

Tarjei S Mikkelsen

List of Publications by Year in Descending Order

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Version: 2024-04-26

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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	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
87	Progenitor identification and SARS-CoV-2 infection in human distal lung organoids. <i>Nature</i> , 2020 , 588, 670-675	50.4	103
86	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. <i>Nature Biotechnology</i> , 2020 , 38, 954-961	44.5	85
85	Progenitor identification and SARS-CoV-2 infection in long-term human distal lung organoid cultures 2020 ,		17
84	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
83	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
82	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
81	Parallel derivation of isogenic human primed and naive induced pluripotent stem cells. <i>Nature Communications</i> , 2018 , 9, 360	17.4	70
80	Defining the human C2H2 zinc finger degrome targeted by thalidomide analogs through CRBN. <i>Science</i> , 2018 , 362,	33.3	171
79	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
78	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	33
77	Massively parallel digital transcriptional profiling of single cells. <i>Nature Communications</i> , 2017 , 8, 14049	17.4	2276
76	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
75	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
74	Organism-Level Analysis of Vaccination Reveals Networks of Protection across Tissues. <i>Cell</i> , 2017 , 171, 398-413.e21	56.2	50
73	Dynamics of lineage commitment revealed by single-cell transcriptomics of differentiating embryonic stem cells. <i>Nature Communications</i> , 2017 , 8, 1096	17.4	92
72	Intestinal Enteroendocrine Lineage Cells Possess Homeostatic and Injury-Inducible Stem Cell Activity. <i>Cell Stem Cell</i> , 2017 , 21, 78-90.e6	18	203

71	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
70	Prospective functional classification of all possible missense variants in PPARG. <i>Nature Genetics</i> , 2016 , 48, 1570-1575	36.3	149
69	LIN28 Regulates Stem Cell Metabolism and Conversion to Primed Pluripotency. <i>Cell Stem Cell</i> , 2016 , 19, 66-80	18	192
68	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , 2016 , 165, 1519-1529	56.2	228
67	Systematic Functional Dissection of Common Genetic Variation Affecting Red Blood Cell Traits. <i>Cell</i> , 2016 , 165, 1530-1545	56.2	204
66	Simultaneous Pathway Activity Inference and Gene Expression Analysis Using RNA Sequencing. <i>Cell Systems</i> , 2016 , 2, 323-334	10.6	19
65	Phenotypic Characterization of a Comprehensive Set of MAPK1/ERK2 Missense Mutants. <i>Cell Reports</i> , 2016 , 17, 1171-1183	10.6	78
64	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
63	Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. <i>Nature Biotechnology</i> , 2016 , 34, 1180-1190	44.5	85
62	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. <i>Cell</i> , 2015 , 162, 412-424	56.2	148
61	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015 , 518, 355-359	50.4	140
60	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
59	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
58	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
57	Genome-scale CRISPR-Cas9 knockout screening in human cells. <i>Science</i> , 2014 , 343, 84-87	33.3	3080
56	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	4.4	95
55	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
54	The regulatory landscape of osteogenic differentiation. <i>Stem Cells</i> , 2014 , 32, 2780-93	5.8	72

53	Massively parallel reporter assays in cultured mammalian cells. <i>Journal of Visualized Experiments</i> , 2014 ,	1.6	32
52	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
51	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
50	Comprehensive mutational scanning of a kinase in vivo reveals substrate-dependent fitness landscapes. <i>Nucleic Acids Research</i> , 2014 , 42, e112	20.1	109
49	ZBED6 modulates the transcription of myogenic genes in mouse myoblast cells. <i>PLoS ONE</i> , 2014 , 9, e94137	13.7	16
48	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
47	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
46	Cellular source and mechanisms of high transcriptome complexity in the mammalian testis. <i>Cell Reports</i> , 2013 , 3, 2179-90	10.6	334
45	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
44	High-resolution mapping reveals a conserved, widespread, dynamic mRNA methylation program in yeast meiosis. <i>Cell</i> , 2013 , 155, 1409-21	56.2	415
43	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
42	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
41	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012 , 489, 57-74	50.4	11449
40	Convergent and divergent evolution of genomic imprinting in the marsupial <i>Monodelphis domestica</i> . <i>BMC Genomics</i> , 2012 , 13, 394	4.5	16
39	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
38	A unique regulatory phase of DNA methylation in the early mammalian embryo. <i>Nature</i> , 2012 , 484, 339-44	56.4	723
37	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
36	FOSL2 promotes leptin gene expression in human and mouse adipocytes. <i>Journal of Clinical Investigation</i> , 2012 , 122, 1010-21	15.9	54

35	A user's guide to the encyclopedia of DNA elements (ENCODE). <i>PLoS Biology</i> , 2011 , 9, e1001046	9.7	1060
34	Mapping and analysis of chromatin state dynamics in nine human cell types. <i>Nature</i> , 2011 , 473, 43-9	50.4	2153
33	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010 , 28, 1045-8	44.5	1284
32	Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. <i>Nature Methods</i> , 2010 , 7, 133-6	21.6	258
31	Comparative epigenomic analysis of murine and human adipogenesis. <i>Cell</i> , 2010 , 143, 156-69	56.2	402
30	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
29	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , 2009 , 458, 223-7	50.4	3230
28	Dissecting direct reprogramming through integrative genomic analysis. <i>Nature</i> , 2008 , 454, 49-55	50.4	1205
27	Genome-scale DNA methylation maps of pluripotent and differentiated cells. <i>Nature</i> , 2008 , 454, 766-70	50.4	1999
26	Genomewide analysis of PRC1 and PRC2 occupancy identifies two classes of bivalent domains. <i>PLoS Genetics</i> , 2008 , 4, e1000242	6	746
25	Solving nonlinear polynomial systems in the barycentric Bernstein basis. <i>Visual Computer</i> , 2008 , 24, 187-200	9	20
24	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007 , 447, 167-77	50.4	577
23	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. <i>Nature</i> , 2007 , 448, 553-60	50.4	3296
22	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
21	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
20	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
19	A bivalent chromatin structure marks key developmental genes in embryonic stem cells. <i>Cell</i> , 2006 , 125, 315-26	56.2	4097
18	Positive natural selection in the human lineage. <i>Science</i> , 2006 , 312, 1614-20	33.3	833

17	DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006 , 439, 331-5	50.4	86
16	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005 , 437, 551-5	50.4	45
15	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005 , 437, 69-87	50.4	1828
14	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005 , 438, 803-19	50.4	1809
13	The case for selection at CCR5-Delta32. <i>PLoS Biology</i> , 2005 , 3, e378	9.7	153
12	Improving genome annotations using phylogenetic profile anomaly detection. <i>Bioinformatics</i> , 2005 , 21, 464-70	7.2	20
11	A human-specific gene in microglia. <i>Science</i> , 2005 , 309, 1693	33.3	94
10	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
9	What makes us human?. <i>Genome Biology</i> , 2004 , 5, 238	18.3	1
8	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004 , 306, 636-40	33.3	1692
7	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001 , 409, 860-921	50.4	17366
6	High-Throughput DNA Sequencing47-67		
5	Characterization of directed differentiation by high-throughput single-cell RNA-Seq		111
4	High-Throughput Screening and CRISPR-Cas9 Modeling of Causal Lipid-Associated Expression Quantitative Trait Locus Variants		3
3	Aligning single-cell developmental and reprogramming trajectories identifies molecular determinants of reprogramming outcome		4
2	Direct capture of CRISPR guides enables scalable, multiplexed, and multi-omic Perturb-seq		9
1	Spatio-temporal analysis of human preimplantation development reveals dynamics of epiblast and trophectoderm		