

Tarjei S Mikkelsen

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

92,190
citations

19657

61
h-index

56724

83
g-index

90
all docs

90
docs citations

90
times ranked

101651
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. Nature, 2001, 409, 860-921.	27.8	21,074
2	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
3	A Bivalent Chromatin Structure Marks Key Developmental Genes in Embryonic Stem Cells. Cell, 2006, 125, 315-326.	28.9	4,773
4	The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells. Nature Biotechnology, 2014, 32, 381-386.	17.5	4,652
5	Massively parallel digital transcriptional profiling of single cells. Nature Communications, 2017, 8, 14049.	12.8	4,535
6	Genome-Scale CRISPR-Cas9 Knockout Screening in Human Cells. Science, 2014, 343, 84-87.	12.6	4,210
7	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. Nature, 2009, 458, 223-227.	27.8	3,801
8	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. Nature, 2007, 448, 553-560.	27.8	3,733
9	Mapping and analysis of chromatin state dynamics in nine human cell types. Nature, 2011, 473, 43-49.	27.8	2,630
10	Genome-scale DNA methylation maps of pluripotent and differentiated cells. Nature, 2008, 454, 766-770.	27.8	2,267
11	Initial sequence of the chimpanzee genome and comparison with the human genome. Nature, 2005, 437, 69-87.	27.8	2,222
12	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	27.8	2,215
13	The ENCODE (ENCyclopedia Of DNA Elements) Project. Science, 2004, 306, 636-640.	12.6	2,121
14	The NIH Roadmap Epigenomics Mapping Consortium. Nature Biotechnology, 2010, 28, 1045-1048.	17.5	1,705
15	Dissecting direct reprogramming through integrative genomic analysis. Nature, 2008, 454, 49-55.	27.8	1,344
16	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	5.6	1,257
17	Positive Natural Selection in the Human Lineage. Science, 2006, 312, 1614-1620.	12.6	1,037
18	Perturbation of m6A Writers Reveals Two Distinct Classes of mRNA Methylation at Internal and 5' Sites. Cell Reports, 2014, 8, 284-296.	6.4	972

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19	Genomewide Analysis of PRC1 and PRC2 Occupancy Identifies Two Classes of Bivalent Domains. PLoS Genetics, 2008, 4, e1000242.	3.5	878
20	A unique regulatory phase of DNA methylation in the early mammalian embryo. Nature, 2012, 484, 339-344.	27.8	860
21	Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences. Nature, 2007, 447, 167-177.	27.8	661
22	Systematic dissection and optimization of inducible enhancers in human cells using a massively parallel reporter assay. Nature Biotechnology, 2012, 30, 271-277.	17.5	602
23	High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis. Cell, 2013, 155, 1409-1421.	28.9	554
24	Cellular Source and Mechanisms of High Transcriptome Complexity in the Mammalian Testis. Cell Reports, 2013, 3, 2179-2190.	6.4	497
25	Comparative Epigenomic Analysis of Murine and Human Adipogenesis. Cell, 2010, 143, 156-169.	28.9	460
26	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. Cell, 2016, 165, 1519-1529.	28.9	378
27	Non-equivalence of Wnt and R-spondin ligands during Lgr5+ intestinal stem-cell self-renewal. Nature, 2017, 545, 238-242.	27.8	327
28	Defining the human C2H2 zinc finger degrome targeted by thalidomide analogs through CRBN. Science, 2018, 362, .	12.6	320
29	Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. Nature Methods, 2010, 7, 133-136.	19.0	302
30	Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. Genome Research, 2013, 23, 800-811.	5.5	298
31	A Second Fatty Acid Amide Hydrolase with Variable Distribution among Placental Mammals. Journal of Biological Chemistry, 2006, 281, 36569-36578.	3.4	294
32	Systematic Functional Dissection of Common Genetic Variation Affecting Red Blood Cell Traits. Cell, 2016, 165, 1530-1545.	28.9	294
33	Intestinal Enteroendocrine Lineage Cells Possess Homeostatic and Injury-Inducible Stem Cell Activity. Cell Stem Cell, 2017, 21, 78-90.e6.	11.1	280
34	LIN28 Regulates Stem Cell Metabolism and Conversion to Primed Pluripotency. Cell Stem Cell, 2016, 19, 66-80.	11.1	278
35	Progenitor identification and SARS-CoV-2 infection in human distal lung organoids. Nature, 2020, 588, 670-675.	27.8	273
36	Systematic discovery of regulatory motifs in conserved regions of the human genome, including thousands of CTCF insulator sites. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7145-7150.	7.1	272

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37	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. Nature Biotechnology, 2020, 38, 954-961.	17.5	232
38	Prospective functional classification of all possible missense variants in PPARC. Nature Genetics, 2016, 48, 1570-1575.	21.4	210
39	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. Cell, 2015, 162, 412-424.	28.9	206
40	The Case for Selection at CCR5-Δ32. PLoS Biology, 2005, 3, e378.	5.6	190
41	Dissecting neural differentiation regulatory networks through epigenetic footprinting. Nature, 2015, 518, 355-359.	27.8	172
42	Comprehensive mutational scanning of a kinase <i>in vivo</i> reveals substrate-dependent fitness landscapes. Nucleic Acids Research, 2014, 42, e112-e112.	14.5	161
43	Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. Genes and Development, 2012, 26, 2802-2816.	5.9	158
44	Dynamics of lineage commitment revealed by single-cell transcriptomics of differentiating embryonic stem cells. Nature Communications, 2017, 8, 1096.	12.8	156
45	Systematic dissection of genomic features determining transcription factor binding and enhancer function. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E1291-E1300.	7.1	150
46	ZBED6, a Novel Transcription Factor Derived from a Domesticated DNA Transposon Regulates IGF2 Expression and Muscle Growth. PLoS Biology, 2009, 7, e1000256.	5.6	149
47	Large, Diverse Population Cohorts of hiPSCs and Derived Hepatocyte-like Cells Reveal Functional Genetic Variation at Blood Lipid-Associated Loci. Cell Stem Cell, 2017, 20, 558-570.e10.	11.1	138
48	Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. Nature Biotechnology, 2016, 34, 1180-1190.	17.5	132
49	Enhanced methods for unbiased deep sequencing of Lassa and Ebola RNA viruses from clinical and biological samples. Genome Biology, 2014, 15, 519.	8.8	129
50	Phenotypic Characterization of a Comprehensive Set of MAPK1 /ERK2 Missense Mutants. Cell Reports, 2016, 17, 1171-1183.	6.4	119
51	DNA sequence and analysis of human chromosome 8. Nature, 2006, 439, 331-335.	27.8	115
52	Evoked brain potentials as indicators of decision-making. Science, 1975, 187, 754-755.	12.6	113
53	microRNA-140 Targets <i>RALA</i> and Regulates Chondrogenic Differentiation of Human Mesenchymal Stem Cells by Translational Enhancement of <i>SOX9</i> and <i>ACAN</i> . Stem Cells and Development, 2014, 23, 290-304.	2.1	109
54	Integrated pseudotime analysis of human pre-implantation embryo single-cell transcriptomes reveals the dynamics of lineage specification. Cell Stem Cell, 2021, 28, 1625-1640.e6.	11.1	108

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55	Parallel derivation of isogenic human primed and naive induced pluripotent stem cells. <i>Nature Communications</i> , 2018, 9, 360.	12.8	104
56	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, 335-350.	9.7	96
57	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, 5364-5369.	7.1	90
58	The Regulatory Landscape of Osteogenic Differentiation. <i>Stem Cells</i> , 2014, 32, 2780-2793.	3.2	85
59	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, 445-453.	4.4	79
60	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.	2.8	69
61	Organism-Level Analysis of Vaccination Reveals Networks of Protection across Tissues. <i>Cell</i> , 2017, 171, 398-413.e21.	28.9	69
62	FOSL2 promotes leptin gene expression in human and mouse adipocytes. <i>Journal of Clinical Investigation</i> , 2012, 122, 1010-1021.	8.2	67
63	Aligning Single-Cell Developmental and Reprogramming Trajectories Identifies Molecular Determinants of Myogenic Reprogramming Outcome. <i>Cell Systems</i> , 2018, 7, 258-268.e3.	6.2	65
64	Identification of nuclear hormone receptor pathways causing insulin resistance by transcriptional and epigenomic analysis. <i>Nature Cell Biology</i> , 2015, 17, 44-56.	10.3	61
65	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005, 437, 551-555.	27.8	53
66	System-wide Genomic and Biochemical Comparisons of Sialic Acid Biology Among Primates and Rodents. <i>Journal of Biological Chemistry</i> , 2006, 281, 25689-25702.	3.4	52
67	Massively Parallel Reporter Assays in Cultured Mammalian Cells. <i>Journal of Visualized Experiments</i> , 2014, , .	0.3	46
68	Altered Chromatin Occupancy of Master Regulators Underlies Evolutionary Divergence in the Transcriptional Landscape of Erythroid Differentiation. <i>PLoS Genetics</i> , 2014, 10, e1004890.	3.5	42
69	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, 35925-35939.	3.4	41
70	Identification of Functional Variants in the <i>FAM13A</i> 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.	5.6	38
71	Registry in a tube: multiplexed pools of retrievable parts for genetic design space exploration. <i>Nucleic Acids Research</i> , 2017, 45, gkw1226.	14.5	37
72	Analysis of the Effects of Five Factors Relevant to In Vitro Chondrogenesis of Human Mesenchymal Stem Cells Using Factorial Design and High Throughput mRNA-Profilng. <i>PLoS ONE</i> , 2014, 9, e96615.	2.5	36

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73	Defining the landscape of ATP-competitive inhibitor resistance residues in protein kinases. Nature Structural and Molecular Biology, 2020, 27, 92-104.	8.2	30
74	Simultaneous Pathway Activity Inference and Gene Expression Analysis Using RNA Sequencing. Cell Systems, 2016, 2, 323-334.	6.2	26
75	Brief Report: Importance of SOX8 for In Vitro Chondrogenic Differentiation of Human Mesenchymal Stromal Cells. Stem Cells, 2014, 32, 1629-1635.	3.2	25
76	Convergent and divergent evolution of genomic imprinting in the marsupial Monodelphis domestica. BMC Genomics, 2012, 13, 394.	2.8	24
77	Solving nonlinear polynomial systems in the barycentric Bernstein basis. Visual Computer, 2008, 24, 187-200.	3.5	23
78	Improving genome annotations using phylogenetic profile anomaly detection. Bioinformatics, 2005, 21, 464-470.	4.1	22
79	ZBED6 Modulates the Transcription of Myogenic Genes in Mouse Myoblast Cells. PLoS ONE, 2014, 9, e94187.	2.5	19
80	Loss of DNA methyltransferase activity in primed human ES cells triggers increased cell-cell variability and transcriptional repression. Development (Cambridge), 2019, 146, .	2.5	9
81	What makes us human?. Genome Biology, 2004, 5, 238.	9.6	1
82	High-Throughput DNA Sequencing. , 0, , 47-67.		1