Martin J Aryee

List of Publications by Year
in descending order

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Version: 2024-02-01

82 papers	30,709 citations	47409 49 h-index	66518 82 g-index
98 all docs	98 docs citations	98 times ranked	56879 citing authors

#	Article	IF	Citations
1	A comparative risk assessment of burden of disease and injury attributable to 67 risk factors and risk factor clusters in 21 regions, 1990â€“2010: a systematic analysis for the Global Burden of Disease Study 2010. Lancet, The, 2012, 380, 2224-2260.	6.3	9,397
2	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. Bioinformatics, 2014, 30, 1363-1369.	1.8	3,192
3	GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. Nature Biotechnology, 2015, 33, 187-197.	9.4	1,757
4	Engineered CRISPR-Cas9 nucleases with altered PAM specificities. Nature, 2015, 523, 481-485.	13.7	1,388
5	Differential methylation of tissue- and cancer-specific CpG island shores distinguishes human induced pluripotent stem cells, embryonic stem cells and fibroblasts. Nature Genetics, 2009, 41, 1350-1353.	9.4	1,076
6	Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. Nature Biotechnology, 2013, 31, 142-147.	9.4	874
7	Dimeric CRISPR RNA-guided FokI nucleases for highly specific genome editing. Nature Biotechnology, 2014, 32, 569-576.	9.4	852
8	CIRCLE-seq: a highly sensitive in vitro screen for genome-wide CRISPRâ€“Cas9 nuclease off-targets. Nature Methods, 2017, 14, 607-614.	9.0	601
9	Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. Nature Biotechnology, 2016, 34, 869-874.	9.4	566
10	Comprehensive methylome map of lineage commitment from haematopoietic progenitors. Nature, 2010, 467, 338-342.	13.7	554
11	Donor cell type can influence the epigenome and differentiation potential of human induced pluripotent stem cells. Nature Biotechnology, 2011, 29, 1117-1119.	9.4	547
12	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. Cell, 2018, 173, 1535-1548.e16.	13.5	545
13	Androgen-induced TOP2B-mediated double-strand breaks and prostate cancer gene rearrangements. Nature Genetics, 2010, 42, 668-675.	9.4	539
14	Global Causes of Diarrheal Disease Mortality in Children <5 Years of Age: A Systematic Review. PLoS ONE, 2013, 8, e72788.	1.1	524
15	Engineered CRISPRâ€“Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. Nature Biotechnology, 2019, 37, 276-282.	9.4	439
16	Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. Nature, 2019, 569, 433-437.	13.7	434
17	Stromal Microenvironment Shapes the Intratumoral Architecture of Pancreatic Cancer. Cell, 2019, 178, 160-175.e27.	13.5	367
18	A cell epigenotype specific model for the correction of brain cellular heterogeneity bias and its application to age, brain region and major depression. Epigenetics, 2013, 8, 290-302.	1.3	353

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19	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. Cell, 2019, 176, 1325-1339.e22.	13.5	345
20	EWS-FLI1ÂUtilizes Divergent Chromatin Remodeling Mechanisms to Directly Activate or Repress Enhancer Elements in Ewing Sarcoma. Cancer Cell, 2014, 26, 668-681.	7.7	334
21	Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. Nature Biotechnology, 2019, 37, 916-924.	9.4	315
22	Reversible switching between epigenetic states in honeybee behavioral subcastes. Nature Neuroscience, 2012, 15, 1371-1373.	7.1	305
23	Personalized Epigenomic Signatures That Are Stable Over Time and Covary with Body Mass Index. Science Translational Medicine, 2010, 2, 49ra67.	5.8	292
24	In vivo CRISPR editing with no detectable genome-wide off-target mutations. Nature, 2018, 561, 416-419.	13.7	274
25	High levels of AAV vector integration into CRISPR-induced DNA breaks. Nature Communications, 2019, 10, 4439.	5.8	257
26	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. Nature Methods, 2015, 12, 230-232.	9.0	248
27	A DNA hypermethylation module for the stem/progenitor cell signature of cancer. Genome Research, 2012, 22, 837-849.	2.4	236
28	CRISPR DNA base editors with reduced RNA off-target and self-editing activities. Nature Biotechnology, 2019, 37, 1041-1048.	9.4	236
29	DNA Methylation Alterations Exhibit Intraindividual Stability and Interindividual Heterogeneity in Prostate Cancer Metastases. Science Translational Medicine, 2013, 5, 169ra10.	5.8	231
30	Epigenome-wide association studies without the need for cell-type composition. Nature Methods, 2014, 11, 309-311.	9.0	205
31	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. Nature Communications, 2019, 10, 1903.	5.8	198
32	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. Nature, 2019, 569, 576-580.	13.7	195
33	Activities and specificities of <scp>CRISPR</scp>/Cas9 and Cas12a nucleases for targeted mutagenesis in maize. Plant Biotechnology Journal, 2019, 17, 362-372.	4.1	192
34	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. Journal of Experimental Medicine, 2017, 214, 2875-2887.	4.2	168
35	A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. Nature Biotechnology, 2020, 38, 861-864.	9.4	168
36	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. Nature Biotechnology, 2021, 39, 451-461.	9.4	150

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37	Interrogation of human hematopoiesis at single-cell and single-variant resolution. Nature Genetics, 2019, 51, 683-693.	9.4	147
38	hichipper: a preprocessing pipeline for calling DNA loops from HiChIP data. Nature Methods, 2018, 15, 155-156.	9.0	139
39	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. Cell, 2020, 182, 1474-1489.e23.	13.5	126
40	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. Cell Reports, 2019, 27, 3228-3240.e7.	2.9	122
41	Genome-Wide DNA Methylation Scan in Major Depressive Disorder. PLoS ONE, 2012, 7, e34451.	1.1	120
42	Estimating Diarrhea Mortality among Young Children in Low and Middle Income Countries. PLoS ONE, 2012, 7, e29151.	1.1	114
43	Alterations in Nucleolar Structure and Gene Expression Programs in Prostatic Neoplasia Are Driven by the MYC Oncogene. American Journal of Pathology, 2011, 178, 1824-1834.	1.9	113
44	MET Exon 14 Skipping in Non-Small Cell Lung Cancer. Oncologist, 2016, 21, 481-486.	1.9	94
45	GeMes, Clusters of DNA Methylation under Genetic Control, Can Inform Genetic and Epigenetic Analysis of Disease. American Journal of Human Genetics, 2014, 94, 485-495.	2.6	93
46	An improved empirical bayes approach to estimating differential gene expression in microarray time-course data: BETR (Bayesian Estimation of Temporal Regulation). BMC Bioinformatics, 2009, 10, 409.	1.2	87
47	DNA methylation shows genome-wide association ofNFIX,RAPGEF2andMSRB3with gestational age at birth. International Journal of Epidemiology, 2012, 41, 188-199.	0.9	71
48	Defining CRISPRâ€“Cas9 genome-wide nuclease activities with CIRCLE-seq. Nature Protocols, 2018, 13, 2615-2642.	5.5	69
49	Accurate genome-scale percentage DNA methylation estimates from microarray data. Biostatistics, 2011, 12, 197-210.	0.9	67
50	diffloop: a computational framework for identifying and analyzing differential DNA loops from sequencing data. Bioinformatics, 2018, 34, 672-674.	1.8	57
51	Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. Nature Communications, 2018, 9, 2905.	5.8	56
52	OTX2 Activity at Distal Regulatory Elements Shapes the Chromatin Landscape of Group 3 Medulloblastoma. Cancer Discovery, 2017, 7, 288-301.	7.7	53
53	Subset Quantile Normalization Using Negative Control Features. Journal of Computational Biology, 2010, 17, 1385-1395.	0.8	52
54	Lysine Demethylase KDM4A Associates with Translation Machinery and Regulates Protein Synthesis. Cancer Discovery, 2015, 5, 255-263.	7.7	51

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55	Open-source guideseq software for analysis of GUIDE-seq data. Nature Biotechnology, 2016, 34, 483-483.	9.4	49
56	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. Cancer Cell, 2021, 39, 827-844.e10.	7.7	49
57	Data-Driven Polymer Model for Mechanistic Exploration of Diploid Genome Organization. Biophysical Journal, 2020, 119, 1905-1916.	0.2	45
58	Smart-RRBS for single-cell methylome and transcriptome analysis. Nature Protocols, 2021, 16, 4004-4030.	5.5	34
59	Inconsistency and features of single nucleotide variants detected in whole exome sequencing versus transcriptome sequencing: A case study in lung cancer. Methods, 2015, 83, 118-127.	1.9	33
60	The early pregnancy placenta foreshadows DNA methylation alterations of solid tumors. Epigenetics, 2017, 12, 793-803.	1.3	31
61	Reverse Transcriptase Inhibition Disrupts Repeat Element Life Cycle in Colorectal Cancer. Cancer Discovery, 2022, 12, 1462-1481.	7.7	30
62	Detection and Analysis of Circulating Epithelial Cells in Liquid Biopsies From Patients With Liver Disease. Gastroenterology, 2018, 155, 2016-2018.e11.	0.6	29
63	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. Nature Biotechnology, 2021, 39, 1086-1094.	9.4	28
64	Survival in Quiescence Requires the Euchromatic Deployment of Clr4/SUV39H by Argonaute-Associated Small RNAs. Molecular Cell, 2016, 64, 1088-1101.	4.5	27
65	High-specificity bioinformatics framework for epigenomic profiling of discordant twins reveals specific and shared markers for ACPA and ACPA-positive rheumatoid arthritis. Genome Medicine, 2016, 8, 124.	3.6	27
66	Defining genome-wide CRISPRâ€“Cas genome-editing nuclease activity with GUIDE-seq. Nature Protocols, 2021, 16, 5592-5615.	5.5	27
67	Response to â€œUnexpected mutations after CRISPRâ€“Cas9 editing in vivoâ€• Nature Methods, 2018, 15, 238-239.	9.0	25
68	Magnetic Resonance Spectroscopy-based Metabolomic Biomarkers for Typing, Staging, and Survival Estimation of Early-Stage Human Lung Cancer. Scientific Reports, 2019, 9, 10319.	1.6	23
69	Diverse repetitive element RNA expression defines epigenetic and immunologic features of colon cancer. JCI Insight, 2017, 2, e91078.	2.3	23
70	Therapeutic Implications of GIPC1 Silencing in Cancer. PLoS ONE, 2010, 5, e15581.	1.1	22
71	Screening human lung cancer with predictive models of serum magnetic resonance spectroscopy metabolomics. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	20
72	EWSR1-ATF1 dependent 3D connectivity regulates oncogenic and differentiation programs in Clear Cell Sarcoma. Nature Communications, 2022, 13, 2267.	5.8	18

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73	Adaptation of the CHARM DNA methylation platform for the rat genome reveals novel brain region-specific differences. Epigenetics, 2011, 6, 1378-1390.	1.3	17
74	Augmenting and directing long-range CRISPR-mediated activation in human cells. Nature Methods, 2021, 18, 1075-1081.	9.0	17
75	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. Blood, 2022, 139, 2534-2546.	0.6	14
76	CRISPR-Cas9 treatment partially restores amyloid-Î² 42/40 in human fibroblasts with the Alzheimerâ€™s disease PSEN1 M146L mutation. Molecular Therapy - Nucleic Acids, 2022, 28, 450-461.	2.3	13
77	Genome-wide DNA methylation patterns reveal clinically relevant predictive and prognostic subtypes in human osteosarcoma. Communications Biology, 2022, 5, 213.	2.0	10
78	A (fire)cloud-based DNA methylation data preprocessing and quality control platform. BMC Bioinformatics, 2019, 20, 160.	1.2	7
79	A Novel Method for Detecting Association Between DNA Methylation and Diseases Using Spatial Information. Genetic Epidemiology, 2014, 38, 714-721.	0.6	3
80	Preprocessing and Computational Analysis of Single-Cell Epigenomic Datasets. Methods in Molecular Biology, 2019, 1935, 187-202.	0.4	2
81	Circularization for In vitro Reporting of Cleavage Effects (CIRCLE-seq). Protocol Exchange, 0, , .	0.3	1
82	Reply. Gastroenterology, 2019, 156, 1933-1934.	0.6	0