 2014 ,	1.6	32
20	Early B-cell factor-1 (EBF1) is a key regulator of metabolic and inflammatory signaling pathways in mature adipocytes. <i>Journal of Biological Chemistry</i> , 2013 , 288, 35925-39	5.4	31
19	Analysis of the effects of five factors relevant to in vitro chondrogenesis of human mesenchymal stem cells using factorial design and high throughput mRNA-profiling. <i>PLoS ONE</i> , 2014 , 9, e96615	3.7	29
18	Registry in a tube: multiplexed pools of retrievable parts for genetic design space exploration. <i>Nucleic Acids Research</i> , 2017 , 45, 1553-1565	20.1	24

17	Identification of Functional Variants in the FAM13A Chronic Obstructive Pulmonary Disease Genome-Wide Association Study Locus by Massively Parallel Reporter Assays. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019 , 199, 52-61	10.2	23
16	Solving nonlinear polynomial systems in the barycentric Bernstein basis. <i>Visual Computer</i> , 2008 , 24, 187-200		20
15	Improving genome annotations using phylogenetic profile anomaly detection. <i>Bioinformatics</i> , 2005 , 21, 464-70	7.2	20
14	Simultaneous Pathway Activity Inference and Gene Expression Analysis Using RNA Sequencing. <i>Cell Systems</i> , 2016 , 2, 323-334	10.6	19
13	Progenitor identification and SARS-CoV-2 infection in long-term human distal lung organoid cultures 2020 ,		17
12	Convergent and divergent evolution of genomic imprinting in the marsupial <i>Monodelphis domestica</i> . <i>BMC Genomics</i> , 2012 , 13, 394	4.5	16
11	ZBED6 modulates the transcription of myogenic genes in mouse myoblast cells. <i>PLoS ONE</i> , 2014 , 9, e94137		16
10	Integrated pseudotime analysis of human pre-implantation embryo single-cell transcriptomes reveals the dynamics of lineage specification. <i>Cell Stem Cell</i> , 2021 , 28, 1625-1640.e6	18	14
9	Defining the landscape of ATP-competitive inhibitor resistance residues in protein kinases. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 92-104	17.6	12
8	Brief report: importance of SOX8 for in vitro chondrogenic differentiation of human mesenchymal stromal cells. <i>Stem Cells</i> , 2014 , 32, 1629-35	5.8	10
7	Direct capture of CRISPR guides enables scalable, multiplexed, and multi-omic Perturb-seq		9
6	Spatio-temporal analysis of human preimplantation development reveals dynamics of epiblast and trophectoderm		8
5	Loss of DNA methyltransferase activity in primed human ES cells triggers increased cell-cell variability and transcriptional repression. <i>Development (Cambridge)</i> , 2019 , 146,	6.6	5
4	Aligning single-cell developmental and reprogramming trajectories identifies molecular determinants of reprogramming outcome		4
3	High-Throughput Screening and CRISPR-Cas9 Modeling of Causal Lipid-Associated Expression Quantitative Trait Locus Variants		3
2	What makes us human?. <i>Genome Biology</i> , 2004 , 5, 238	18.3	1
1	High-Throughput DNA Sequencing47-67		