

Tarjei S Mikkelsen

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

92,190
citations

19608

61
h-index

56606

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. <i>Nature</i> , 2001, 409, 860-921.	13.7	21,074
2	An integrated encyclopedia of DNA elements in the human genome. <i>Nature</i> , 2012, 489, 57-74.	13.7	15,516
3	A Bivalent Chromatin Structure Marks Key Developmental Genes in Embryonic Stem Cells. <i>Cell</i> , 2006, 125, 315-326.	13.5	4,773
4	The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells. <i>Nature Biotechnology</i> , 2014, 32, 381-386.	9.4	4,652
5	Massively parallel digital transcriptional profiling of single cells. <i>Nature Communications</i> , 2017, 8, 14049.	5.8	4,535
6	Genome-Scale CRISPR-Cas9 Knockout Screening in Human Cells. <i>Science</i> , 2014, 343, 84-87.	6.0	4,210
7	Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals. <i>Nature</i> , 2009, 458, 223-227.	13.7	3,801
8	Genome-wide maps of chromatin state in pluripotent and lineage-committed cells. <i>Nature</i> , 2007, 448, 553-560.	13.7	3,733
9	Mapping and analysis of chromatin state dynamics in nine human cell types. <i>Nature</i> , 2011, 473, 43-49.	13.7	2,630
10	Genome-scale DNA methylation maps of pluripotent and differentiated cells. <i>Nature</i> , 2008, 454, 766-770.	13.7	2,267
11	Initial sequence of the chimpanzee genome and comparison with the human genome. <i>Nature</i> , 2005, 437, 69-87.	13.7	2,222
12	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	13.7	2,215
13	The ENCODE (ENCyclopedia Of DNA Elements) Project. <i>Science</i> , 2004, 306, 636-640.	6.0	2,121
14	The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , 2010, 28, 1045-1048.	9.4	1,705
15	Dissecting direct reprogramming through integrative genomic analysis. <i>Nature</i> , 2008, 454, 49-55.	13.7	1,344
16	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). <i>PLoS Biology</i> , 2011, 9, e1001046.	2.6	1,257
17	Positive Natural Selection in the Human Lineage. <i>Science</i> , 2006, 312, 1614-1620.	6.0	1,037
18	Perturbation of m6A Writers Reveals Two Distinct Classes of mRNA Methylation at Internal and 5' Sites. <i>Cell Reports</i> , 2014, 8, 284-296.	2.9	972

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19	Genomewide Analysis of PRC1 and PRC2 Occupancy Identifies Two Classes of Bivalent Domains. <i>PLoS Genetics</i> , 2008, 4, e1000242.	1.5	878
20	A unique regulatory phase of DNA methylation in the early mammalian embryo. <i>Nature</i> , 2012, 484, 339-344.	13.7	860
21	Genome of the marsupial <i>Monodelphis domestica</i> reveals innovation in non-coding sequences. <i>Nature</i> , 2007, 447, 167-177.	13.7	661
22	Systematic dissection and optimization of inducible enhancers in human cells using a massively parallel reporter assay. <i>Nature Biotechnology</i> , 2012, 30, 271-277.	9.4	602
23	High-Resolution Mapping Reveals a Conserved, Widespread, Dynamic mRNA Methylation Program in Yeast Meiosis. <i>Cell</i> , 2013, 155, 1409-1421.	13.5	554
24	Cellular Source and Mechanisms of High Transcriptome Complexity in the Mammalian Testis. <i>Cell Reports</i> , 2013, 3, 2179-2190.	2.9	497
25	Comparative Epigenomic Analysis of Murine and Human Adipogenesis. <i>Cell</i> , 2010, 143, 156-169.	13.5	460
26	Direct Identification of Hundreds of Expression-Modulating Variants using a Multiplexed Reporter Assay. <i>Cell</i> , 2016, 165, 1519-1529.	13.5	378
27	Non-equivalence of Wnt and R-spondin ligands during Lgr5+ intestinal stem-cell self-renewal. <i>Nature</i> , 2017, 545, 238-242.	13.7	327
28	Defining the human C2H2 zinc finger degrome targeted by thalidomide analogs through CRBN. <i>Science</i> , 2018, 362, .	6.0	320
29	Genome-scale DNA methylation mapping of clinical samples at single-nucleotide resolution. <i>Nature Methods</i> , 2010, 7, 133-136.	9.0	302
30	Systematic dissection of regulatory motifs in 2000 predicted human enhancers using a massively parallel reporter assay. <i>Genome Research</i> , 2013, 23, 800-811.	2.4	298
31	A Second Fatty Acid Amide Hydrolase with Variable Distribution among Placental Mammals. <i>Journal of Biological Chemistry</i> , 2006, 281, 36569-36578.	1.6	294
32	Systematic Functional Dissection of Common Genetic Variation Affecting Red Blood Cell Traits. <i>Cell</i> , 2016, 165, 1530-1545.	13.5	294
33	Intestinal Enteroendocrine Lineage Cells Possess Homeostatic and Injury-Inducible Stem Cell Activity. <i>Cell Stem Cell</i> , 2017, 21, 78-90.e6.	5.2	280
34	LIN28 Regulates Stem Cell Metabolism and Conversion to Primed Pluripotency. <i>Cell Stem Cell</i> , 2016, 19, 66-80.	5.2	278
35	Progenitor identification and SARS-CoV-2 infection in human distal lung organoids. <i>Nature</i> , 2020, 588, 670-675.	13.7	273
36	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, 7145-7150.	3.3	272

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37	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. <i>Nature Biotechnology</i> , 2020, 38, 954-961.	9.4	232
38	Prospective functional classification of all possible missense variants in PPARC. <i>Nature Genetics</i> , 2016, 48, 1570-1575.	9.4	210
39	Integrative Analyses of Human Reprogramming Reveal Dynamic Nature of Induced Pluripotency. <i>Cell</i> , 2015, 162, 412-424.	13.5	206
40	The Case for Selection at CCR5-Δ32. <i>PLoS Biology</i> , 2005, 3, e378.	2.6	190
41	Dissecting neural differentiation regulatory networks through epigenetic footprinting. <i>Nature</i> , 2015, 518, 355-359.	13.7	172
42	Comprehensive mutational scanning of a kinase <i>in vivo</i> reveals substrate-dependent fitness landscapes. <i>Nucleic Acids Research</i> , 2014, 42, e112-e112.	6.5	161
43	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, 2802-2816.	2.7	158
44	Dynamics of lineage commitment revealed by single-cell transcriptomics of differentiating embryonic stem cells. <i>Nature Communications</i> , 2017, 8, 1096.	5.8	156
45	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.	3.3	150
46	ZBED6, a Novel Transcription Factor Derived from a Domesticated DNA Transposon Regulates IGF2 Expression and Muscle Growth. <i>PLoS Biology</i> , 2009, 7, e1000256.	2.6	149
47	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.	5.2	138
48	Genome-scale high-resolution mapping of activating and repressive nucleotides in regulatory regions. <i>Nature Biotechnology</i> , 2016, 34, 1180-1190.	9.4	132
49	Enhanced methods for unbiased deep sequencing of Lassa and Ebola RNA viruses from clinical and biological samples. <i>Genome Biology</i> , 2014, 15, 519.	3.8	129
50	Phenotypic Characterization of a Comprehensive Set of MAPK1 /ERK2 Missense Mutants. <i>Cell Reports</i> , 2016, 17, 1171-1183.	2.9	119
51	DNA sequence and analysis of human chromosome 8. <i>Nature</i> , 2006, 439, 331-335.	13.7	115
52	Evoked brain potentials as indicators of decision-making. <i>Science</i> , 1975, 187, 754-755.	6.0	113
53	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.	1.1	109
54	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.	5.2	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.	5.8	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.	4.5	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.	3.3	90
58	The Regulatory Landscape of Osteogenic Differentiation. <i>Stem Cells</i> , 2014, 32, 2780-2793.	1.4	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.	2.4	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.	1.2	69
61	Organism-Level Analysis of Vaccination Reveals Networks of Protection across Tissues. <i>Cell</i> , 2017, 171, 398-413.e21.	13.5	69
62	FOSL2 promotes leptin gene expression in human and mouse adipocytes. <i>Journal of Clinical Investigation</i> , 2012, 122, 1010-1021.	3.9	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.	2.9	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.	4.6	61
65	DNA sequence and analysis of human chromosome 18. <i>Nature</i> , 2005, 437, 551-555.	13.7	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.	1.6	52
67	Massively Parallel Reporter Assays in Cultured Mammalian Cells. <i>Journal of Visualized Experiments</i> , 2014, , .	0.2	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.	1.5	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.	1.6	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.	2.5	38
71	Registry in a tube: multiplexed pools of retrievable parts for genetic design space exploration. <i>Nucleic Acids Research</i> , 2017, 45, gkw1226.	6.5	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-Profiling. <i>PLoS ONE</i> , 2014, 9, e96615.	1.1	36

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73	Defining the landscape of ATP-competitive inhibitor resistance residues in protein kinases. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 92-104.	3.6	30
74	Simultaneous Pathway Activity Inference and Gene Expression Analysis Using RNA Sequencing. <i>Cell Systems</i> , 2016, 2, 323-334.	2.9	26
75	Brief Report: Importance of SOX8 for In Vitro Chondrogenic Differentiation of Human Mesenchymal Stromal Cells. <i>Stem Cells</i> , 2014, 32, 1629-1635.	1.4	25
76	Convergent and divergent evolution of genomic imprinting in the marsupial <i>Monodelphis domestica</i> . <i>BMC Genomics</i> , 2012, 13, 394.	1.2	24
77	Solving nonlinear polynomial systems in the barycentric Bernstein basis. <i>Visual Computer</i> , 2008, 24, 187-200.	2.5	23
78	Improving genome annotations using phylogenetic profile anomaly detection. <i>Bioinformatics</i> , 2005, 21, 464-470.	1.8	22
79	ZBED6 Modulates the Transcription of Myogenic Genes in Mouse Myoblast Cells. <i>PLoS ONE</i> , 2014, 9, e94187.	1.1	19
80	Loss of DNA methyltransferase activity in primed human ES cells triggers increased cell-cell variability and transcriptional repression. <i>Development (Cambridge)</i> , 2019, 146, .	1.2	9
81	What makes us human?. <i>Genome Biology</i> , 2004, 5, 238.	13.9	1
82	High-Throughput DNA Sequencing. , 0, , 47-67.		1